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82

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Table of Contents

Fagraeus, A., Norberg, R.: Anti-Actin Antibodies	1
Kääriäinen, L., Söderlund, H.: Structure and Replication of α -Viruses . .	15
Zechel, K.: Initiation of DNA Synthesis by RNA	71
Zinkernagel, R.M.: Speculations on the Role of Major Transplantation Antigens in Cell-Mediated Immunity Against Intracellular Parasites .	113
<i>Indexed in Current Contents</i>	

Anti-Actin Antibodies

ASTRID FAGRAEUS and RENÉE NORBERG¹

I. Introduction	1
II. Experimentally Produced Anti-Actin Antibodies	2
A. Immunizing Antigen; Source and Preparation	2
III. Human Anti-Actin Antibodies	4
A. Actin Specificity of SMA	4
B. Incidence and Diagnostic Significance of Human Anti-Actin Antibodies	6
C. Etiology of Spontaneously Occuring Anti-Actin Antibodies	7
IV. The Use of Anti-Actin Antibodies as a Diagnostic Tool	7
A. Preparation of Test-Material	8
B. Comparison of Human and Rabbit Anti-Actin Antibodies	9
References	10

I. Introduction

Although antibodies against actin were claimed to have been experimentally produced by *Kesztyüs* et al. (1949) and subsequently by several others (*Marshall* et al., 1959; *Tunik* and *Holtzer*, 1961; *Pepe*, 1966; *Hirabayashi* and *Hayashi*, 1972), the specificity of the antisera produced was nevertheless questioned (*Bray*, 1974). Actin, which is present in almost every cell of all animals, has even been considered nonantigenic because of its strongly conserved structure with very small differences between species. Thus, all animals should be tolerant, and this would explain the many unsuccessful attempts to produce antisera against actin.

In the last few years, however, the production of actin antibodies in experimental animals has been convincingly demonstrated (*Trenchev* et al., 1974; *Lazarides* and *Weber*, 1974; *Lazarides*, 1975; *Trenchev* and *Holborow*, 1976). Moreover, antibodies against actin have been shown to occur in many human diseases.

Interaction between actin and other contractile proteins provides the molecular basis of motility in muscles but also in numerous other biologic systems. Actin is present within the muscles in an easily recognized, well-organized form, whereas in nonmuscle cells it can be demonstrated in at least two states, as bundles of filaments and as poorly defined, diffusely distributed meshwork. It is obvious that the mesh can convert into filaments and vice versa by, e.g., contact-mediated signals emanating from the cell's periphery.

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Although the cell's locomotive system might be influenced by preparative methods and by fixation procedures necessary for immunofluorescence experiments (IFL), anti-actin antibodies are valuable tools in studying the contractile machinery under various conditions.

This review will deal with anti-actin antibodies experimentally produced in animals or spontaneously occurring in man. The production and characteristics of anti-actin antibodies of various origins will be compared and the applications hitherto most used will be related. Moreover, the use of human anti-actin antibodies as a diagnostic tool will be considered.

II. Experimentally Produced Anti-Actin Antibodies

The first attempt to produce anti-actin serum experimentally was made by *Keszyüs et al.* (1949). They produced antibodies in two out of three rabbits by immunizing them with rabbit skeletal actin. The antisera precipitated the antigen used for immunization but not a myosin preparation.

Later on, several others (*Marshall et al.*, 1959; *Tunik and Holtzer*, 1961; *Pepe*, 1966; *Hirabayashi and Hayashi*, 1972; *Wilson and Finck*, 1971) prepared antisera to skeletal muscle actin, but the monospecificity of these sera has been questioned. Since 1974, however, several anti-actin sera have been produced and characterized according to specificity and reactivity with various kinds of cells (*Trenchev et al.*, 1974; *Lazarides and Weber*, 1974; *Lazarides*, 1975; *Trenchev and Holborow*, 1976; *Owaribe and Hatano*, 1975; *Fagraeus et al.*, 1977).

A. Immunizing Antigen; Source and Preparation

Actins of various species and tissues seem to be very similar in several of their physiologic, physical and chemical properties. Amino sequence analyses have shown very small differences, e.g., between skeletal muscle actin of rabbit and actin from fish (*Elzinga et al.*, 1973; *Collins and Elzinga*, 1975).

Within the same species, actins from cardiac and skeletal muscle are essentially indistinguishable and the sequence differences observed in these actins do not seem to affect their functional characteristics. But, it is nevertheless clear that there are several actins within a species and that muscle and cytoplasmic actins are slightly different in amino acid sequences (*Elzinga et al.*, 1976). Moreover, a large fraction of actin present in, e.g., brain and fibroblasts (*Bray and Thomas*, 1976), as well as in platelets (*Gallagher et al.*, 1976), differ functionally from muscle actin. There is, on the other hand, no proven antigenic difference between actins of different species and tissues. Antisera against skeletal muscle actin react with actin-containing structures of nonmuscle cells and vice versa (*Lazarides*, 1975; *Trenchev and Holborow*, 1976; *Fagraeus, Biberfeld, and Norberg*, 1977). *Owaribe and Hatano* (1975), however, have reported an exception as their rabbit antiserum against actin from *Plasmodium myxomycete* did not react with actin from rabbit skeletal muscle.

The immunizing actins have been isolated according to standard procedures (*Fagraeus et al.*, 1977) (Fig. 1) and further purified by gel filtration (*Trenchev*

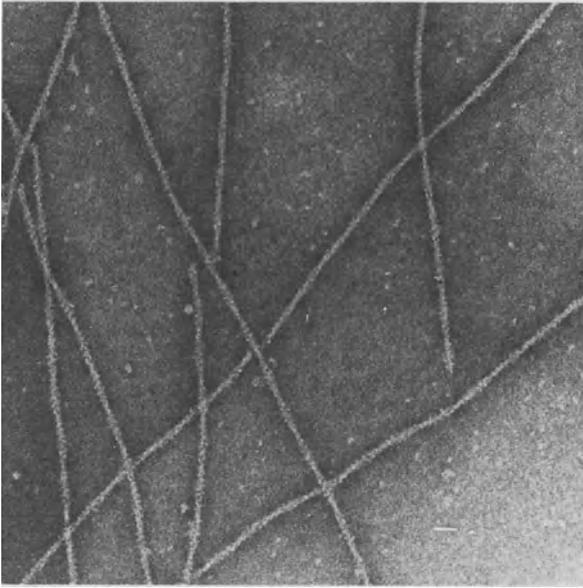


Fig. 1. Electron micrograph showing F-actin prepared from rabbit skeletal muscle. Negative staining with 2% sodiumtungstosilicate. $\times 150000$

et al., 1974; *Owaribe and Hatano, 1975; Trenchev and Holborow, 1976*). A very elegant method was introduced when *Lazarides and Weber (1974)* isolated actin from mouse fibroblasts and purified it further through sodium dodecyl sulfate (SDS) slab gel electrophoresis. The proteins comigrating with actin on SDS slab gels were recovered from the gel by elution and then used as immunogen.

Actin is considered to be a poor antigen, which has been attributed to its widespread distribution in nature. However, actin denatured by SDS or by storage for at least a week at $+4^{\circ}\text{C}$ is considered more immunogenic than a native preparation. It is also the experience of many researchers that only a restricted number of animals produced antibodies after immunization. According to our research (*Fagraeus et al., 1977*) one out of ten rabbits immunized with rabbit skeletal muscle actin produced antibodies in satisfactory amounts. *Trenchev and Holborow (1976)* found precipitating antibodies in 14 out of 36 rabbits injected with human smooth muscle actin. They did not mention if some animals produced nonprecipitating antibodies (see below).

The amount of antigen used has varied from 0.5–10 mg per injection, given in *Freund's* (complete or incomplete) adjuvant at different intervals. When testing the immunogenicity of actin it is necessary to take pre-immunization serum samples since the incidence of spontaneously occurring antibodies reacting with muscles and actin-containing structures in nonmuscle cells is high in rabbits. The reason for this antibody production is unknown. It seems to vary with the rabbits' origin and might be related to various virus infections affecting the animals (see below).

III. Human Anti-Actin Antibodies

Human antibodies (SMA) reacting with smooth muscle antigens were first described by *Johnson et al.* (1965) in patients with chronic active hepatitis (CAH). SMA-positive sera from CAH-patients were also shown to react with renal glomeruli (*Whittingham et al.*, 1966), liver cells (*Farrow et al.*, 1971), thyroid cells (*Biberfeld et al.*, 1974; *Sutton et al.*, 1974), the brush border of renal tubular and intestinal epithelial cells (*Gabbiani et al.*, 1973; *Fagraeus, Lidman, and Norberg*, 1975), microfilaments in fibroblasts grown on glass (*Gabbiani et al.*, 1973), lymphoid cells (*Fagraeus et al.*, 1973), and platelets (*Gabbiani et al.*, 1972; *Norberg et al.*, 1975). (Fig. 2)

A. Actin Specificity of SMA

The specificity of SMA characterized by the broad reactivity described above was unknown until *Gabbiani et al.* (1973) were able to abolish the staining of SMA-positive sera by absorption with thrombosthenin A, the actin moiety of platelets.

The actin specificity of SMA-positive sera, however, was not generally accepted until 1976 when the results were confirmed by adsorbing such sera with rabbit skeletal muscle actin (*Lidman et al.*, 1976; *Chaponnier et al.*, 1976), actin prepared from human uterus or ox stomach (*Botazzo et al.*, 1976) and actin from rabbit skeletal muscle or gizzard muscle (*Andersen et al.*, 1976). In all experiments absorptions with other contractile proteins prepared from smooth or striated muscle were unsuccessful.

Broad-reacting SMA stain the actin-rich I-bands of isolated skeletal muscle myofibrils (*Andersen et al.*, 1976; *Chaponnier et al.*, 1977). Analysis through SDS slab gel electrophoresis of precipitates formed between actin and SMA demonstrated only bands corresponding to IgG and actin (*Lidman et al.*, 1976; *Utter et al.*, 1977). By electronmicroscopy, *Utter et al.* (1977) studied the complexes formed by F-actin and broad-reacting SMA. The immune complexes consisted of parallel arrays of actin filaments cross-linked by antibodies. Thus, the actin specificity of SMA-positive sera from patients with CAH seems to be well-documented.

The actin specificity of other SMA-positive sera, however, has so far been confirmed only in a restricted number of sera, mostly from patients with liver diseases and with EB virus infections (*Lidman et al.*, 1976; *Botazzo et al.*, 1976; *Lamelin et al.*, 1977), although broad-reacting SMA are found under many other conditions (*Whitehouse and Holborow*, 1971; *Holborow et al.*, 1973; *Andersen*, 1975; *Wasserman et al.*, 1975; *Biberfeld and Sterner*, 1976; *Lidman*, 1976; *Lamelin et al.*, 1977). In this context it should be mentioned that not all human sera reacting by IFL with smooth muscle exhibit actin specificity. Several other specificities are known (*Lidman et al.*, 1976; *Andersen et al.*, 1976; *Botazzo et al.*, 1976; *Fairfax and Groeschel-Stewart*, 1977). Most of the latter sera, however, do not give the broad cell-staining pattern shown by anti-actin sera. Thus, it is necessary to perform thorough analyses including absorption experiments before establishing the actin specificity of human SMA.

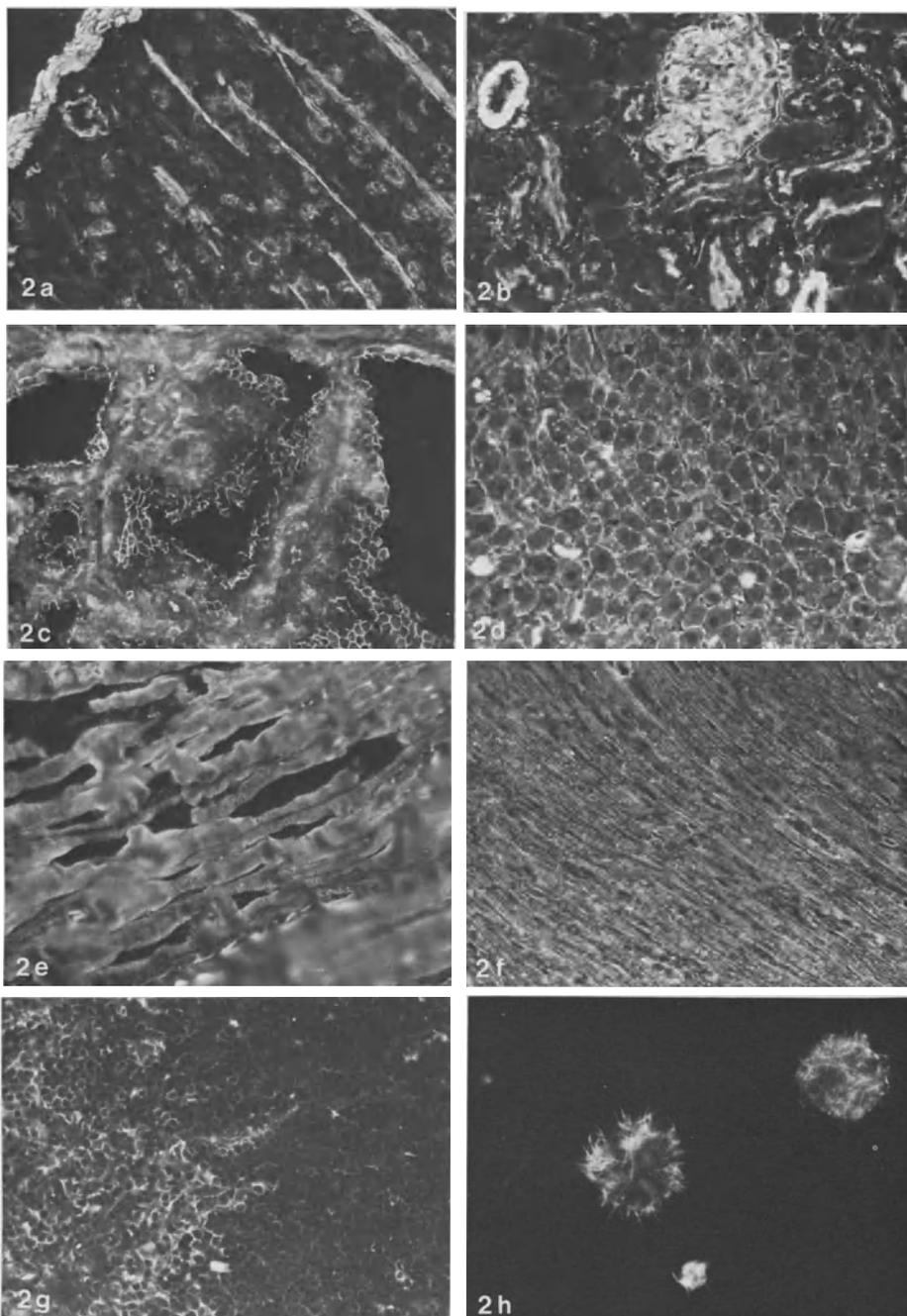


Fig. 2a-h. Indirect immunofluorescence experiments showing staining produced by human anti-actin SMA-positive serum. (a) Positive reaction in muscularis mucosae and the smooth muscle fibres between the mucosal cells in sections of rat stomach. $\times 325$. (b) Staining of walls of blood vessels, glomerulus, the brush borders of proximal renal tubules and basal parts of tubular cells of rat kidney. $\times 325$. (c) Fluorescence in the membrane region of the epithelial cells in sections of human thyrotoxic thyroid. $\times 325$. (d) Pericellular, "polygonal" pattern of sections of rat liver cells. $\times 325$. (e), (f) Striated pattern on monkey skeletal and rat cardiac muscle. $\times 325$. (g) Staining of medullary cells of sections of mouse thymus. $\times 325$. (h) Fluorescent surface microvilli of smeared lymphoblastoid cells. Note also a free bunch of "hairs". $\times 1000$

B. Incidence and Diagnostic Significance of Human Anti-Actin Antibodies

In healthy human controls the incidence of SMA, demonstrated by immunofluorescence techniques, has been 3%–18% (*Wasserman et al.*, 1975; *Shu et al.*, 1975; *Lidman et al.*, 1976; *Biberfeld and Sterner*, 1976). The titers are low (<25). We found, however, in immunodiffusion experiments according to Ouchterlony that 30 out of 100 undiluted blood donor sera precipitated actin prepared from rabbit skeletal muscle (unpublished results).

High titers (≥ 80) of SMA with actin specificity (*Gabbiani et al.*, 1973; *Lidman et al.*, 1976; *Andersen et al.*, 1976; *Botazzo et al.*, 1976) are essentially found in patients with CAH where the incidence in Caucasian patients with a definite diagnosis is 70% or more (*Whittingham et al.*, 1966; *Galbraith et al.*, 1974). Some studies (*Whittingham et al.*, 1966; *Olsson and Hultén*, 1975; *Lidman et al.*, 1976) have shown that in CAH the anti-actin titers varied at least to some extent according to the disease activity. Thus, clinical impairment was mostly accompanied by increased anti-actin titers, whereas after successful therapy the titers mostly decreased or even disappeared. On the other hand, *Murray-Lyon et al.* (1973), in their controlled trial of treatment in adult patients with CAH, found no apparent relationship between changes in titers of SMA and treatment or alterations in liver function tests.

Broad-reacting SMA are occasionally found, usually at low titers (<80) in a variety of chronic diseases with or without liver involvement (*Lidman*, 1976). The actin specificity of these sera, however, has hitherto been documented only in a minority of cases. With actin prepared from rabbit skeletal muscle *Lidman* (1976) absorbed out all SMA activity of 20 sera randomly selected out of 49 SMA-positive sera from patients with nonliver diseases. Anti-actin antibodies found in CAH and other chronic diseases are mainly of IgG class. Their diagnostic importance is obvious, especially in liver diseases where the finding of high titers might indicate a chronic active hepatitis.

Broad-reacting SMA, mostly of IgM class have been reported in various acute viral diseases. *Farrow et al.* (1970) found SMA in 87% of patients with acute viral hepatitis. The antibodies occurred both in HB_sAg-positive and -negative cases. The incidence of SMA was highest during the first month after onset of symptoms and disappeared gradually thereafter. *Andersen et al.* (1976) found that the specificity of IgM-SMA in sera from patients with acute hepatitis varied. Some sera were completely absorbed out by F-actin, others were not.

In cases of *Paul-Bunnell* positive infectious mononucleosis, *Holborow et al.* (1973) reported the finding of SMA in 81% of patients tested within one month of the onset of symptoms. Similar figures have later on been published by *Sutton et al.* (1974) and *Andersen* (1975). SMA have also been demonstrated in measles and mumps (*Haire*, 1972; *Biberfeld*, personal communication), cytomegalovirus infections (*Ajdukiewicz et al.*, 1972; *Andersen and Andersen*, 1975), and wart virus infections (*McMillan and Haire*, 1975). The only nonviral, acute infection where an increased incidence of SMA has been described is *Mycoplasma pneumoniae* infection (*Biberfeld and Sterner*, 1976).

C. Etiology of Spontaneously Occurring Anti-Actin Antibodies

Anti-actin antibodies may develop in most individuals in certain viral infections. The presence of virus is in some way of crucial importance for the anti-actin production, since these antibodies are only exceptionally demonstrable in connection with cell damage caused by other agents. *Li et al.* (1977) were able to produce anti-actin antibodies—and antibodies reacting with heavy meromyosin—in rats by ligation of a liver lobe or by cryosurgical damage to a liver lobe provided the damaged tissue was not removed. Other methods causing cell necrosis did not cause production of SMA. The actin-virus complex may in some way act like a hapten-carrier complex. The recent finding of actin, derived from the host cell within RNA tumor viruses (*Lamb et al.*, 1976; *Wang et al.*, 1976) and paramyxoviruses (*Wang et al.*, 1976; *Tyrrell and Norrby*, 1977), might be of relevance in this context. The production of anti-actin antibodies in acute viral infections might well be elicited by actin-virus complexes. Additional evidence for the importance of the hapten-carrier theory is the appearance of SMA after drug therapy (*Reynolds et al.*, 1971). *Lidman* (1976) showed the actin specificity of these SMA in two patients with hepatitis after oxyphenisatin therapy. After viral infection and also after withdrawal of oxyphenisatin the antibodies gradually disappear. Thus, the occurrence of anti-actin antibodies at low titer in sera from normal human subjects and normal rabbits may be a consequence of earlier viral infections.

In patients with CAH of unknown etiology there is mostly a continuous production of large amounts of IgG anti-actin antibodies. These patients, however, might have a genetic predisposition for an abnormal immune response related to the observed increased frequency of HL-A 1 and 8 in patients with CAH (*Mackay and Morris*, 1972).

The anti-actin antibodies are not considered to be directly involved in liver cell destruction as they do not react with the surface of normal living cells (*Farrow et al.*, 1971; *Gabbiani et al.*, 1973; *Fagraeus et al.*, 1975; *Andersen et al.*, 1976) and as there is no evidence that SMA are cytotoxic to liver cells (*Paronetto et al.*, 1973).

IV. The Use of Anti-Actin Antibodies as a Diagnostic Tool

The interpretation of staining patterns obtained by direct or indirect immunofluorescence is closely connected with the properties of the reactants used. This is valid for all systems but perhaps especially for experiments involving cellular contractile proteins and anti-actin antibodies. It might be discussed whether the experimental conditions permit a preservation of the cellular contractile proteins in their native state. Although important biochemical characteristics are shared by actins from muscle and nonmuscle cells, it is evident that their properties within the cells may differ and that therefore *in vitro* treatment, e.g., fixation, may give different results depending on the type of cell investigated.

A. Preparation of Test Material

Ordinary cryostat sections of various tissues have mostly been used unfixed, or fixed in dry acetone. Cells grown on glass were fixed in dry acetone at -20° for 20 min (Norberg et al., 1975) or used fixed for 30 min in 3.5% formaldehyde in PBS followed by various time periods in acetone (Lazarides, 1976). When making preparations of suspended cells, e.g., lymphoid cells and platelets we have shown (Fagraeus et al., 1975) that a prerequisite for obtaining a positive staining reaction with anti-actin serum was to deprive the suspending medium of Ca^{2+} , e.g., by using a chelating agent. The reason for this is unknown but might be connected with the organization of cellular actin in the presence or absence of Ca^{2+} . A suitable suspending medium was 0.034 M sodium citrate. Smears on glass slides were fixed for 20 min in dry acetone at -20°C .

Within the muscle cell actin constitutes the thin filaments – the I-bands – which are sharply stained by anti-actin antibodies. Within the nonmuscle cells the organization of actin seems to vary both within a specific cell and between cells of various kind. Several investigations indicate (Bray and Thomas, 1975; Bray and Thomas, 1976; Gallagher et al., 1976; Tilney, 1976; Weihing, 1976) that actin in nonmuscle cells exists in two forms. Bray and Thomas (1975) estimated that in fibroblasts about half the actin was present in an unpolymerized form (G-actin) and the remaining part was filamentous and distributed largely in bundles beneath the cell cortex and within filopodia.

According to most results human or experimentally produced anti-actin sera react in immunofluorescence experiments mainly with actin distributed in microfilaments (Lazarides and Weber, 1974; Goldman and Lazarides, 1975; Norberg et al., 1975). Norberg et al. (1977) compared the staining pattern of anti-actin antibodies on various cells smeared on glass to the relative amount of cellular actin estimated by SDS gel electrophoresis with subsequent scanning of the gel. Although the cells showed a varying stainability under different conditions the cellular actin content was fairly constant. Thus, the staining differences seemed to reflect changes in the organization of cellular actin rather than actual differences in the amount of actin.

There is no definite explanation of the decreased reactivity of anti-actin antibodies with nonfilamentous actin. Recently several researchers (Tilney, 1976; Kane, 1976; Weihing, 1976; Carlsson et al., 1977) have pointed out the existence of cellular proteins that interact with actin and keep it in an unpolymerized storage form. The proteins interacting with actin might in some way interfere with the stainability of unpolymerized actin. This is supported by our experience of the influence of DNase I on the anti-actin staining of smeared lymphoblastoid cells. DNase I causes depolymerization of filamentous actin and forms complexes consisting of 1 mol of actin and 1 mol of the enzyme (Hitchcock, et al., 1976). The presence of myosin and tropomyosin highly influences the depolymerization of the F-actin and the formation of DNase I–actin complexes. Treatment of smeared lymphoblastoid cells with DNase I totally blocked the anti-actin staining of these cells. On the other and, the staining of cryostat sections from smooth or skeletal muscle was not influenced by DNase I treatment, nor was the staining of cells, e.g., fibroblasts, grown on glass. This might depend upon

the different organization of the contractile proteins in the smeared lymphoblastoid cells and the other tissues used.

In this context it should be mentioned that human sera as well as sera from all animals examined (dog, cattle, sheep, rabbit, guinea pig, rat, and mouse) contain a substance which competes with antibodies in the same way as DNase I. Its reaction with actin is Ca^{2+} -dependent and destroyed by heating the serum to 56° C for 30 min (to be published). Therefore all anti-actin sera, human as well as animal sera, should be heated before use.

B. Comparison of Human and Rabbit Anti-Actin Antibodies

The human sera can easily be obtained in ample amounts whereas the production of experimental antisera is time consuming and highly laborious. Thus, it seems to be extremely important to characterize and compare the reactivity of anti-actin antibodies of different origin in order to find out whether they can be used alternatively or whether their reactions with actin diverge in any respect.

Both human and experimentally produced rabbit anti-actin antibodies have been used to study muscular structures. They stain the thin filaments (I-bands) of myofibrils in the same way (*Andersen et al.*, 1976; *Trenchev and Holborow*, 1976; *Chaponnier et al.*, 1977). The staining of sections of smooth muscles in, e.g., vessels, stomach and uterus is also indistinguishable (*Trenchev et al.*, 1974; *Trenchev and Holborow*, 1976; *Fagraeus et al.*, 1977). The actin-containing structures of mouse fibroblasts and rat embryo cells grown on glass have been extensively studied by *Lazarides* (1975) using IFL and rabbit antibodies against actin isolated from smooth muscle or mouse fibroblasts. In our studies using human skin fibroblasts (*Norberg et al.*, 1975; *Fagraeus et al.*, 1978), human anti-actin antibodies and rabbit antibodies against rabbit or pig skeletal muscle actin gave the same IFL-staining with fibers showing a continuous fluorescence along their lengths. Nor have we been able to show any difference between human and rabbit anti-actin antibodies in staining lymphoid cells and platelets (*Norberg et al.*, 1977). Thus, so far human and experimentally produced rabbit anti-actin antibodies seem to be exchangeable in indirect tests, such as IFL experiments, although several results in other in vitro systems indicate that their antigen specificity might not be identical.

Most human sera containing anti-actin antibodies precipitate easily with actin in gel diffusion experiments (*Gabbiani et al.*, 1973; *Lidman et al.*, 1976; *Andersen et al.*, 1976; *Chaponnier et al.*, 1977) whereas in our experience rabbit anti-actin sera do not. We have used our own antisera against pig and rabbit skeletal muscle actin, rabbit sera against pig skeletal actin (kindly provided from Dr. M. Crumpton, MRC, Mill Hill, London), and rabbit antiserum against gizzard actin purified on SDS-polyacrylamide gel electrophoresis (a generous gift from Dr. K. Burridge, Cold Spring Harbor Laboratory). They all gave negative results in immunodiffusion experiments using pig or rabbit skeletal F-actin which had been reduced by 0.0005 M mercaptoethanol in order to make the actin diffusible. However, F-actin heated for 30 minutes at 70° C was precipitated by the rabbit anti-actin sera (*Norberg et al.*, unpublished).

Other researchers (*Lazarides and Weber, 1974; Lazarides, 1975; Trenchev and Holborow, 1976*) have reported precipitin reactions of their rabbit anti-actin sera but they have not stated how the actin used as antigen was treated. Human and rabbit anti-actin sera also reacted differently in passive hemagglutination tests (*Fagraeus et al., 1977*). Rabbit sera readily agglutinated actin-coated sheep red cells whereas human anti-actin sera did not. The agglutination capacity of rabbit sera was restricted to the IgM fraction obtained by gradient centrifugation of rabbit anti-actin sera. None of human sera with anti-actin antibodies of IgG class gave a positive passive hemagglutination reaction. A further support of the differences in specificity between human and experimentally produced antisera might be deduced from the result of *Lessard et al. (1977)*. They have developed a sensitive and specific radioimmunoassay to quantitate anti-actin antibodies. The method involves the detection of an immune complex between actin, covalently linked to agarose, and IgG on the basis of the specific binding of ^{125}I -labeled protein A from *Staphylococcus aureus*. The method has been used to follow the appearance of anti-actin antibodies in rabbits immunized with SDS-denatured and electrophoretically purified murine skeletal muscle actin. However, two of our human anti-actin sera and a number of SMA-positive sera from local patients with CAH failed to react in this radioimmunoassay (*Lessard, personal communication*).

So far, there are no definite explanations for the differing behaviors of human and experimentally produced anti-actin sera. The type and availability of the antigenic determinants of actin may vary depending on the source and on the methods used for preparation of actin, the way of immunization, whether they are spontaneously occurring or experimentally produced etc. Moreover, the test system used may influence the availability of the antigenic determinants of actin.

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Structure and Replication of α -Viruses

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I. Introduction	15
II. Structure	16
A. Nucleocapsid	17
1. RNA	17
2. Capsid Protein	18
3. Structure of the Nucleocapsid	18
B. Envelope	20
1. Envelope Proteins	20
2. Lipids	21
3. Structure of the Envelope	22
C. Virion Structure	23
III. Replication	26
A. Growth	26
B. Early Events	27
C. α -Virus-Directed RNA Synthesis	29
1. α -Virus-Specific RNAs	29
2. Synthesis of 42 S and 26 S RNAs	30
3. Regulation of 26 S RNA Synthesis	32
4. RNA Polymerase in α -Virus-Infected Cells	34
D. α -Virus-Directed Protein Synthesis	35
1. Translation of Structural Proteins	35
2. Translation of Nonstructural Proteins	37
3. Control of Protein Synthesis in α -Virus-Infected Cells	39
E. Assembly of Nucleocapsid	42
F. Assembly of Viral Envelope	43
1. Glycosylation of Envelope Proteins	43
2. Transport of Envelope Proteins to the Plasma Membrane	44
G. Maturation of α -Virus	46
IV. Defective Interfering Particles in α -Virus-Infected Cells	47
V. Conclusions	49
References	51

I. Introduction

The α -virus family presently contains 20 members of closely related viruses. These viruses were previously known as group A arboviruses but are currently classified as togaviruses together with flaviviruses (previously group B arboviruses) and some nonarboviruses such as rubella and lactic dehydrogenase viruses (Wildy, 1971, Fenner, 1976). In nature, the α -viruses are spread to their mamma-

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lian or avian hosts by arthropods, mainly mosquitoes. The viruses multiply in both vertebrate and invertebrate hosts (*Casals and Clarke, 1965; Mussgay et al., 1975*). A great deal of research has been carried out to clarify the ecology, epidemiology, and pathology of these viruses since several α -viruses are of great importance in veterinary and human medicine (*Casals and Clarke, 1965; Casals, 1975*).

This review concentrates on the molecular biology of the α -viruses, for which a huge body of literature exists. However, only 2 out of the 20 members, the nonpathogenic Semliki Forest (SF) virus and the Sindbis virus, have been extensively studied. Some data also exist on the chikungunya, eastern equine encephalitis (EEE), Venezuelan equine encephalitis (VEE), and western equine encephalitis (WEE) viruses. The viruses seem to be remarkably similar in molecular terms, and here we have often made generalizations based on the data obtained from one or two of the members, which do not of course, represent valid assumptions in all cases.

II. Structure

Production of α -virus particles on a milligram scale for morphologic, chemical, and physical studies is a relatively simple task. The virus is released from the infected cells by budding through the plasma membrane and can then be recovered from the culture medium. Several purification methods have been described, but the one generally adopted includes concentration of the virus from the culture fluid by ultracentrifugation or by precipitation, e.g., with polyethylene glycol. Purification of the concentrated preparation is then achieved by rate zonal and/or isopycnic centrifugation on sucrose or tartrate density gradients (*Kääriäinen et al., 1969; Strauss et al., 1969; David, 1971*). The purified virus particles consist of RNA, protein, protein-bound carbohydrate, and lipids (Table 1). The particle has a sedimentation constant of about 280 S and a density of 1.18–1.20 g/cm³ in sucrose (*Cheng, 1961; Aaslestad et al., 1968; Osterrieth, 1968; Strauss et al., 1968; Horzinek and Mussgay, 1969; Kääriäinen et al., 1969; Fuscaldo et al., 1971; Mussgay et al., 1973*).

In electron micrographs, the negatively stained α -viruses appear as spheric particles of about 50–55 nm in diameter, to which 7-nm long spikes are attached

Table 1. Overall composition of α -viruses

Virus	Component (%)				Reference
	RNA	Protein	Carbohydrate (in glyco- protein)	Lipid	
Sindbis virus	5.5	61	6.5	27	<i>Pfefferkorn and Shapiro (1974)</i> ^a
SF virus	6.3	56.6	6.3	30.8	<i>Laine et al. (1973)</i>

^a Data combined from *Pfefferkorn and Hunter (1963 a)* and *Strauss et al. (1970)*

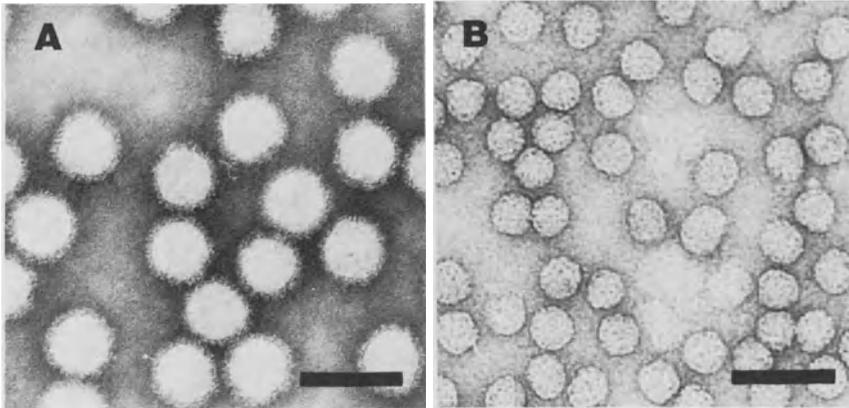


Fig. 1. Negatively stained electron micrographs of (A) SF virus particles and (B) isolated Sindbis virus nucleocapsids. Bar 100 nm (Courtesy of Dr. C.H. von Bonsdorff)

in radial orientation (Fig. 1). An internal core, or nucleocapsid, which is surrounded by a lipid bilayer can be visualized in thin sections.

The viral envelope can be disrupted with mild detergents and the nucleocapsid separated from the solubilized envelope components by sucrose gradient centrifugation (reviewed by *v. Bonsdorff*, 1973; *Higashi*, 1973; *Horzinek*, 1975). Treatment of the virion with strong detergents, such as sodium dodecyl sulfate, causes a total disintegration of the particle, making it possible to study the proteins and RNA (reviewed by *Pfefferkorn* and *Shapiro*, 1974; *Strauss* and *Strauss*, 1977; *Simons et al.*, 1978).

A. Nucleocapsid

1. RNA

The genome of the virion consists of one continuous single-stranded RNA molecule which has a sedimentation value of 40–49 S (*Pfefferkorn* and *Shapiro*, 1974; *Strauss* and *Strauss*, 1977). Polyacrylamide gel electrophoresis has given molecular weight estimates ranging from $3.6\text{--}4.6 \times 10^6$ (*Cartwright* and *Burke*, 1970; *Dobos* and *Faulkner*, 1970b; *Arif* and *Faulkner*, 1971; *Levin* and *Friedman*, 1971; *Agabalyan et al.*, 1972; *Boulton* and *Westaway*, 1972; *Simmons* and *Strauss*, 1972a). The electrophoretic mobility of double-stranded genome RNA indicates a molecular weight of 4.4×10^6 (*Simmons* and *Strauss*, 1972b) and sedimentation in sucrose gradients in the presence of formaldehyde of 4.1×10^6 (*Simmons* and *Strauss*, 1972a). Electron microscopic length measurement of glyoxal-denatured Sindbis RNA gives a value of 4.6×10^6 daltons (*Hsu et al.*, 1973). The wide range is probably due to difficulties in determining the molecular weight of a large single-stranded RNA rather than to true variation. A commonly used figure is $4.3 \pm 0.2 \times 10^6$ which corresponds to about 13,000 nucleotides.

The genome RNA shares properties with eukaryotic messenger RNAs; the

3' end contains a poly (A) tract, which is on the average about 60 nucleotides long, and possibly has some heterogeneity (*Armstrong et al., 1972; Eaton and Faulkner, 1972; Johnston and Bose, 1972; Hsu et al., 1973; Wittek et al., 1974; Deborde and Leibowitz, 1976*), while the 5' end of at least the Sindbis virus RNA has an inverted 7-methylguanosine, i.e., a cap (*Hefti et al., 1976; Dubin et al., 1977*).

Protein-free Sindbis virus RNA has some secondary structure (*Sprecher-Goldberger, 1967; Engelhardt, 1972; Brawner et al., 1977*). This RNA can circularize as reported by *Hsu et al. (1973)*, probably due to cohesive ends which form a stem, about 250 nucleotides long, in a panhandle-like structure. In spite of the close similarity between different α -viruses, their RNAs have a strikingly low base sequence homology, as revealed by cross-hybridization and oligonucleotide fingerprinting of Sindbis, SF, chikungunya, and O'nyong-nyong RNAs (*Wengler et al., 1977*).

2. Capsid Protein

In addition to the RNA, the nucleocapsid contains 200–300 capsid protein molecules, which is 66% of the particle's weight (*Strauss et al., 1968; Kääriäinen et al., 1969; Acheson and Tamm, 1970b; Igarashi et al., 1970; Laine et al., 1973*). The capsid protein has a molecular weight of 30,000–33,000 as determined by SDS polyacrylamide gel electrophoresis and gel filtration (*Strauss et al., 1968; Simons and Kääriäinen, 1970; Kennedy and Burke, 1972*). The molecular weight seems to be approximately the same in the six most commonly studied α -viruses (chikungunya, EEE, SF, Sindbis, VEE, and WEE) (*Pedersen et al., 1974*). The capsid proteins from different α -viruses also share common antigenic determinants (*Dalrymple et al., 1973*). The capsid protein has a high lysine content (SF virus, *Simons and Kääriäinen, 1970; Kennedy and Burke, 1972*) or a high lysine plus arginine content (Sindbis virus, *Burke and Keegstra, 1976*). A low level of phosphorylation, less than 0.05 M phosphate per mole protein, has been reported for the capsid protein of the Sindbis virus (*Waite et al., 1974*).

3. Structure of the Nucleocapsid

The nucleocapsid particle isolated from purified virions after treatment with mild detergents, or from infected cells, has been studied intensively. The sedimentation value of the particle is 140–150 S and density values of 1.40–1.47 g/cm³ in CsCl after fixation with glutaraldehyde have been reported. (*Dobos and Faulkner, 1968; Strauss et al., 1968; Kääriäinen et al., 1969; Acheson and Tamm, 1970a; Appleyard et al., 1970; Horzinek and Mussgay, 1971; Uryayev et al., 1971; Zhdanov et al., 1972; Igarashi et al., 1973; Karabatsos, 1973*). The nucleocapsids are spheric with a diameter of 35–40 nm (*Osterrieth and Calberg-Bacq, 1966; Kääriäinen et al., 1969; Acheson and Tamm, 1970a; v. Bonsdorff, 1972, 1973; Söderlund et al., 1972; Horzinek, 1975*). Small angle X-ray scattering studies of whole virions have revealed diameter values of 40 nm for the Sindbis and 38 nm

for the SF virus nucleocapsids (Harrison et al., 1971; Harrison and Kääriäinen, unpublished data). Thus, the smaller diameter values reported are probably artifacts due to a shrinkage of the nucleocapsids during the specimen preparation. However, Brown and Gliedman (1973) have reported the existence of smaller nucleocapsids together with the normal ones in persistently infected mosquito cells.

Most authors agree that the particle is icosahedral (McGee-Russel and Gosztonyi, 1967; Faulkner and McGee-Russel, 1968; Osterrieth, 1968; Simpson and Hauser, 1968; Horzinek, 1973 a, b). Since no staining methods have revealed distinct surface structures, the exact symmetry has not been established. Triangulation numbers of T=3 (Horzinek and Mussgay, 1969), T=4 (v. Bonsdorff, 1973; Harrison et al., 1974), and T=9 (Brown et al., 1972; Brown and Gliedman, 1973) have been suggested.

The protein shell of at least SF virus nucleocapsid is not closed as in most naked virions (e.g., picorna, Rueckert, 1976 or isometric plant viruses, Bancroft, 1970), since the RNA is sensitive to the action of ribonuclease (Acheson and Tamm, 1970c; Kääriäinen and Söderlund, 1971). A structural role for the RNA has been proposed because ribonuclease digestion of the SF virus nucleocapsid causes a contraction of the nucleocapsid diameter to 32 nm (v. Bonsdorff, 1972). Exposure of SF virus nucleocapsids to slightly acid pH (5.6–6.2) results in irreversible contraction of particles from 38 to 32 nm in diameter. The contracted particle has an increased sedimentation value of 166 *S*, but the RNA to protein ratio remains unchanged (Söderlund et al., 1972). The mechanism and significance of this phenomenon is unknown, but it is interesting to note that the configurational change occurs at the same pH range at which the carboxyl-carboxylate pair of tobacco mosaic virus capsid protein dissociates (Butler, 1971). This pair apparently controls the TMV assembly. Furthermore, the SF-virus nucleocapsid can be “unfolded” to a slowly sedimenting strand-like structure without loss of protein or RNA by treatment with EDTA in low salt. Similar structures are produced in low concentrations of sodium dodecyl sulfate (Söderlund and Kääriäinen, 1974; Söderlund et al., 1975). The SF virus nucleocapsid is completely dissociated into RNA and protein at 0.2 mM SDS. This sensitivity to SDS is indicative of strong RNA protein interactions in the particle according to Kaper (1973). Some properties of the SF virus nucleocapsid are summarized in Table 2.

Table 2. Properties of SF virus nucleocapsid in its different configurations

Parameter	pH 7.2	pH 6.2	EDTA	RNase	SDS 0.05 mM
Size (nm)	39	32	> 50	32	> 50
<i>S</i> value	150 <i>S</i>	166 <i>S</i>	100 <i>S</i>	100–130 <i>S</i>	100 <i>S</i>
Density (g/cm ³)	1.43	1.43	1.43	1.38–1.41	ND
RNA/protein	0.5	0.5	0.5	0.25–0.45	0.5

From Söderlund et al. (1975)

B. Envelope

1. Envelope Proteins

Two different envelope glycoproteins E1 and E2 with molecular weights of about 50,000 can be resolved by polyacrylamide gel electrophoresis from EEE, SF, Sindbis, VEE, and WEE viruses (*Schlesinger M. et al.*, 1972; *Garoff et al.*, 1974; *Ivanic*, 1974; *Pedersen et al.*, 1974). Since the mobility of the two proteins in polyacrylamide gels can vary greatly between different viruses, it has been suggested that E2 should be defined as a protein which is formed by cleavage of a precursor protein p62 (or pE₂) (see Sect. III. D. 1). This nomenclature [(recommendation of the International Arbovirus Meeting in Helsinki 1975, *J. Gen. Virol.* 30, 273 (1976))] is adopted here. In a comparative study by *Pedersen et al.* (1974), the chikungunya virus failed to give two envelope protein bands. This is apparently due to difficulties in separation rather than real qualitative differences. SF virus has an additional small, highly glycosylated protein E3 with a molecular weight of about 10,000 (*Garoff et al.*, 1974), first found in infected cells treated with canavanine (*Ranki et al.*, 1972). This protein has not yet been reported in other α -viruses.

The envelope proteins of the SF and Sindbis viruses have been purified by chromatography on hydroxylapatite in the presence of SDS or on DEAE cellulose in the presence of triton (*Garoff et al.*, 1974; *Burke and Keegstra*, 1976). Sindbis virus E1 and E2 separate at pI 6 and pI 9, respectively, in preparative isoelectric focusing, carried out in the presence of triton (*Dalrymple et al.*, 1976). The three envelope proteins of the SF virus can be separated by sucrose gradient centrifugation in the presence of sodium deoxycholate (*Helenius et al.*, 1976).

The amino acid compositions of the envelope proteins do not show higher proportion of hydrophobic amino acids than ordinary soluble proteins (*Garoff et al.*, 1974; *Burke and Keegstra*, 1976). Their amphiphilic nature can, however, be detected by their affinity to detergents like triton and deoxycholate which are known to bind to hydrophobic regions of integral membrane proteins (*Helenius and Simons*, 1972; *Uterman and Simons*, 1974; *Becker et al.*, 1975; *Helenius and Simons*, 1975).

The hemagglutinating activity resides in E1 in both the Sindbis and SF viruses (*Dalrymple et al.*, 1976; *Helenius et al.*, 1976). The hemagglutinin also seems to be only one of the envelope proteins in the VEE virus (*Pedersen and Eddy*, 1974). Sindbis E1 protein carries antigenic determinants which cross-react with related α -virus antibodies while E2 is antigenically distinct (*Dalrymple et al.*, 1976). Strain specificity of the envelope proteins is also shown by differences in their electrophoretic mobility (*Pedersen et al.*, 1974; *Pedersen and Eddy*, 1975). The phosphokinase activity reported to be found in the intact virion has not been localized (*Tan and Sokol*, 1974; *Tan*, 1975).

The carbohydrate moieties of the envelope proteins have been characterized fairly well. Glycopeptides have been isolated after pronase digestion and their sugar composition determined (Table 3) (*Burge and Huang*, 1970; *Burge and Strauss*, 1970; *Strauss et al.*, 1970; *Sefton and Keegstra*, 1974; *Keegstra et al.*,

Table 3. Carbohydrate composition of SF virus oligosaccharides

Glyco-protein	Type of oligo-saccharide	No. of chains per protein	Moles of carbohydrate per oligosaccharide				
			Sialic acid	Galactose	Fucose	Mannose	N-acetyl glucosamine
E1	A	1 (-2)	2	2	1	3	4
E2	A	1 (-2)	2	2	1	3	4
E2	B	3	—	—	—	5-7	2
E3	A	1 (-2)	3	3	1	3-4	5-6

Data collected from *Mattila et al., 1976; Pesonen and Renkonen, 1976; Pesonen and Renkonen, 1977*

1975; *Burke and Keegstra, 1976; Mattila et al., 1976*). The Sindbis virus E1 and E2 both contain one A-type and one B-type oligosaccharide chain (nomenclature of *Johnson and Clamp, 1971*), while the SF virus contains one to two A-type chains in E1 and E3 and one A-type and two to three B-type chains in E2 (Table 3). The previously reported uncharacterized chain X in the E2 (*Mattila et al., 1976; Kääriäinen and Renkonen, 1977*) is probably an A-type chain (*Pesonen, personal communication*).

Sequential degradation of the oligosaccharide chains with exo- and endoglycosidases has been carried out and the structures for the A chains of the SF virus have been deduced (*Pesonen and Renkonen, 1976; Renkonen et al., 1976; Haahtela and Renkonen, 1978*). Typical N-glycosidic A-type chains similar to those of soluble serum glycoproteins appear to be present (cf. *Spiro, 1973*). The A chains carried by the individual proteins appear to be mixtures of several glycans, and the average molecular weight of the oligosaccharides carried by E3 is distinctly larger than that of E1 glycans, which in turn may be a little larger than the average E2 oligosaccharides (*Rasilo and Renkonen, 1978*). The largest glycans of the SF virus, those of E3, are believed to be the most exposed ones in the intact virion, because they react most readily with sialidase and galactose oxidase (*Luukkonen et al., 1977a*).

Virions which lack the terminal sialic acids in their envelope proteins, either after enzymic removal (*Kennedy, 1974*) or when grown in *Aedes albopictus* cells (*Stollar et al., 1976*), retain their infectivity and hemagglutinating activity. Even the terminal glucosamine and galactose residues may be lacking without decreased biologic activity, suggesting that the glucoseamine-mannose core of the A-type oligosaccharide is sufficient for these activities (*Schlesinger S. et al., 1976*). For the Sindbis virus envelope proteins, *Waite et al. (1974)* have reported a low level of phosphorylation, while *Pinter and Compans (1975)* have shown that radiolabeled sulfate is incorporated into Sindbis virus envelope proteins.

2. Lipids

About 30% of the virion or 37% of the envelope consists of lipids (*Pfefferkorn and Hunter, 1963a; Laine et al., 1973*). The main components are phospholipid

and cholesterol. The lipids are derived from the host cell (*Pfefferkorn* and *Hunter*, 1963 b), and the composition resembles that of the plasma membrane of the host (*Renkonen* et al., 1971; *Renkonen* et al., 1972a, b). This is also true for the fatty acid composition within the different phospholipid classes (*Laine* et al., 1972) and for the glycolipids (*Renkonen* et al., 1971; *Hirshberg* and *Robbins*, 1974). The viral envelope however contains, more cholesterol compared to phospholipid than the host (*Renkonen* et al., 1971). Because of the host influence, the lipid composition in virus preparations propagated in mammalian or mosquito cells, for example, may vary considerably without other obvious alterations in virus structure (*Luukkonen* et al., 1976; *Luukkonen* et al., 1977b, *Heydrick* et al., 1971). However, an abnormal lipid composition may also destabilize the virion (*Sly* et al., 1976). *Friedman* and *Pastan* (1969) have reported that about 60% of the phospholipids in the virion can be digested with phospholipase C without loss of infectivity.

3. Structure of the Envelope

The envelope of the α -viruses consists of a lipid bilayer with two to three proteins anchored to it. In many respects, this viral membrane resembles cellular membranes, but it is simpler in protein composition, homogenous, and easy to purify. Thus, it has been extensively studied as a membrane model (*Simons* et al., 1974; 1977; 1978; *Kääriäinen* and *Renkonen*, 1977).

The action of detergents on the SF virus has been studied using triton X-100, sodium dodecyl sulfate, and sodium deoxycholate. The solubilization process begins with the binding of the detergent to the virus, then it proceeds with increasing detergent concentration to lysis of the membrane, solubilization into lipid-protein-detergent complexes, and terminates with complete delipidization of the proteins (*Helenius* and *Söderlund*, 1973; *Becker* et al., 1975; *Helenius* et al., 1976).

The mode of attachment of the envelope proteins to the membrane and the interaction with the nucleocapsid have attracted a great deal of interest. Several lines of evidence indicate that the bulk of the proteins are located on the surface of the virion. A hydrophobic tail of E1 and E2 is embedded in the lipid bilayer, anchoring the proteins, and at least one of them penetrates the membrane, making contact with the capsid protein.

The external localization of the proteins has been shown by surface labeling techniques (*Gahmberg* et al., 1972a; *Sefton* et al., 1973), by the accessibility of the proteins to proteolytic and glycolytic enzymes (*Osterrieth*, 1965; *Calberg-Bacq* and *Osterrieth*, 1966; *Compans*, 1971; *Ravid* and *Goldblum*, 1973; *Kennedy*, 1974), and also by the agglutinability of the virus with concanavaline A (*Oram* et al., 1971; *Birdwell* and *Strauss*, 1973). The different proteins and glycans react with varying efficiency, probably reflecting the organization of the viral surface. From the envelope proteins of the SF virus, the E3 is labeled most efficiently after treatment with galactose oxidase followed by reduction with tritiated borohydride (*Luukkonen* et al., 1977a). The A-type oligosaccharide in Sindbis virus E2 is the only glycan, which can be completely removed by treatment with glycosidases (*McGarthy* and *Harrison*, 1977).

Treatment of the SF virus with thermolysin or subtilisin results in the formation of spike-less particles from which the glycoproteins have been removed. A short membrane protein fragment is, however, protected from proteolysis in the membrane (*Gahmberg et al.*, 1972 b). This hydrophobic fragment of about 5,000 daltons is very rich in hydrophobic amino acids. Both E1 and E2 contain such a peptide (*Uterman and Simons*, 1974), while E3 is probably not an integral membrane protein (*Simons et al.*, 1978). These hydrophobic fragments apparently give the membrane proteins their tendency to aggregate into star-shaped oligomers or "rosettes" (*Simons et al.*, 1973 a; *Helenius and Bonsdorff*, 1976).

In a recent experiment, *Garoff and Söderlund* (1978), by synchronization of protein synthesis with high salt, produced virions which contain an increasing or decreasing specific activity gradient of ^{35}S -methionine from the N-terminal of the capsid protein toward the C-terminal of E1 (cf. Sect. III. D. 1.). By this approach, it was possible to show that the hydrophobic fragments are located at the carboxy-terminus of both E1 and E2.

When the virus is treated with protein cross-linking reagents, dimers consisting of E1 and E2 are preferentially formed (*Garoff*, 1974; *Simons et al.*, 1978). Immunoprecipitation with specific antisera of such cross-linked material suggests that the spike structure of the SF virus is a trimer containing one each of E1, E2, and E3 (*Ziemiecki and Garoff*, 1977).

Only a small proportion, less than 10%, of the lipid bilayer is occupied by the penetrating hydrophobic fragment as shown by small angle x-ray scattering (*Harrison et al.*, 1971; 1974). The protein part affects the organization of the lipids in the bilayer, since the microviscosity is higher in the presence of envelope proteins or hydrophobic fragments than in liposomes or cellular membranes (*Sefton and Gaffney*, 1974; *Hughes and Pedersen*, 1975; *Moore et al.*, 1976). It should be noted that because of the small radius of the virus the outer leaflet of the lipid bilayer contains 50% more lipid than the inner one (*Harrison et al.*, 1971). This may cause some stress to the membrane since the even higher curvature of the small Sindbis virus particles formed in persistently infected mosquito cells seems to significantly destabilize the envelope (*Brown and Gliedman*, 1973). The lipids are at least partly assymmetrically distributed in the membrane since the glycolipids are found in the outer leaflet (*Stoffel and Sorgo*, 1976).

C. Virion Structure

Electron micrographs of α -viruses show spheric particles with a diameter of about 50 nm, which are surrounded by the spike layer. Electron microscopy and small angle x-ray scattering give the dimensions of the nucleocapsid, the lipid bilayer, and the spike layer (*Cheng*, 1961; *Morgan et al.*, 1961; *Mussgay and Weibel*, 1963; *Mussgay and Rott*, 1964; *Chain et al.*, 1966; *Osterrieth and Calberg-Bacq*, 1966; *Acheson and Tamm*, 1967; *Erlanson et al.*, 1967; *Higashi et al.*, 1967; *Faulkner and McGee-Russel*, 1968; *Osterrieth*, 1968; *Simpson and Hauser*, 1968; *Bykovsky et al.*, 1969; *Lascano et al.*, 1969; *Harrison et al.*, 1971;

Brown et al., 1972; *v. Bonsdorff*, 1973; *Harrison et al.*, 1974; *v. Bonsdorff and Harrison*, 1975) as shown in Figure 2.

Analysis of the surface structure of negatively stained Sindbis virus has revealed that the glycoproteins are organized with trimer clustering in a T=4 icosahedral surface lattice (*v. Bonsdorff and Harrison*, 1975) (Fig. 3). This highly organized surface structure explains why the pelleted virus is found in crystalline lattices (*Wiley and v. Bonsdorff*, 1978) and why the virus crystallizes from solution under suitable conditions (*Simons et al.*, 1978). In thin sections of infected cells, crystalline arrays of extracellular virus have also been observed (*Higashi*, 1966; 1973).

The fact that the SF virus envelope proteins can be cross-linked to the nucleocapsid by dimethyl suberimidate indicates that at least one of the envelope proteins spans the lipid bilayer and is probably in direct contact with the underlying nucleocapsid (*Garoff and Simons*, 1974). Additional evidence for spanning of the envelope proteins has been obtained by labeling with formyl-³⁵S-methylthionyl sulfone-methyl phosphate of triton-solubilized proteins (*Gahmberg et al.*, 1972a) or nucleocapsid-free membranes (*Garoff and Simons*, 1974). Under these conditions, new labeled oligopeptides appear which are probably derived from E2 (*Simons et al.*, 1978). Treatment of the Sindbis virus with formaldehyde results in "cross-linking" of envelope proteins to the nucleocapsid, suggesting similar interaction of envelope and nucleocapsid in this virus (*Brown et al.*, 1973).

It seems logical to assume that the symmetric arrangement of the glycoproteins in the membrane would be dictated by the direct interaction with the icosahedral nucleocapsid. This would mean that the proteins of the nucleocapsid are also organized in a T=4 surface lattice. Such an exactly defined particle should contain 240 copies of each of the structural proteins, assuming that one capsid protein interacts with one envelope protein trimer (E1-E2-E3, SF virus) or dimer (E1-E2, Sindbis virus). This model defines the number of polypeptides and the total amount of protein in the virus particles. Setting the molecular weight of the RNA at 4.3×10^6 , the amount of phospholipids can be estimated from direct chemical measurements of total phosphorus in the virus compared to lipid and RNA phosphorus (*Laine et al.*, 1973) or distribution of radioactive phosphorus between RNA and phospholipids in ³²P equilibrium-labeled SF virus particles (*Luukkonen et al.*, 1976).

The values obtained with both methods agree well, giving an RNA to phospholipid ratio of 0.82. This would give 16,000–17,000 phospholipid-cholesterol pairs for the whole virus particle; hence the total molecular weight of SF virus would be close to 60×10^6 (Table 4).

If the chemical composition of this idealized particle is calculated back and compared to that based on direct measurements, there is an obvious discrepancy (Table 4B). The reason for this is not known, and further studies are needed to establish the detailed molecular structure of the α -viruses. Among these, direct molecular weight determination of the whole particle would be essential. Part of the discrepancy must lie in the inherent difficulty of determining the exact molecular weights of the envelope glycoproteins (*Garoff et al.*, 1974).

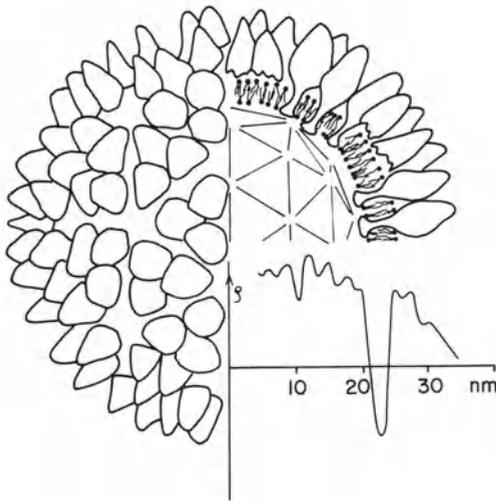


Fig. 2. A schematic drawing (modified from *McCarthy and Harrison 1977*) of an idealized α -virus particle showing the trimer clustering of the envelope glycoproteins in a $T=4$ icosahedral surface lattice. Each subunit at the surface consists of glycoproteins E1 and E2 (plus E3 in SF virus). The surface of the nucleocapsid is drawn according to $T=4$ symmetry. The inset shows the relative electron density (in arbitrary units) obtained by small angle x-ray scattering of the SF virus (*Harrison and Käriäinen*, unpublished results). The deep minimum corresponds to the hydrocarbon region of the lipid bilayer

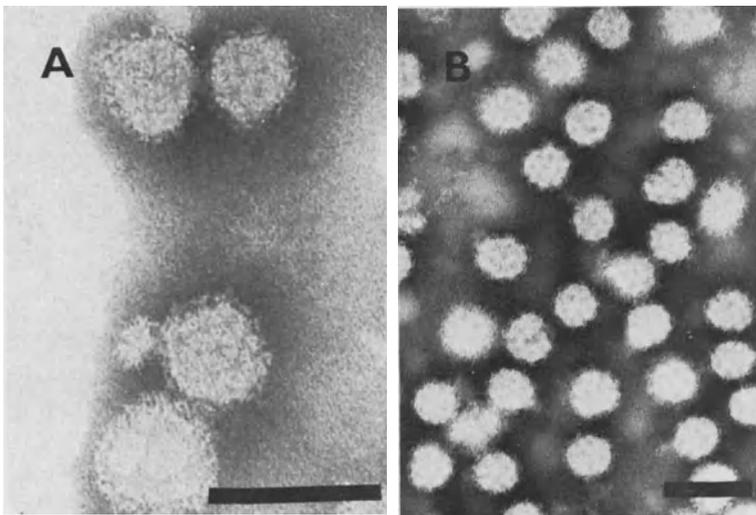


Fig. 3. Electron micrographs of negatively stained (A) Sindbis and (B) SF virus particles showing regular surface lattice. Bar 100 nm (Courtesy of *Dr. C.H. von Bonsdorff*)

Table 4A. The molecular composition of α -viruses as deduced from the T=4 symmetry model

Component	Mol wt of component	Molecules per virion	Total mol wt $\times 10^{-6}$
Nucleocapsid			11.3–12.4
RNA	4.1–4.5 $\times 10^6$	1	4.1–4.5
Protein (C)	30–33 $\times 10^3$	240	7.2–7.9
Envelope			46.0–47.2
Proteins			23.8–26.9
E1	49–50 $\times 10^3$	240	11.8–12.0
E2	50–52 $\times 10^3$	240	12.0–12.5
(E3)	10 $\times 10^3$	240	2.4
Lipids			19.6–20.8
Phospholipids	775	16,000–17,000	12.3–13.1
Cholesterol	385	16,000–17,000	6.1–6.5
Glycolipids	1200	1000	1.2
Virion			54.7–60.1

The number of each component was deduced as described in the text

Table 4B. The chemical composition of α -viruses

	Dry weight %				
	RNA	Capsid protein	Envelope glycoprotein	Lipid	Particle weight $\times 10^{-6}$
Determined ^a	6.3	12.2	50.7	30.8	68 ^c
Deduced ^b	7.3	12.9	45.3	34.5	58.6

^a Laine et al. (1973)

^b From Table 4A, using the mean values when ranges are given, E3 included

^c Based on RNA mol wt 4.3×10^6

III. Replication

A. Growth

The α -viruses grow in the cytoplasm of a large variety of vertebrate and invertebrate cell cultures in a wide temperature range between 20° and 41° C (Pfefferkorn and Shapiro, 1974; Follet et al., 1975; Strauss and Strauss, 1977). At 37° C, the one-step growth curve (Fig. 4) is completed usually after 6–10 h (Dulbecco and Vogt, 1954; Rubin et al., 1955; Veckenstedt and Wagner, 1973), whereas at 27°–29° C, the time is about twice as long (Burge and Pfefferkorn, 1966a; Tan et al., 1969; Davey et al., 1973; Atkins et al., 1974; Keränen and Kääriäinen, 1974; Renz and Brown, 1976). In most cases, the multiplication of α -virus usually causes severe cytopathic changes and the host cell dies within 10–20 h at 37° C (Hardy and Brown, 1961; Acheson and Tamm, 1967; Erlandson

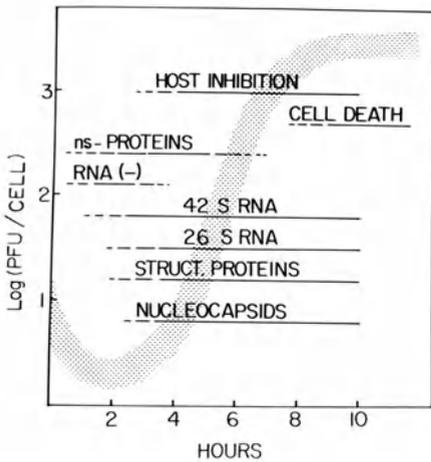


Fig. 4. One-step growth curve of the SF virus in cell culture. Schematic presentation of the duration of the major intracellular events during the virus replication

et al., 1967). The host cell protein, RNA and DNA syntheses, are inhibited within 3–5 h after infection (*Taylor, 1965; Lust, 1966; Strauss et al., 1969; Mussgay et al., 1970; Mantani and Kato, 1975; Atkins, 1976; Simizu et al., 1976*) by mechanisms which are still largely unknown. Persistent infections in vertebrate cells have also been described (*Schwoebel and Ahl, 1972; Inglot et al., 1973; Precious et al., 1974; Seamer, 1974; Schwobel et al., 1975; Eaton and Hapel, 1976*). In the cytolitic infection, up to 20,000 progeny particles are released from the cells into the medium (*Pfefferkorn and Shapiro, 1974; Tuomi et al., 1975; Strauss and Strauss, 1977*), representing in some cases close to 10% of the phospholipid mass of the host cell plasma membrane (*Brotherus and Renkonen, 1977; Tuomi et al., 1975*). Growth in cultivated invertebrate cells at 28° C takes place more slowly and often without cytopathic effect and inhibition of host macromolecular syntheses (*Mims et al., 1966; Singh and Paul, 1968; Buckley, 1969; Peleg, 1969; Stevens, 1970; Peleg, 1972; Davey et al., 1973; Raghov et al., 1973; Gliedman et al., 1975*). Infection becomes limited, even if all cells are infected at the start, leading to persistent infection with a small percentage of cells producing virus (*Davey and Dalgarno, 1974; Bras-Hereng, 1975; Esparza and Sanches, 1975; Schlesinger R.W., 1975*). Appearance of temperature-sensitive mutants from persistently infected mosquito cells has also been described (*Stollar et al., 1973; Shenk et al., 1974; Igarashi et al., 1977*). *Sarver and Stollar (1977)* have reported cytolitic infection of cloned mosquito cells.

In the following discussion, we will concentrate mainly on the cytolitic infection of vertebrate cells, the biochemical events of which are well-known (see also the excellent reviews by *Pfefferkorn and Shapiro, 1974* and *Strauss and Strauss, 1977*).

B. Early Events

The adsorption of WEE virus to chick embryo fibroblasts was shown to be rapid and effective, more than 80% of the infectious virus being adsorbed

within 30 min (*Dulbecco and Vogt, 1954*). Smaller percentages (20%–50%) have been shown to adsorb when radioactive virus has been used (*Birdwell and Strauss, 1974b; Marker et al., 1977*). This may be due to the presence of noninfectious, labeled particles which are unable to adsorb to the cells. There are about 10^5 receptor sites for the Sindbis virus in both chick and BHK 21 cells. These receptors are distributed evenly on the cell surface provided that the cells are fixed prior to adsorption of the virus (*Birdwell and Strauss, 1974b*). The nature of the receptors is still unknown. Different lipid receptors have been suggested by several investigators on the basis of the ability of different lipids to inhibit the hemagglutination of the virus (*Quersin-Thiry, 1961; Quersin-Thiry and Nihoul, 1961; Salminen, 1962; Nicoli, 1965; v. Frish-Niggemayer, 1967; Gorman, 1970*). Binding of the Sindbis virus to liposomal model membranes has been demonstrated by *Mooney et al. (1975)*. The binding of radio-labeled Sindbis virus was almost quantitative to liposomes consisting of phosphatidyl ethanolamine and cholesterol. The optimum pH range was, however, from pH 6 to pH 3, suggesting that this model system does not reflect the physiologic adsorption.

Adsorption of the Sindbis virus to chick cells is dependent on the ionic strength of the medium (*Pierce et al., 1974*). More virus is bound to the cells at low ionic strength but about half of this is loosely bound and can be detached by treatment with 0.25 M NaCl. Virus binds tightly at an ionic strength of 0.15–0.17 M salt and cannot be washed away. An optimum pH of close to 6.5 has been reported for adsorption of some α -viruses (*Negro-Ponzi, 1967; Marker et al., 1977*).

Removal of the virion glycoprotein spikes by proteolytic enzymes renders the virus inactive (*Osterrieth, 1965; Compans, 1971; Sefton and Gaffney, 1974; Uterman and Simons, 1974*), indicating that the envelope proteins are responsible for the attachment of virus to the cells. It has also been shown that the membrane-free nucleocapsid is noninfectious under normal assay conditions (*Sreevalsan and Allen, 1968; Bose and Sagik, 1970; Dobos and Faulkner, 1970a*). Envelope protein E1 is responsible for the hemagglutinating activity of the Sindbis (*Dalrymple et al., 1976*) and SF viruses (*Helenius and v. Bonsdorff, 1976*), whereas E2 protein of the Sindbis virus elicited antibodies which specifically neutralized only this virus (*Dalrymple et al., 1976*). The recent results by *Burge* indicate that Sindbis virus E2 protein has hemolytic activity and may thus be responsible for the possible fusion with host cell plasma membrane (*Burge, personal communication; see also Ueba and Kimura, 1977*). The exact roles of the individual proteins, however, remain to be determined, for example, by competition experiments with isolated proteins. The subsequent steps of virus entry are poorly understood. Does the viral envelope fuse with the plasma membrane (*Morgan and Howe, 1968*) or is the virus taken into the cell by pinocytosis? Serious attempts to solve this question have not yet been made.

α -Viruses were among the first which were shown to have infectious RNA (*Wecker and Schäfer, 1957; Cheng, 1958; Wecker, 1959a, b; Sonnabend et al., 1967; Yoshinaka and Hotta, 1971*). This observation proved that the parental viral proteins are not needed for the initiation of the α -virus replication process. It was soon shown that protein synthesis was required during the early phase

of infection (*Wecker et al.*, 1962; *Wecker*, 1963; *Sreevalsan and Lockart*, 1964). These results indicated that the parental RNA of α -viruses served as a messenger for the synthesis of their own RNA polymerase, which then starts the replication of RNA. Support for this hypothesis was obtained from experiments with interferon, which inhibits the multiplication of α -viruses (*Friedman and Sonnabend*, 1965). In interferon-treated cells, the parental RNA was not converted into a double-stranded form (*Friedman et al.*, 1967; *Pfefferkorn et al.*, 1967), which was considered to be the first sign of the newly formed RNA polymerase activity (*Burge and Pfefferkorn*, 1967; *Pfefferkorn and Burge*, 1967; 1969). The parental RNA associates with membrane structures (*Friedman and Sreevalsan*, 1970). Protein synthesis may be required for this association to take place, since cycloheximide can inhibit it. In any case, RNA polymerase activity is not needed for the binding since parental RNA of temperature-sensitive RNA-negative mutants of the Sindbis virus do attach to the intracellular membranes (*Sreevalsan*, 1970).

C. α -Virus-Directed RNA Synthesis

1. α -Virus-Specific RNAs

Labeling of α -virus-infected cells with ^3H -uridine in the presence of actinomycin D reveals cytoplasmic RNA species with sedimentation values of 42 S, 26 S, and 18–22 S (*Sonnabend et al.*, 1964; *Friedman et al.*, 1966; *Friedman and Berezsky*, 1967; *Sreevalsan and Lockart*, 1966; *Sreevalsan et al.*, 1968; *Poiree et al.*, 1972; *Lubinieccki and Henry*, 1974). The 42 S and 26 S RNAs are single-stranded and only the former is infectious (*Sonnabend et al.*, 1967). Some of the material sedimenting at about 20 S is RNase-resistant double-stranded RNA. Short pulses of ^3H -uridine have revealed a heterogeneously sedimenting (20–30 S), partially RNase-resistant structure which consists of nascent single strands and a double-stranded core (*Sreevalsan and Lockart*, 1966; *Friedman*, 1968b; *Kääriäinen and Gomatos*, 1969; *Stern and Friedman*, 1969; *Cartwright and Burke*, 1970; *Scholtissek et al.*, 1972; *Simmons and Strauss*, 1972b; *Segal and Sreevalsan*, 1974; *Bruton and Kennedy*, 1975). This structure has been designated as replicative intermediate in analogy with the corresponding structure found from poliovirus-infected cells (*Baltimore and Girard*, 1966).

A genuine double-stranded RNA can be isolated from the α -virus-infected cells (*Kääriäinen and Gomatos*, 1969; *Stollar and Stollar*, 1970; *Stollar et al.*, 1972; *Yoshinaka and Hotta*, 1972; *Martin and Burke*, 1974), which may represent a dead end in the RNA replication since it contains continuous 42 S RNA, which is infectious (*Wengler et al.*, 1976). In addition to the above-listed RNAs, minor amounts of single-stranded 38 S, 33 S, and 20–22 S RNA have been found from α -virus-infected cells (*Kääriäinen and Gomatos*, 1969; *Levin and Friedman*, 1971; *Kennedy*, 1972; *Martin and Burke*, 1974; *Simmons and Strauss*, 1974a; *Colbere and Hannoun*, 1974; *Kennedy*, 1976). The puzzling phenomenology of the α -virus RNA pattern has been clarified by the investigations of *Simmons and Strauss* (1972a, 1974a), *Wengler and Wengler* (1976a), and *Kennedy* (1976).

The virion 42 S RNA and the intracellular 26 S RNA are both of positive polarity, and the 26 S RNA is identical to about one-third of the 42 S RNA as shown by hybridization competition experiments (*Simmons and Strauss, 1972a*). Oligonucleotide analysis has shown that 26 S RNA is identical to the 3' end of the 42 S RNA (*Kennedy, 1976; Wengler and Wengler, 1976a*). The 38 S and 33 S RNAs are probably conformational variants of 42 S and 26 S RNAs, respectively (*Simmons and Strauss, 1974a; Kennedy, 1976*).

As is the case in 42 S RNA, the 3' end of 26 S RNA has a polyadenylic acid tract of 60–70 residues long (*Eaton et al., 1972; Clegg and Kennedy, 1974a*). Shorter poly (A) tracts of 30–40 residues have also been reported (*Wittek et al., 1974; Deborde and Leibowitz, 1976*). The 5' terminus of 26 S RNA is blocked by a cap, mG (5') pppAp, which is methylated as m₂^{2,7}G or m₃^{2,2,7}G (*Dubin and Stollar, 1975; Hsueh and Dubin, 1976; Dubin et al., 1977*). Internal methylation in m⁵C of 26 S but not 42 S RNA has been reported by the above authors.

2. Synthesis of 42 S and 26 S RNAs

Some early experiments suggested that the 26 S RNA is produced by a specific cleavage from the 42 S RNA (*Sreevalsan et al., 1968; Dobos and Faulkner, 1969; Dobos et al., 1971*) or that 42 S RNA is formed by ligase enzymes from 26 S and 33 S RNA (*Michel and Gomatos, 1973*) or from smaller pieces (*Koblet et al., 1974*). These possibilities have been disproved by pulse-chase experiments, using glucosamine after the pulse to bind the excess of labeled ³H-UTP (*Scholtissek et al., 1972; Keränen, 1977c*). In these experiments, no interconversion of 42 S and 26 S RNA was observed. The finding of continuous 42 S RNA-negative strands in replicative intermediate structures and the lack of evidence of 26 S RNA-negative strands have established the mode of transcription in α -virus-infected cells (*Simmons and Strauss, 1972b; Bruton and Kennedy, 1975; Sawicki and Gomatos, 1976*). Analysis of the "replicative forms" obtained after mild RNase treatment shows the presence of three different double-stranded cores, RF I (mol wt 8.8×10^6), RF II (mol wt 5.6×10^6), and RF III (mol wt 3.2×10^6), which represent double-stranded forms of 42 S RNA, a 2.8×10^6 dalton RNA, and 26 S RNA, respectively. The RFs are considered to be derived from two different replicative intermediates RIa and RIb, which synthesize 42 S and 26 S RNA, respectively (*Simmons and Strauss, 1972b*) (Fig. 5, a, b). Short pulses with ³H-uridine given in the middle of the infectious cycle label only RF I and RF III in their nascent positive strands, indicating that 42 S and 26 S RNA are synthesized with similar kinetics. Pulses of 40 min are required to fully label the RF II, showing that transcription in this part takes place, but very slowly compared to the 26 S RNA synthesizing part of the RIb (Fig. 5a). Yet no 2.8×10^6 daltons single-stranded RNA is released from the RIb. The poly (A) tract of both 42 S and 26 S RNA is transcribed from a poly (U) sequence with an average length of about 60 residues at the 5' end of the 42 S RNA-negative strand (*Sawicki and Gomatos, 1976; see also Bruton and Kennedy, 1975; Pisano et al., 1975; Margotat et al., 1976; Wittek et al., 1977*).

The maximum rate of synthesis of 42 S RNA-negative strands is reached

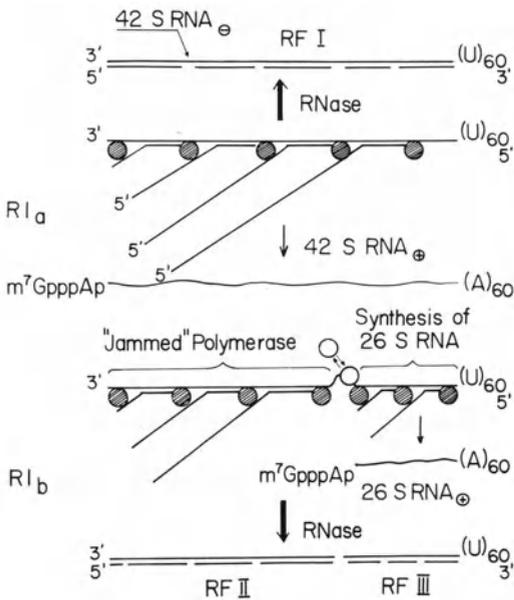


Fig. 5A. Schematic presentation of the transcription of α -virus-specific 42 S and 26 S RNA-positive strands from the 42 S RNA-negative strand template. The evidence for the existence of two different replicative intermediates, RIa and RIb, is based on their response to mild ribonuclease treatment which yields RF I or RF II and RF III. Interaction between interconversion protein (o) and the replication complex synthesizing 42 S RNA converts RIa into RIb, allowing an internal initiation of 26 S RNA synthesis. Proximal to this initiation site, a ribonuclease-sensitive site is created. Polymerase molecules (⊙) which started the transcription of 42 S RNA-positive strands prior to the action of the interconversion protein cannot continue their transcription over the initiation site of 26 S RNA synthesis and become "jammed." When the interconversion protein detaches, RIb is converted into RIa, and the jammed polymerase molecules can complete the interrupted transcription of the 42 S RNA-positive strands

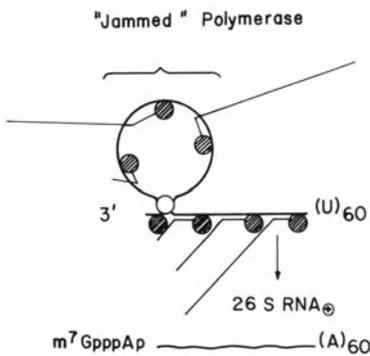


Fig. 5B. An alternative model for the action of interconversion protein. In this model, a common initiation site for transcription of 42 S and 26 S RNA is postulated. Here the interconversion protein creates a loop corresponding to RF II

at about 2¹/₂ h postinfection, declining rapidly thereafter. The rate of synthesis of positive strands, i.e., 42 S and 26 S RNAs, grows exponentially up to 3 h postinfection remaining constant thereafter up to 6–7 h postinfection. The amount of 42 S and 26 S RNA molecules can reach values close to 200,000

per cell at 8 h postinfection as determined by equilibrium labeling with ^{32}P orthophosphate (Tuomi et al., 1975). The massive RNA synthesis is paralleled by a significant decrease in the nucleotide pool size of the infected cells (Hammer et al., 1976).

3. Regulation of 26 S RNA Synthesis

Temperature-sensitive mutants deficient in 26 S RNA synthesis have been isolated from both the Sindbis and SF viruses by mutagen treatment (Scheele and Pfefferkorn, 1969b; Atkins et al., 1974; Keränen and Kääriäinen, 1974; Bracha et al., 1976; Saraste et al., 1977). One SF virus mutant, ts-4, which is phenotypically RNA negative, has a reversible temperature-dependent defect in the synthesis of 26 S RNA (Saraste et al., 1977). When ts-4 is grown at the permissive temperature (28° C), both 42 S and 26 S RNA are synthesized, but upon shift to restrictive temperature (39° C), only the synthesis of 26 S RNA stops. When the cultures are shifted back to 28° C, the synthesis of 26 S RNA starts again even in the presence of cycloheximide.

The fate of 42 S RNA-negative strands in RF I, II, and III before and after temperature shifts was followed by exposing the cells to ^3H -uridine early during infection at 28° C. Further labeling of viral RNAs was stopped using glucosamine and an excess of unlabeled uridine (Sawicki et al., 1978). When the 26 S RNA synthesis stopped at 39° C, there was a quantitative shift of label from RF II plus RF III to RF I. When shifted back to 28° C, part of the label from RF I was again found in RF II and RF III (Sawicki et al., 1978). These results confirm the proposed interconvertibility between RIa and RIb (Simmons and Strauss, 1972b), i.e., that 42 S RNA-negative strands used as templates for 26 S RNA synthesis are shifted to templates of 42 S RNA-positive strand synthesis and vice versa.

The interconversion is regulated by a virus-specific protein which is mutated in ts-4. This "interconversion protein" (Scheele and Pfefferkorn, 1969b) or "26 S protein" (Keränen and Kääriäinen, 1974) must be different from the RNA polymerase synthesizing 42 S RNA since the synthesis of this RNA is unaffected by the upward shift in ts-4. Another mutant deficient in 26 S RNA has been isolated from the SF virus. This ts-1 mutant has an RNA-positive phenotype and synthesizes the same amount of RNA as the wild type (Keränen and Kääriäinen, 1974; Kääriäinen et al., 1975b). This means that the function of the interconversion protein is neither necessary in the synthesis of 42 S RNA-negative nor 42 S RNA-positive strands. Some RNA-negative ts-mutants of the SF virus can at least partly restore the 26 S RNA deficiency of ts-1 at 39° C, giving further evidence for the different functions of RNA polymerase and interconversion protein (Keränen, 1977a). The possibility that the latter is in fact a different polymerase specific for the synthesis of 26 S RNA cannot be excluded at present, but we consider it to be unlikely. Our view of the regulation of 26 S RNA synthesis is presented in Figure 5a. When interconversion protein binds to RIa, possibly to the negative strand template, it creates a single-stranded area or loop, which can be easily hydrolyzed by ribonuclease leading to formation of RF II and RF III (Simmons and Strauss, 1972b). Those polymerase molecules

which had started transcription from the 3' end of the 42 S RNA-negative strand cannot continue due to alterations in the template caused by the interconversion protein. An internal initiation by new RNA polymerase molecules becomes possible leading to the synthesis of 26 S RNA. Detachment of the factor (e.g., by an upward shift of temperature of ts-4 infected cultures) converts the RIb to RIa allowing the "jammed" polymerase molecules to complete the nascent 42 S RNA-positive strands, which were started before the interconversion protein was attached. The temperature dependence of 26 S RNA synthesis (Scheele and Pfefferkorn, 1969b; Atkins et al., 1974; Keränen and Kääriäinen, 1974; Wengler and Wengler, 1976b; Sawicki et al., 1978) would be easily explained if the interconversion protein bound more easily to the template at the lower temperature. At lower temperatures, the binding is favored and more 26 S RNA is produced. The difference in the 42 S/26 S RNA ratios between the Sindbis and SF viruses would also reflect the different binding constants of the interconversion protein of these two viruses. This model would also explain the slow labeling of RF II which would reflect the rate of interconversion between RIa and RIb.

If puromycin is added to the Sindbis virus-infected cultures 90 min after infection, practically no 26 S RNA is formed, whereas the synthesis of 42 S RNA is found in almost normal quantities (Scheele and Pfefferkorn, 1969b). Assuming that the interconversion protein is a soluble protein, which in its free form is not associated with membranes or with the replication complex, the result of Scheele and Pfefferkorn can be understood. Higher concentrations of this protein would be required to initiate the 26 S RNA synthesis than to start the actual RNA polymerase function, which is tightly membrane-bound and most probably also template associated (Friedman et al., 1972; Clewley and Kennedy, 1976). The interconversion protein has not been identified. The recent results by Bracha et al. (1976) and ourselves (Kääriäinen et al., 1978) suggest that at least one of the nonstructural proteins is involved in this function.

The circular model of regulation of 26 S RNA synthesis shown in Figure 5b cannot be excluded at present. It postulates that the 5' ends of both 42 S and 26 S RNA would be transcribed from the same sequence in the 3' end of the 42 S RNA-negative strand. The function of the interconversion protein would be to align the sequences from the 3' and 5' ends to create a large loop equivalent to RF II. Transcription beginning from the 3' end of the negative strand either continues through the loop or "jumps over" the loop. In the former case, newly synthesized positive strands should be specifically destroyed as has been suggested to occur during the processing of adenovirus mRNA (Berget et al., 1977; Chow et al., 1977; Gelinas and Roberts, 1977; Klessig, 1977). The finding of RF II and RF III in equimolar ratios after long labeling with ^3H -uridine speaks against this possibility. The model in which the polymerase molecule jumps over the loop (Fig. 5b) would probably cause the formation of a gap in the synthesized RNA strand and would thus require ligase activity. The validity of the circular model proposed above can be tested by sequencing the 5' ends of both 42 S and 26 S RNA. If the sequences are different the model is incorrect. Translation of 42 S RNA under some conditions also yields structural proteins (Smith et al., 1974; Glanville et al., 1976a), indicating

that the initiation site for structural proteins exists in that part of 42 S RNA which is equivalent to 26 S RNA. These results would speak against the circular model. This model would, however, easily explain the creation of defective interfering RNAs of different lengths, which consist of part of the 5' terminus and larger or smaller part of the poly (A)-containing 3' end (*Bruton and Kennedy, 1976; Bruton et al., 1976; Kennedy, 1976*).

4. RNA Polymerase in α -Virus-Infected Cells

The ability to incorporate labeled nucleotides or phosphate into RNA in the presence of actinomycin D can be considered to be a rough measure of RNA polymerase activity in the infected cells. Kinetic studies carried out throughout the infectious cycle have revealed that the viral RNA synthesis is hardly detectable during the first hour postinfection and thereafter slowly increases during the next hour. An exponential increase follows which lasts to 4–5 h postinfection, whereafter the rate of RNA synthesis remains almost constant (*Sonnabend et al., 1967; Kääriäinen and Gomatos, 1969; Simmons and Strauss, 1972b; Bruton and Kennedy, 1975; Wengler and Wengler, 1975b*). Addition of protein synthesis inhibitors after 3 h postinfection affects the RNA synthesizing capacity of the cells little if at all, indicating that enough stable RNA polymerase has been formed (*Friedman and Grimley, 1969; Scheele and Pfefferkorn, 1969b; Ranki and Kääriäinen, 1970; Wengler and Wengler, 1975b; Kääriäinen et al., 1978*) to ensure the continuation of RNA synthesis. The RNA polymerase activity has been demonstrated directly by several investigators in subcellular fractions derived from α -virus-infected cells (*Martin and Sonnabend, 1967; Martin, 1969; Sreevalsan and Yin, 1969; Ranki and Kääriäinen, 1970; Sreevalsan, 1970; Ershov et al., 1971; Takehara, 1971; Friedman et al., 1972; Michel and Gomatos, 1973*).

In all cases, the polymerase-template complex is bound to large-sized intracellular membranes often capable of synthesizing 42 S and 26 S RNA, replicative intermediates, and double-stranded RNA. Fractionation of the membranes further revealed the presence of typical cytoplasmic vacuoles (CPV I) (*Grimley et al., 1968*) in fractions enriched in RNA polymerase activity (*Friedman et al., 1972*).

Only recently, *Clewley and Kennedy (1976)* purified the RNA polymerase activity further from discontinuous sucrose gradient fractions. The solubilized enzyme preparation was applied to an affinity chromatography column in which 42 S RNA was bound to oligo(dT)cellulose. By this means, two virus-specific and one host cell protein with apparent molecular weights of 90,000, 63,000, and 40,000 were eluted in a fraction which still stimulated incorporation of ^3H -GTP into acid-insoluble form. There was a drastic decrease in enzymatic activity when the membrane fraction was solubilized with Triton X-101, indicating the importance of membranes in protecting the enzyme-template complex against cellular nucleases.

The problems of α -virus-directed RNA synthesis are far from being solved. The function of all four nonstructural proteins has yet to be established either in the synthesis of 42 S RNA-negative and positive strands or 26 S RNA. The possible contribution of host components in the RNA polymerase(s) is

also unknown. The role of viral structural proteins in the regulation of RNA synthesis cannot be excluded either, as suggested by a recent report of *Keränen* (1977b). UV-irradiated ts-mutant of the SF virus was able to interfere with the RNA replication of the wild type, showing that structural proteins, possibly the capsid protein, might directly inhibit the RNA polymerase action.

D. α -Virus-Directed Protein Synthesis

1. Translation of Structural Proteins

The mode of translation of α -virus structural proteins has been clarified to a large extent during the recent past (for review, see *Strauss and Strauss*, 1977). The messenger for the structural proteins is the intracellular 26 S RNA as has been shown by in vitro translation in different cell-free systems derived from mammalian and wheat germ cells (*Cancedda et al.*, 1974a, b; *Clegg and Kennedy*, 1974b; *Simmons and Strauss* 1974b; *Wengler et al.*, 1974; *Clegg and Kennedy*, 1975a, b, c; *Glanville et al.*, 1976a) (Fig. 6).

Association of 26 S RNA with polysomes in infected cells confirms the messenger role of this RNA (*Kennedy*, 1972; *Mowshowitz*, 1973; *Poiree et al.*, 1973; *Söderlund et al.*, 1973; *Simmons and Strauss*, 1974a; *Wengler and Wengler*, 1974; *Wengler et al.*, 1974; *Eaton and Regnery*, 1975; *Martire et al.*, 1977). The 26 S RNA polysomes are membrane bound (*Kennedy*, 1972; *Wirth et al.*, 1977) as is the synthesis of structural proteins (*Friedman*, 1968a). The structural proteins are principally translated as a polyprotein with a molecular weight of 130,000–140,000 as shown by three independent lines of evidence:

1. When 26 S RNA is translated in vitro in the presence of formyl- ^{35}S methionyl-transfer RNA_f, only one labeled tryptic (or pronase) peptide is detected (*Cancedda et al.*, 1975; *Clegg and Kennedy*, 1975b; *Glanville et al.*, 1976b), which yields f-met-asn as a dipeptide (*Glanville et al.*, 1976b). The same dipeptide (met-asn) is obtained in the 26 S RNA-directed in vitro system when elongation is inhibited by diphtheria toxin (*Clegg and Kennedy*, 1975b). Polyacrylamide gel analysis of the product labeled with formyl- ^{35}S -methionine in an in vitro

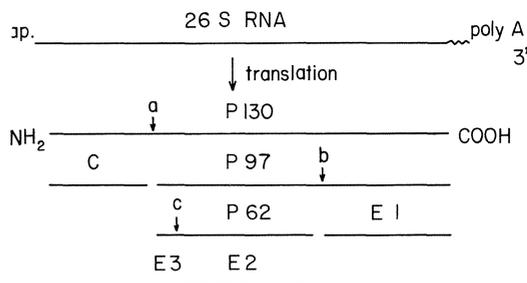


Fig. 6. Translation of structural protein as a polyprotein from the 26 S RNA. The cleavage of capsid protein is nascent (a), cleavage between p62 and E1 takes place rapidly after translation (b), whereas p62 is cleaved during the maturation of the virus (c)

system programmed with 26 S RNA yields only labeled capsid protein, indicating that this protein is N-terminal in the structural polyprotein.

2. Temperature-sensitive, RNA-positive mutants have been isolated from the Sindbis and SF viruses, which produce a large 130,000–140,000 daltons protein. This protein has the tryptic peptides of the capsid and all envelope proteins (*Schlesinger M. and Schlesinger S.*, 1973; *Keränen and Kääriäinen*, 1975; *Lachmi et al.*, 1975).

3. Sequential labeling of structural proteins takes place when infected cells are released from the hypertonic block of initiation (*Saborio et al.*, 1974); capsid protein is labeled first, followed by envelope proteins E3, E2, and finally by E1 (*Clegg*, 1975; *Clegg and Kennedy*, 1975b, c; *Lachmi and Kääriäinen*, 1976; *Garoff and Söderlund*, 1978).

The gene order of the structural proteins in 26 S RNA revealed by sequential labeling has been independently proved by tryptic peptide mapping of some aberrative cleavage products found in cells infected with some temperature-sensitive mutants of the SF virus (*Kääriäinen et al.*, 1975b; *Lachmi et al.*, 1975). The capsid protein is cleaved from the nascent polyprotein both in vivo (*Burke*, 1975; *Strauss and Strauss*, 1976) and in vitro (*Cancedda et al.*, 1974a, b; *Clegg and Kennedy*, 1974b; *Wengler et al.*, 1974; *Glanville and Ulmanen*, 1976), probably immediately after the ribosome has finished the translation of the sequence coding for capsid protein (*Clegg* 1975; *Söderlund*, 1976). The nature of the cleavage enzyme is not clear, but recent evidence by *Scupham et al.* (1977) obtained in mixed infections with Sindbis ts-mutants suggests that the enzyme is virus specific. Since the N-terminal amino acid of capsid protein is probably lysine (*Kennedy and Burke*, 1972), there must be another cleavage whereby at least met-asn or a longer oligopeptide is removed from the N-terminus of the primary translational product of the capsid protein. This type of "lead-in" sequence was previously demonstrated in the mengovirus-directed polyprotein (*Smith*, 1973).

The cleavage between the envelope proteins takes place at the time when most of the polyprotein has been translated (*Söderlund*, 1976). The products of this cleavage are the envelope protein E1 and the 62,000–68,000 daltons precursor protein of E2 and E3, i.e., the p62 (NSP 68, NVP 68, or pE₂) (*Schlesinger S. and Schlesinger M.*, 1972; *Simons et al.*, 1973b; *Garoff et al.*, 1974; *Lachmi et al.*, 1975). The cleavage between the capsid protein and the envelope protein is probably the only one which takes place in reticulocyte lysate programmed with the Sindbis virus 26 S RNA (*Simmons and Strauss*, 1974b), leading to production of 100,000 daltons envelope protein "precursor" and capsid protein in almost a 1:1 molar ratio. If membranes from isolated endoplasmic reticulum are added to the incubation mixture, cleavage between E1 and p62 seems to take place (*Dobberstein*, 1977), showing the importance of membranes in the processing of these proteins.

The capsid protein attaches to the 60 S ribosomal subunit in the polysomes immediately after its synthesis (*Glanville and Ulmanen*, 1976; *Ulmanen et al.*, 1976), while the p62 (pE₂) and E1 associate with membranes of the endoplasmic reticulum and become glycosylated, as will be discussed later.

The possibility of premature termination after the translation of capsid

protein has been suggested as an explanation for excessive synthesis of capsid protein in Sindbis virus-infected cells (*Cancedda and Schlesinger, 1974*). This may not be a general rule in α -virus protein synthesis since in SF virus-infected cells, capsid and envelope proteins are synthesized in about a 1:1 molar ratio (*Morser et al., 1973; Morser and Burke, 1974; Keränen and Kääriäinen, 1975*). The overproduction of capsid protein may also not be the rule in the Sindbis virus-infected cells, as judged from the earlier published results by several investigators (*Strauss et al., 1969; Scheele and Pfefferkorn, 1970; Pfefferkorn and Boyle, 1972; Snyder and Sreevalsan, 1974*).

The molecular weight of 26 S RNA has been estimated to be between 1.6 and 1.8×10^6 (*Levin and Friedman, 1971; Simmons and Strauss, 1972a; Martin and Burke, 1974*). Its theoretic coding capacity is thus at least 160,000 daltons of protein. From this capacity, about 130,000 is used to code for the known structural proteins. It will be interesting to see whether hitherto unknown proteins can be demonstrated in the α -virus-infected cells in the future.

2. Translation of Nonstructural Proteins

Recently, several other-than-structural proteins have been detected in SF and Sindbis virus-infected cells (*Lachmi et al., 1975; Bracha et al., 1976; Kaluza, 1976; Kaluza et al., 1976; Brzeski and Kennedy, 1977*). These proteins are designated as nonstructural proteins until their function has been definitely established. Two nonstructural proteins with apparent molecular weights of 86,000 and 72,000 were first identified by tryptic peptide mapping from cells infected with a temperature-sensitive mutant, ts-1, of the SF virus (*Lachmi et al., 1975*). In ts-1-infected cells, these proteins are produced in an excessive amount compared to the wild type (*Keränen and Kääriäinen, 1975; Kääriäinen et al., 1975a, b*).

When ts-1-infected cell cultures were released from the hypertonic block of initiation, sequential labeling of four stable nonstructural proteins with molecular weights of 70,000 (ns70), 86,000 (ns86), 72,000 (ns72, previously ns78), and 60,000 (ns60) were demonstrated (*Lachmi and Kääriäinen, 1976*). Two short-lived large proteins with molecular weights of about 155,000 (ns155 or A) and 135,000 (ns135 or B) were also labeled. The former was seen after a short labeling, whereas ns135 appeared only after 10 min or a longer labeling period, following synchronous initiation of protein synthesis. These results suggested a precursor-product relationship between the large short-lived proteins and the more stable ones. The evidence for the existence of ns60 is still indirect and based on the labeling of a protein of this size in pactamycin-treated cells in which the structural protein synthesis was already stopped (*Lachmi and Kääriäinen, 1976*). Comparison of tryptic peptides of ns155, ns135, ns70, ns86, and ns72 has to a large extent confirmed the proposed precursor-product relationship. First, the primary structures of ns155 and ns135 are different, indicating that the total molecular weight of the nonstructural proteins is close to 300,000 (*Glanville and Lachmi, 1977*). Secondly, the tryptic peptides of ns70 and ns86 are found in ns155 and those of ns72 are found in ns135 (*Glanville et al., 1978*). In ns135, there are peptides not found in ns72, and these may be derived from ns60.

The sequential labeling of the different nonstructural proteins suggested that they are translated as a polyprotein in analogy to the structural proteins (*Lachmi and Kääriäinen, 1976*). Support of this view has been obtained from the results of translation of 42 S RNA in vitro in the presence of formyl ³⁵S-methionyl-transfer RNA_f. Analysis of tryptic (or pronase) peptides of the translational product yielded only one labeled peptide, suggesting that the translation of 42 S RNA is initiated from a single initiation site (*Glanville et al., 1976b*). The initiation dipeptide was identified to be f-met-ala. Similar results have been reported by *Cancedda et al. (1975)*, although they found small amounts of radioactivity which evidently was derived from an internal initiation site, respective to the initiation site of 26 S RNA.

The viral origin of the nonstructural proteins of SF virus, at least of ns155 (i.e., ns70 and ns86) and partly of ns72, has been confirmed by comparing the tryptic peptides of the above proteins with those derived from the translational product of 42 S RNA in wheat germ cell-free extract (*Glanville and Lachmi, 1977*).

The presence of the nonstructural proteins has also been demonstrated in the SF virus wild type-infected cells in which their maximum rate of synthesis takes place between 3 and 4 h postinfection, declining thereafter (*Lachmi and Kääriäinen, 1977*). *Clegg et al. (1976)* have shown two nonstructural proteins with molecular weights of 90,000 and 63,000. These proteins are probably equivalent to ns86 and ns70. They are presumably formed from larger precursors which have molecular weights of 200,000, 184,000, and 150,000.

The 42 S RNA is most probably the messenger for the nonstructural proteins in the infected cells, since this RNA has been found in the polysomes by several investigators (*Mowshowitz, 1973*; *Söderlund et al., 1973*; *Simmons and Strauss, 1974a*; *Wengler and Wengler, 1975a*; *Martire et al., 1977*). *Bracha et al. (1976)* have shown the existence of a 200,000 daltons nonstructural protein in cells infected with the temperature-sensitive mutants ts-21 and ts-24 of the Sindbis virus. The protein accumulated only at the restrictive temperature, suggesting a cleavage defect of the nonstructural polyprotein with these RNA negative mutants.

Brzeski and Kennedy (1977) have found several nonstructural proteins with molecular weights of 230,000, 215,000, 150,000, 89,000, 82,000, 76,000, and 60,000 in Sindbis virus wild type-infected cells. The large proteins accumulated when zinc ions were used to inhibit the cleavages of the nonstructural polyprotein (*Bracha and Schlesinger, 1976a*). The ns89, ns82, and ns60 are stable products, whereas the others are their precursors. Exposure of the infected cells to ³⁵S-methionine after release from the hypertonic block of initiation labeled the proteins sequentially in the order ns60, ns89, and ns82, suggesting that they are made from a large polyprotein which the authors think is ns230.

A 220,000 daltons protein (ns220) was recently demonstrated with a temperature-sensitive mutant, ts-4, of the SF virus (*Kääriäinen et al., 1978*). This protein is detected only at the restrictive temperature as is the case with the similar size protein from the Sindbis virus ts-mutants (*Bracha et al., 1976*). Short pulses given after release from the hypertonic block of initiation labels the ns220 as well as ns155, suggesting that both are derived from the N-terminal part of the nonstructural polyprotein.

Waite (1973) has reported an interesting result using an RNA-negative mutant, ts-11, of the Sindbis virus. When ts-11-infected cultures were shifted to the restrictive temperature, a protein with an apparent molecular weight of 133,000 accumulated into the cells. This protein remained stable even if the cultures were shifted back to the permissive temperature. *Waite* suggested that the large protein was the structural polyprotein. It would be more plausible to assume that the 133,000 daltons protein is a nonstructural precursor protein, perhaps similar to that of ns135 of the SF virus, which accumulates because of a cleavage defect caused by a mutation in one of the nonstructural proteins.

Kaluza has demonstrated the presence of at least some of the nonstructural proteins in SF virus-infected cells pretreated with fowl plague virus which shuts off the host protein synthesis (*Kaluza*, 1976; *Kaluza et al.*, 1976). *Friedman* (1968c) may have detected some of the nonstructural proteins in guanidine-treated SF virus-infected cells. The identification of the proteins is, however, difficult because of the different polyacrylamide gel systems used.

The mode of translation of α -virus nonstructural proteins is nearly solved. In spite of the slightly different results obtained with SF and Sindbis viruses, there are also striking similarities:

1. Results with both viruses suggest that the nonstructural proteins are translated as a large polyprotein of at least 230,000 but probably 290,000 molecular weight.
2. The identification of the different stable nonstructural proteins is facilitated by their order of labeling after synchronous initiation. Thus the N-terminal protein, ns70, in the SF virus has its counterpart in ns60 in Sindbis virus-infected cells, followed by ns86 (SF virus), ns89 (Sindbis virus) and ns72 (SF virus), ns82 (Sindbis virus) (Fig. 7a, b).

The existence of the fourth nonstructural protein has been difficult to show in either virus, due to its migration at the position of p62 (pE₂). The differences in apparent molecular weights obtained by research groups may be real, but they may also reflect technical differences. For example, with the SF virus, ns72, ns70, and p62 migrate together in the discontinuous polyacrylamide gel system by *Laemmli* (1970), whereas ns72 migrates far from p62 and allows the detection of ns70 between ns72 and p62 in the *Neville* gel system (1971) (unpublished results). The different primary structures of ns155 and ns135 strongly suggest that a fourth nonstructural protein exists, and thus we should be able to find the whole nonstructural polyprotein in the future.

As mentioned previously, two of the nonstructural proteins, ns90 (probably identical with our ns86 and the ns89 of the Sindbis virus) and ns63 (possibly our ns70 and equivalent to ns60 of the Sindbis virus), are associated with purified preparations of RNA polymerizing activity (*Clegg et al.*, 1976; *Clewley and Kennedy*, 1976). The functions of the other nonstructural proteins remain to be solved in the future (*Pfefferkorn*, 1975).

3. Control of Protein Synthesis in α -Virus-Infected Cells

A drastic inhibition of host cell protein synthesis takes place in vertebrate cells infected with different α -viruses (*Lust*, 1966; *Hay et al.*, 1968; *Strauss et al.*, 1969; *Igarashi*, 1970; *Mussgay et al.*, 1970; *Takehara*, 1972; *Keränen and Kääriäinen*, 1975; *Lubiniecki*, 1975), usually between 3–5 h postinfection.

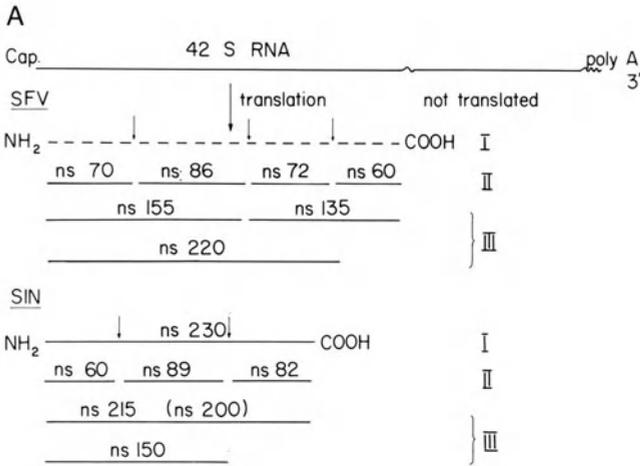


Fig. 7A. Translation of Semliki Forest (SFV) and Sindbis virus (SIN) nonstructural proteins from 42 S RNA. I indicates the postulated primary translational product, II the stable cleavage products, and III the detected intermediates. Arrows indicate the cleavage sites. Dotted line refers to a protein which has not been found

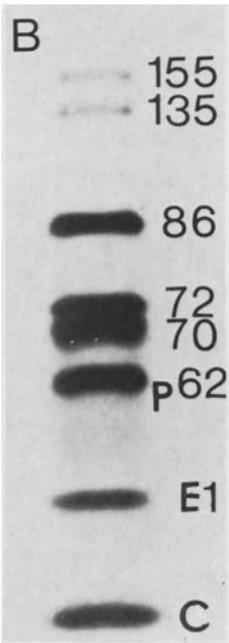


Fig. 7B. Fluorogram of polyacrylamide gel showing SF virus-specific structural and nonstructural proteins

The mechanism of this inhibition is not known. Competition between viral and host messenger RNAs has been suggested to explain the host cell inhibition (Keränen and Kääriäinen, 1975; Wengler and Wengler, 1976b; Atkins, 1976). Tuomi et al. (1975) calculated that there are about equal amounts of viral and cellular mRNAs competing for the ribosomes at 4 h postinfection. This indicates

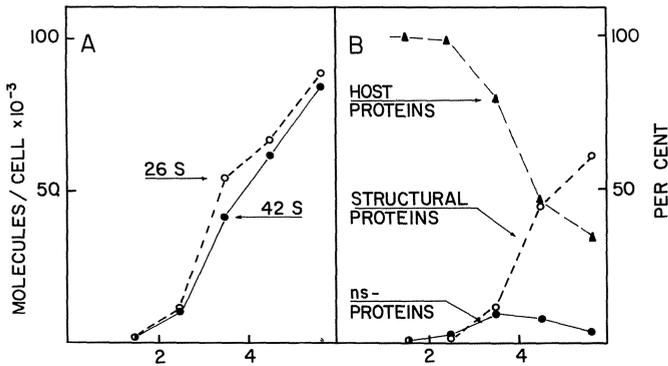


Fig. 8. RNA and protein synthesis in SF virus-infected cells according to *Tuomi et al.* (1975) and *Lachmi and Kääriäinen* (1977). (A) The number of virus-specific RNAs is compared to the rate (B) of synthesis of host- and virus-specific proteins

that the affinity of ribosomes to the viral messenger is greater than to the host cell messenger. The required difference in affinity may be so small that it would be difficult to verify experimentally *in vitro*, as has turned out to be the case in cell-free extracts from picornavirus-infected cells (*Lawrence and Thach*, 1974; *Abreu and Lucas-Lenard*, 1976).

Another type of protein synthesis control in α -virus-infected cells has been described (*Kääriäinen et al.*, 1976; *Lachmi and Kääriäinen*, 1977). The maximum rate of synthesis of nonstructural proteins is reached between 3 and 4 h postinfection at a time when only about 50% of 42 S RNA has been synthesized. Thereafter, the rate of synthesis of the nonstructural proteins declines continuously despite the increase in the amount of 42 S RNA. The efficiency of the 42 S RNA as a messenger declines by an overall factor of six. This decline is at least partly due to an increased encapsidation rate of 42 S RNA molecules into nucleocapsids (*Ulfmanen et al.*, unpublished results). However, a nucleocapsid-negative, RNA-positive mutant of the SF virus (ts-3) shows the same shutoff (*Keränen and Kääriäinen*, 1975) in the synthesis of nonstructural proteins as does the wild type, indicating that mechanisms other than encapsidation of 42 S RNA must be involved in this translational control. The synthesis of structural proteins does not seem to be regulated at the translational level, since their rate of synthesis closely reflects the amount of 26 S RNA in the infected cells (*Lachmi and Kääriäinen*, 1977) (Fig. 8).

The excessive synthesis of nonstructural proteins in the SF virus ts-1 mutant-infected cells has been studied to some extent (*Kääriäinen et al.*, 1976). Ts-1-infected cells initially maintained at the permissive temperature accelerate the synthesis of nonstructural proteins only slowly when shifted to the restrictive temperature. If the infection is started at 39°C and the cultures thereafter shifted to 28°C, the shut off of nonstructural protein synthesis takes about 2 h. The synthesis continues somewhat longer if cycloheximide is added at the moment of shift-down. These observations would suggest that the factors controlling the shut off must be synthesized after the shift-down and that a fairly large amount of these factors must be made before most of the 42 S RNAs are

shut off from the synthesis of nonstructural proteins. The shift-up experiment suggests that those 42 *S* RNA molecules which had been shut off from the synthesis of nonstructural proteins at 28° C are not able to start it again when shifted to 39° C. Rather, it would mean that new 42 *S* RNA molecules are needed which are not affected by the control mechanism operating at the permissive temperature. These experiments rule out a temperature-sensitive reversible control mechanism similar to that seen in the regulation of 26 *S* RNA synthesis discussed earlier.

E. Assembly of Nucleocapsid

The assembly of α -viruses differ from most icosahedral plant and animal viruses because no empty nucleocapsids can be seen in the infected cells (*Acheson and Tamm, 1967; Erlandson et al., 1967; McGee-Russell and Gosztonyi, 1967*) nor have fractionation of infected cells revealed RNA-free structures or "top components" which could be regarded as empty capsids (*Ben-Ishai et al., 1968; Friedman, 1968a; Friedman and Grimley, 1969; Söderlund, 1973*).

Kinetic studies carried out by amino acid labeling have shown that the capsid protein is transferred to the cytoplasmic nucleocapsids within 2–10 min (*Söderlund, 1973*) and to released virions within 10–30 min (*Scheele and Pfefferkorn, 1969a*). Free capsid protein cannot be demonstrated even after short pulses, suggesting that capsid protein binds rapidly to sedimenting structures. After short pulses with ³⁵S-methionine, most of the newly formed capsid protein was associated with polysomes from which it could be chased to nucleocapsids. This process was inhibited if cycloheximide was added after the pulse (*Söderlund, 1973*). The inhibition of nucleocapsid assembly by cycloheximide was first demonstrated by *Friedman and Grimley (1969)*.

The recent findings that nascent capsid protein binds to the large ribosomal subunit in the polysomes explains why no free capsid protein has been found (*Ulmanen et al., 1976*). Pulse-chase experiments show that the capsid protein is rapidly transferred from the large subunits to 42 *S* RNA (*Söderlund and Ulmanen, 1977*). The transfer takes place with two different kinetics; initially about 30% of the pulse-labeled capsid protein is chased within 2 min, whereafter the transfer is considerably slower. This result must mean that the initial transfer from the large ribosomal subunit to 42 *S* RNA takes place at the polysomes. The second phase may take place after the ribosomes have been released into the monosome pool. How the transfer of capsid protein takes place is not known. The kinetics suggest that the nucleocapsid may be assembled by the continuous addition of capsid protein to 42 *S* RNA, but no intermediates or nucleocapsid precursors have been isolated so far. The possible linkage between polysomes and assembling nucleocapsids could explain why nucleocapsids have been isolated from the polysomal fraction (*Mowshowitz, 1973; Simmons and Strauss, 1974a*).

The attachment of capsid protein is specific for 42 *S* RNA since 26 *S* RNA does not bind this protein (*Ulmanen et al., 1976*) in contrast to predictions based on earlier experiments (*Söderlund and Kääriäinen, 1974*). This means that

the 5' two-thirds of the 42 S RNA, which is different from the 26 S RNA, has a specific binding region for capsid protein. These sequences must have been preserved in the defective interfering RNAs because these are encapsidated (*Bruton and Kennedy, 1976*).

The information available on the assembly of α -virus nucleocapsids suggests that it is a unique process. It will be interesting to see whether similar assembly processes will be found among those small isometric plant viruses, like cucumber chlorotic mottle viruses, which apparently have strong RNA-protein interactions as the stabilizing force in the virion (*Kaper, 1975*).

Nucleocapsid seems to be formed in great excess compared to the amount which actually is released from the cell as mature virus. Intermediate and late in the infection, most of the genome RNA is encapsidated (*Ulmanen, personal communication*), but only 5%–10% is released (*Tuomi et al., 1975*). Nucleocapsids accumulate to such an extent that paracrystalline arrays can be visualized by electron microscopy in the cytoplasm of infected cells (*Morgan et al., 1961; Acheson and Tamm, 1967; Wagner et al., 1975*).

F. Assembly of Viral Envelope

In this section, we will mainly discuss the most recent findings since the earlier literature was recently reviewed by *Kääriäinen and Renkonen (1977)* and *Simons et al. (1978)*.

1. Glycosylation of Envelope Proteins

The structural proteins are translated from 26 S RNA in membrane-bound polysomes (*Wirth et al., 1977*). The envelope proteins are inserted into the membranes of endoplasmic reticulum and protrude through the membrane into the cisternal side of the rough endoplasmic reticulum (Fig. 9). The nascent chains of p62 (pE₂) and E1 are glycosylated by lipid-containing oligosaccharide intermediates, probably a dolichol oligosaccharide (*Krag and Robbins, 1977; Sefton, 1977*). In this process, the glucosamine-containing mannose-rich core of the A-oligosaccharide type chain (*Johnston and Clamp, 1971; Spiro, 1973*) and the probably identical B-type chain are transferred to the envelope proteins. If primary glycosylation is inhibited by tunicamycin, which is a specific inhibitor of oligosaccharide lipid intermediate synthesis (*Takatzuki et al., 1975; Tkacz and Lampen, 1975; Struck and Lennarz, 1977*), envelope proteins p62 (pE₂) and E1, which have increased mobility in polyacrylamide gels, are found from infected cells (*Schwarz et al., 1976; Leavitt et al., 1977*). The same "apoproteins" are formed if the cells are incubated in glucose-free medium (*Kaluza, 1975; Sefton, 1977*). These may not be able to accept oligosaccharides, e.g., due to a wrong configuration (*Sefton, 1977*). Similar apoproteins, or poorly glycosylated envelope proteins, are synthesized in the presence of glucosamine (*Duda and Schlesinger, 1975*), 2-deoxy-D-glucose (*Kaluza et al., 1973; Scholtissek and Kaluza,*

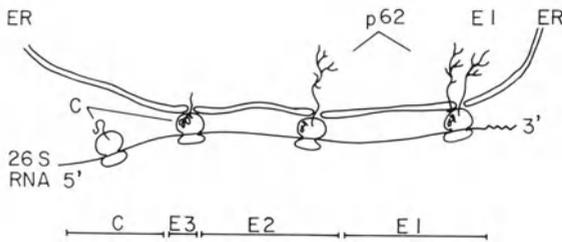


Fig. 9. The structural proteins of α -viruses are translated from 26 S RNA on membrane-bound polysomes on the cytoplasmic side of the endoplasmic reticulum membranes (ER). Translation of capsid protein takes place on free ribosomes. After completion of translation of the capsid protein, nascent cleavage takes place and the protein attaches to the 60S ribosomal subunit. The nascent N-terminus of the envelope protein precursor directs the binding of the ribosome to the ER membrane, and the growing polypeptide chain is protruded through the membrane to the cisternal side and becomes glycosylated by lipid-bound oligosaccharide intermediates. Cleavage between p62 (pE₂) and E1 takes place but the two proteins remain closely associated. The envelope glycoproteins remain in the membrane by their C-terminal hydrophobic fragments and can only move at the plane of the membrane

1975; Scholtissek et al., 1975; for review see Scholtissek, 1975), 2-deoxy-2-fluoro-D-glucose, and mannose (Schmidt et al., 1976).

These studies imply that the cleavage between envelope protein E1 and p62 takes place even if glycosylation is inhibited, probably as a result of penetration through the endoplasmic reticulum membrane. As an exception to this rule, the common envelope protein precursor, the 100,000 daltons B protein (Strauss et al., 1969; Schlesinger M. and Schlesinger S., 1973), which is not glycosylated (Sefton and Burge, 1973), is protected from the action of added proteases in vitro (Wirth et al., 1977), suggesting that it has been transported through the endoplasmic reticulum membrane without cleavage and glycosylation.

The addition of the distal sugars of the A-type chain, such as glucosamine, galactose, and sialic acid, takes place later within approximately 20 min (Sefton, 1977). At this stage, part of the mannose residues are probably removed from the "core" before addition of the distal sugars (Sefton and Burge, 1973; Rasilo and Renkonen, 1978). The most exposed glycans like the A-type chain of E3 of the SF virus may be more easily glycosylated and is, therefore, larger than A-type chains of E1 and E2 (Renkonen, personal communication). The somewhat incomplete glycosylation does not affect the transport of envelope proteins to the plasma membrane and incorporation into the virions, as has been shown by Schlesinger et al. (1976). The Sindbis virus was grown in cells deficient in *N*-acetyl-glucosaminyl transferase activity with normal yields of infectious virus.

2. Transport of Envelope Proteins to the Plasma Membrane

The envelope proteins E1 and E2 have hydrophobic tails by which they are attached to the lipid bilayer in the virus envelope (Uterman and Simons, 1974). The same interaction must take place in intracellular membranes after the poly-

peptides have been completed. In both E1 and E2, the hydrophobic regions are close to the C-terminus, as recently shown by *Garoff and Söderlund (1978)*, making the association to the membranes the final event in the synthesis of polypeptide. Unlike the secretory glycoproteins (*Palade, 1975*), the envelope glycoproteins must migrate in the cells by lateral diffusion at the plane of the membrane (*Hirano et al., 1972*).

Schlesinger and Schlesinger (1972) showed by pulse-chase experiments, devised by *Scheele and Pfefferkorn (1969a)*, that both E1 and E2 were released in the virus particles to the medium with similar kinetics. This suggests that p62 and E1 remain associated with each other after their synthesis and are transported together to the plasma membrane and finally to the virus. Support of this idea was obtained from studies with temperature-sensitive mutants of the Sindbis virus belonging to complementation groups D and E (*Burge and Pfefferkorn, 1966b; 1968*). All the mutants show the same defect, namely the inability to cleave p62 (pE₂) at the restrictive temperature (*Jones et al., 1974; Bracha and Schlesinger, 1976b; Jones et al., 1977; Smith and Brown, 1977*; for similar observations with SFV mutants see *Keränen and Kääriäinen, 1975*).

In cells infected with ts-20 mutant of the Sindbis virus (with postulated defect in E2 protein) (*Jones et al., 1974*), E1 protein is transported to the outside of the plasma membrane. This is evident since the cells adsorb goose erythrocytes (*Burge and Pfefferkorn, 1968*) and E1 can be labeled with lactoperoxidase-mediated iodination as in the wild type infected cells (*Sefton et al., 1973; Smith and Brown, 1977*). The cells also show membrane fluorescence with antiserum against E1 (*Bell and Waite, 1977*). The p62 is present in the plasma membrane fractions (*Jones et al., 1974*), but it can neither be labeled with the lactoperoxidase technique (*Smith and Brown, 1977*) nor fluorescent antibodies against E2 (*Bell and Waite, 1977*). The crucial demonstration that p62 is on the outside of the plasma membrane would require other methods, e.g., specific antiserum against p62.

The cleavage of p62 (pE₂) in wild type-infected cells can be prevented by antiserum against E1, strongly suggesting that both E1 and p62 are on the outside of the plasma membrane and indeed interact so that inhibition of the free mobility of E1 affects p62 so that it cannot be cleaved (*Bracha and Schlesinger, 1976b; Smith and Brown, 1977*). Further support for the interaction between E1 and p62 was obtained from studies with ts-mutants of complementation group D (ts-10 and ts-23), which are supposed to have the defect in the hemagglutinating E1 protein (*Burge and Pfefferkorn, 1968; Yin, 1969; Dalrymple et al., 1976*).

Neither iodination with lactoperoxidase nor ferritin-antibody labeling could demonstrate the envelope proteins on the outside of the plasma membrane (*Smith and Brown, 1977*), suggesting that transport to the outside of the plasma membrane of both proteins had failed due to the mutation in E1. This observation also explains why nucleocapsid cannot be seen attached to the cytoplasmic side of the plasma membrane in ts-23-infected cells maintained at the restrictive temperature (*Brown and Smith, 1975*). A similar mutant of the WEE virus was reported recently by *Hashimoto et al. (1977)*.

Birdwell and *Strauss* (1974a) have nicely demonstrated the presence of envelope proteins at the surface of Sindbis wild type-infected cells as early as 2 h postinfection. The proteins are evenly distributed and patched, easily showing that they are free to move laterally at the plane of the membrane. The amount of envelope proteins on the cell surface increased throughout the infection, but their distribution remained random, showing no prevalent areas of "viral patches" (*Lenard* and *Compans*, 1974).

G. Maturation of α -Virus

Morphogenetic studies with different α -viruses have shown that viral nucleocapsid aligns below the plasma membrane and that the virus is formed by budding through the plasma membrane (*Acheson* and *Tamm*, 1967; *Erlandson* et al., 1967; *Grimley* and *Friedman*, 1970; *Grimley* et al., 1972; *Bykovsky* et al., 1969; *Lascano* et al., 1969; *Tan*, 1970; *Waite* et al., 1972; *Birdwell* et al., 1973; *Gil-Fernandez* et al., 1973; *Virtanen* and *Wartiovaara*, 1974). At this time, there are only projections visible at the site of budding (*Acheson* and *Tamm*, 1967).

The transmembrane interaction between nucleocapsid and the envelope proteins demonstrated in SF virus particles by *Garoff* and *Simons* (1974) would explain how the nucleocapsid can recognize the envelope proteins at the other side of the plasma membrane. The interactions created between nucleocapsid and envelope proteins prevent the free lateral movement of the latter but not the movement of the host cell plasma membrane proteins, which become excluded from the maturing virus particle. If the free lateral mobility is inhibited, e.g., by plant lectins (*Becht* et al., 1971; *Birdwell* and *Strauss*, 1973) or by specific antiserum, virus maturation is inhibited (*Bracha* and *Schlesinger*, 1976b; *Jones* et al., 1977; *Smith* and *Brown*, 1977). The driving force in the assembly is the increasing number of interactions leading to the budding and finally release of the virus particle from the cell membrane (*Brown* et al., 1972; *v. Bonsdorff* and *Harrison*, 1975). During the budding, the virus obtains the lipids from the host cell plasma membrane (*Renkonen* et al., 1971; 1972a, b; 1974; *Laine* et al., 1972; *Hirschberg* and *Robbins*, 1974). *Richardson* and *Vance* (1976) recently demonstrated how labeled proteins from the microsomal fractions are transferred to plasma membrane fraction and finally to released virus particles.

In *Aedes albopictus* cells, the α -viruses probably mature at the intracellular membranes, budding into vacuoles, which release the virus particles into the medium by fusing with the plasma membrane (*Whitfield* et al., 1971; *Raghow* et al., 1973; *Gliedman* et al., 1975; see also *Strauss* and *Strauss*, 1977). The lipids of SF grown in *A. albopictus* cells are drastically different from those derived from BHK 21 cells (*Renkonen* et al., 1974; *Luukkonen* et al., 1976), demonstrating that the host cell specifies the lipid components, whereas the viral genome is responsible for the proteins (*Pfefferkorn* and *Clifford*, 1964; *Luukkonen* et al., 1977b). Variation in the oligosaccharides of the glycoproteins is also a host-specific phenomenon, as has been shown by several investigators (*Keegstra* et al., 1975; *Schlesinger* S. et al., 1976; *Stollar* et al., 1976).

The amino acid sequence of the envelope proteins determines the number and type of the oligosaccharide chains which are added to the glycoproteins by cellular enzymes (*Burge and Huang, 1970; Grimes and Burge, 1971; Froger and Louisot, 1972a, b; Sefton, 1976*). The recognition of envelope proteins through the membrane is sometimes inaccurate, leading to incorporation of several nucleocapsids into giant particles (*Simizu et al., 1973; Hashimoto et al., 1975, 1977; Strauss E. et al., 1976, 1977*). The reason for this "inaccuracy" may be mutation in the capsid protein rather than envelope proteins, at least in one of the cases studied more closely (*Strauss E. et al., 1977*).

Simultaneous infection of mouse peritoneal macrophages with the Sindbis and lactic dehydrogenase viruses (a nonarboviral virus) may result in phenotypic mixing, i.e., Sindbis genotypes with LDH envelopes, suggesting that the capsid-envelope protein interaction is not absolutely specific (*Lagwinska et al., 1975*). The phenotypic mixing occurs easily among the α -viruses but cannot be accomplished between α - and rhabdoviruses (*Burge and Pfefferkorn, 1966c; Chopin and Compans, 1970*). The concept of virus maturation presented above is mostly based on experiments performed with cultured cells. The process may be much more complicated in the living organism (*Johnson, 1965; Murphy et al., 1970; Pathak and Webb, 1974; Pathak et al., 1976*).

IV. Defective Interfering Particles in α -Virus-Infected Cells

Serial passage of the Sindbis and SF viruses with high multiplicities of infection results in an abrupt drop in infectivity and hemagglutination titers in the culture medium. This autointerference phenomenon is due to accumulation of defective interfering particles (*Schlesinger S. et al., 1972, 1975; Eaton and Faulkner, 1973; Inglot et al., 1973, 1977; Shenk and Stollar, 1972, 1973a, b; Weiss and Schlesinger, 1973; Eaton, 1975; Johnston et al., 1975; Bruton and Kennedy, 1976*). The progeny particles isolated from the medium after high multiplicity passages interfere with the multiplication of homologous but not with heterologous standard viruses (*Bruton and Kennedy, 1976*). The particles with interfering properties (DI particles) have all the proteins of standard viruses in the same proportions but usually contain RNAs which are smaller than the 42 S RNA (*Schlesinger S. et al., 1974, 1975; Johnston et al., 1975; Bruton and Kennedy, 1976; Kennedy et al., 1976; Guild and Stollar, 1977*).

In some cases, the DI particles can be separated from the standard virus by size (*Johnston et al., 1975*) or by density (*Bruton and Kennedy, 1976; Shenk and Stollar, 1973a*). Purified DI particles alone cannot direct any virus-specific functions except adsorption, penetration, and uncoating (*Bruton et al., 1976*), which are probably host functions (*Bracha et al., 1977*). The DI particles isolated so far require the functions of standard viruses to manifest their effects (*Schlesinger S. et al., 1972; Shenk and Stollar, 1973a, b; Schlesinger S. et al., 1974, 1975; Bruton and Kennedy, 1976*).

A typical effect of DI particles, in addition to their interfering ability, is the stimulation of synthesis of single-stranded RNAs different from the normal

42 S and 26 S RNA (Weiss et al., 1974; Schlesinger S. et al., 1974, 1975; Bruton et al., 1976). The predominant species has been a single-stranded RNA sedimenting at about 20 S (mol wt $0.8-1.0 \times 10^6$). Abnormal single-stranded RNA formation is accompanied by a significant reduction in the synthesis of 42 S and 26 S RNA. The aberrative RNAs are apparently synthesized from different templates than the normal α -virus-specific RNAs, since double-stranded RNAs sedimenting at 12 S–16 S (Eaton and Faulkner, 1973; Guild and Stollar, 1975; Guild et al., 1977), probably derived from specific replicative intermediates, have been regularly found (Bruton et al., 1976).

The single-stranded DI-RNAs are of positive polarity but cannot stimulate protein synthesis *in vitro* (Weiss et al., 1974; Bruton et al., 1976; Guild and Stollar, 1977). They contain poly (A) and different lengths of sequences from the 3' end of 42 S RNA, which is identical to 26 S RNA (Schlesinger S. et al., 1974, 1975; Weiss et al., 1974; Bruton et al., 1976; Kennedy et al., 1976; Guild and Stollar, 1977). The single-stranded DI-RNAs can be derived predominantly from the "26 S" RNA region (Kennedy et al., 1976) or from the region of 42 S RNA, which codes for nonstructural proteins (Bruton et al., 1976; Kennedy et al., 1976). In both cases, they contain sequences from the 5' end of 42 S RNA (Kennedy, 1976; Kennedy et al., 1976).

The synthesis of single-stranded DI-RNAs must originally take place from the 42 S RNA-positive or negative strand. One possibility is that they are transcribed from the 42 S RNA-negative strand by formation of a loop, which the RNA polymerase does not transcribe but rather "jumps over" (Fig. 10). Once formed, the DI-RNA can autoreplicate, using the RNA polymerase provided by the standard virus. The interfering property of the DI-RNAs is considered to be their ability to prevalently bind to the RNA polymerase (Schlesinger et al., 1975; Bruton et al., 1976; see also Cole and Baltimore, 1973; Huang, 1973). The binding ability and the structure of RNA must be interrelated. It is evident from the work done so far that the 3' end containing poly (A) cannot be the only signal for the RNA polymerase. If it were so, the 26 S RNA should be replicated independently. The finding that part of the 5' end of 42 S RNA is present in the DI-RNAs suggests that both ends are necessary for the binding of polymerase. This conclusion would again speak against the possibility that 26 S RNA has an identical 5' end with the 42 S RNA discussed in the context of RNA replication, favoring the model of internal initiation in the synthesis of 26 S RNA.

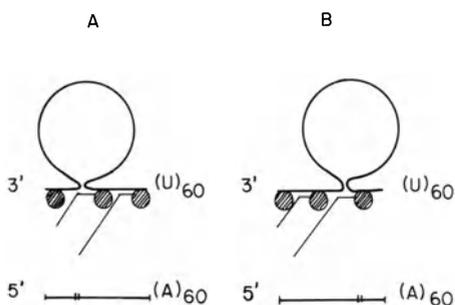


Fig. 10. Hypothetic model for creation of two different types of defective interfering RNAs by transcription of 42 S RNA-negative strand template

The presence of the 5' end of 42 S RNA in the DI-RNAs raises the question of the presence of "caps" in these RNAs. Why do they not serve as messenger, even for incomplete products of translation, as the poliovirus DI-RNA does (*Villa-Komaroff et al.*, 1975)? One would predict that DI-RNAs with translational capacity would be isolated. The other important property provided by the 5' end sequences is probably the binding site for capsid proteins, which makes it possible to encapsidate the DI-RNA (*Bruton et al.*, 1976). As is well-known, the 26 S RNA is not encapsidated during the normal infection and does not seem to bind capsid protein in the cells (*Ulmanen et al.*, 1976). The possible role of defective interfering particles as a cause for chronic infections has been discussed by *Huang and Palma* (1975).

The reason for accumulation of DI particles is not known. It seems evident that DI-RNAs must be produced in every cycle of normal replication, possibly as mistakes in the synthesis of 26 S RNA. These DI-RNAs are encapsidated and obtain entrance to the cell. With the aid of the RNA polymerase of the standard virus, they replicate independently and their proportion increases during the further undiluted passages, causing interference in the replication of the standard virus RNA (*Huang*, 1973). As soon as the amount of standard virus becomes limiting, the replication of DI-RNAs stops. This type of interaction between DI particles and standard virus leads to fluctuation in the yields of standard virus and sometimes to an equilibrium yield of both particles, as has been described by *Johnston et al.* (1975) and *Guild and Stollar* (1975) (for VSV see *Huang*, 1973).

The role of host cells in the ability to replicate DI particles is evidently important, since DI particles isolated in vertebrate cells neither interfere nor stimulate synthesis of aberrant RNAs in *A. albopictus* cells (*Eaton*, 1975; *Igarashi and Stollar*, 1976). In murine cells, the dormant DI particles of the SF virus were readily replicated, causing interference and synthesis of DI-RNAs (*Levin et al.*, 1973). These results suggest that recognition of the binding sites in the DI-RNAs may be regulated by host-specific components.

V. Conclusions

In this review, we have tried to outline the present knowledge about the structure and replication of the α -viruses. The different events of replication are schematically presented in Figure 11. It is obvious that the mechanism for many of the steps needs to be solved. The early events of interaction between host cells and α -viruses is so far poorly known. To date, neither the functions of the envelope glycoproteins nor the nature of the receptors has been determined. The isolated envelope proteins in their water soluble octamer form are presently used in the isolation of receptors, and hopefully this approach will solve the problem (*Helenius*, personal communication).

The mode of penetration and uncoating of α -viruses could be studied, e.g., by using radiolabeled virus and cell fractionation. Immunologic techniques combined with electron microscopy should show whether envelope proteins remain in the plasma membrane or are taken inside the cell.

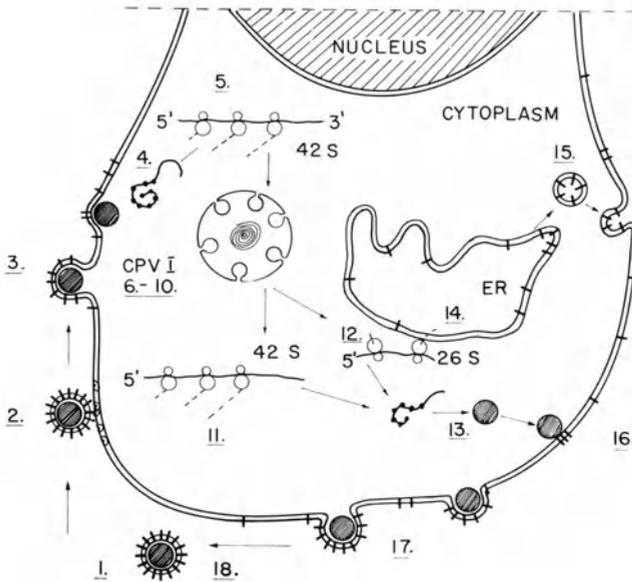


Fig. 11. Simplified scheme of α -virus replication. The virus (1) adsorbs to specific receptors (2) at the plasma membrane, fusing (?) with it (3). The nucleocapsid is released to the cytoplasm and uncoated (4). Ribosomes associate with the 42 S RNA genome, translating nonstructural proteins which are components of the RNA polymerase (*primary translation*, 5). When enough RNA polymerase has been assembled, the translation of the parental RNA is replaced by *primary transcription*, first producing 42 S RNA-negative strands (6) and by their transcription a first progeny of 42 S RNA-positive strands (7). These are used as messengers in the production of more nonstructural proteins during the *secondary translation* (8). Part of the positive strands are used parallelly as templates for synthesis of more negative 42 S RNAs, which in turn are used as templates for synthesis of positive strands (*secondary transcription*, 9). When the concentration of the interconversion protein is high enough, the synthesis of 26 S RNA begins (10). The RNA synthesis probably takes place in cytoplasmic vacuoles (CPV I). The translation of 42 S RNA takes place in free polysomes (11), and the structural proteins are translated into membrane-bound polysomes (12). The progeny 42 S RNA and the capsid protein assemble into nucleocapsids (13). The envelope proteins are protruded into the cisternal side (14) of the endoplasmic reticulum membrane (ER), become glycosylated, first in ER and finally in the Golgi apparatus from which they are transported (15) to the plasma membrane. The nucleocapsid recognizes the spanning part of the envelope protein dimer (p62-E1), preventing its free lateral mobility (16). Increasing interactions between nucleocapsid and envelope proteins lead to protrusion of nucleocapsid into the plasma membrane (17). At this stage, the host cell proteins are excluded from the forming virion and p62 is cleaved to E2 and E3 (?). Finally, the mature virion is released into the medium (18).

The early events of protein synthesis remain a difficult problem because the viral synthesis is minimal in the beginning of infection compared to the host protein synthesis. The early phases of RNA synthesis can perhaps only be studied *in vitro* when the RNA polymerase components have been purified in active form. The mechanism of inhibition of host cell macromolecular synthesis has turned out to be a difficult task with all animal viruses so far.

Perhaps the use of temperature-sensitive mutants will help to solve these problems, as has been approached by *Atkins* (1976).

The shut off of the synthesis of nonstructural proteins late in the α -virus infection in favor of the structural proteins is an interesting problem. Do 42 S and 26 S RNA have different affinities to the ribosomes due to different nucleotide sequences at their 5' ends or are there other factors involved? Actually, direct evidence is lacking that the initiation site for the structural proteins cannot be expressed in the 42 S RNA where this site is internal (*Cancedda et al.*, 1975).

The translation and processing of the structural proteins still leave many unanswered questions; the nascent cleavage of capsid protein is probably essential for the further processing of the whole polyprotein. If the signal hypothesis of *Blobel* and *Dobberstein* (1975 a, b) is applicable for membrane glycoproteins, as it may be (*Katz et al.*, 1977; *Wirth et al.*, 1977), this cleavage is a necessary prerequisite for the release of the signal sequence which should immediately follow the capsid protein in the structural polyprotein. If the cleavage does not occur, the envelope proteins are not transported through the membrane.

Recently, the α -virus glycoproteins have been generally accepted as models for glycoprotein transport. There is fair hope that they will, together with the use of vesicular stomatitis virus G protein, help to establish the transport pathway of membrane glycoproteins from the site of translation to the plasma membrane. They will also provide models for the study of the glycosylation in different cells of vertebrate and invertebrate origin.

Finally, the analysis of the structure of the virus and especially the viral envelope by X-ray crystallographic methods has now become possible when proper crystals of the SF virus have been obtained (*Simons et al.*, 1978). The detailed structural analysis of this virus with its homogenous piece of a biologic membrane is a tremendous task which will yield valuable information in the future.

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Initiation of DNA Synthesis by RNA

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I. Introduction	72
II. Existence of Several Initiation Mechanisms for DNA Synthesis Involving RNA Primers	73
A. DNA Synthesis Starting from an Origin of Replication	74
B. Discontinuous DNA Synthesis	75
C. Replication of Bacteriophage DNA	76
1. Bacteriophages Containing Double-Stranded DNA	76
2. Bacteriophages Containing Single-Stranded DNA	77
D. DNA Replication in Small Animal Viruses	78
E. DNA Synthesis by Reverse Transcriptase	78
III. Evidence for RNA Priming of DNA Synthesis	79
A. Direct Evidence for RNA Priming	79
1. Comigration under Denaturing Conditions of RNA and DNA Labeled with Different Isotopes	79
2. Density Shift in Isopycnic Centrifugation Experiments	79
3. Label Transfer Experiments	80
4. Evidence Derived from Phosphorylation of Terminal Nucleotides	81
5. The Spleen Exonuclease Assay	82
6. Inclusion of Primer RNA in a DNA Strand by Joint Action of T4-DNA Polymerase and T4 Ligase	82
B. Indirect Evidence for RNA Priming	83
1. Inhibition of DNA Synthesis by Drugs Known to Inhibit Transcription	83
a) Rifampicin	83
b) Streptolydigin	84
c) Actinomycin D	84
2. Other Indirect Evidence	85
a) Requirement for a Functional RNA Polymerase in Bacterial Systems	85
3. Requirement of Four Ribonucleoside Triphosphates for Replication	85
IV. The Structure of Primer RNAs	87
V. Proteins Involved in RNA Primer Formation	92
A. RNA Polymerase of <i>E. coli</i>	92
B. DNA Primases	93
1. T7 Gene 4 Protein	94
2. The <i>dnaG</i> Protein	95
VI. Excision of the RNA Primer	97
A. The 5'→3' Exonuclease Activity of DNA Polymerase I	97
B. Ribonuclease H	98
VII. Conclusions	98
References	100

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Abbreviations: Col E1=colicinogenic factor E1 (plasmid coding for colicin E1); *E. coli*=*Escherichia coli*; Eco RI= restriction endonuclease from *E. coli* bearing the resistance transfer factor I (plasmid); Hpa II= restriction endonuclease from *Haemophilus parainfluenza*; iRNA=initiator RNA; RF I=closed, circular, double-stranded replicative form of DNA; RF II= circular, double-stranded replicative form of DNA having a discontinuity in one strand; SS=single-strand; SV 40=simian virus 40.

I. Introduction

Up to the present one of the basic problems for the understanding of DNA replication is how the synthesis of DNA chains is initiated *in vivo*. So far none of the known DNA polymerases of prokaryotic or eukaryotic origin has been shown to initiate the synthesis of a DNA chain *de novo*. All DNA polymerases need a primer, which, in its simplest form, may be an oligoribo- or an oligodeoxyribonucleotide having a free 3'-hydroxyl end (*Karkas and Chargaff, 1966*). This primer terminus can be extended at its 3'-OH end by addition of new nucleotides as directed by the polynucleotide template to which the primer is linked through hydrogen bonds. Although the requirement for a primer has always been realized, earlier studies on DNA synthesis focused more on the mechanism of chain elongation than on the initiation process.

In order to explain how the necessary primer termini could become available inside a cell, several possibilities were considered. One was, for example, that a pool of small oligonucleotides may exist in the cells, consisting of either partial breakdown products of cellular nucleic acids or of specific primer oligonucleotides that would base-pair with the DNA and serve as primers. The basis for this hypothesis was provided by the observation that DNA synthesis by DNA polymerase I *in vitro* could be stimulated by heated extracts from *E. coli*, which were shown to contain fragmented DNA (*Goulian, 1968*). However, despite extensive search no such cellular primer oligonucleotides have been detected.

An alternative model calls for specific nucleases that would introduce scissions into a DNA strand at one or several specific site(s). In that way, 3'-OH ends could be created that would serve as primer terminus for extension by DNA polymerase. For this model, a number of nucleases have been discussed as possible initiators of DNA replication. The formation of the DNA protein relaxation complexes, which may be involved in the replication of the colicinogenic factors E1 and E2 DNAs, may require the action of a specific nuclease (*Blair et al., 1971*), and a model was proposed involving a hypothetical phage-coded "nickase" for the initiation of the replication of T4 DNA (*Kozinski, 1968*). The creation of a 3'-OH end for primer purposes by a specific nuclease seems to be exemplified in the initiation of the viral DNA synthesis of the bacteriophages ϕ X174 and M13. A specific nuclease is coded for by the gene A of bacteriophage ϕ X174 (*Francke and Ray, 1972; Henry and Knippers, 1974; Fujisawa and Hayashi, 1976; Ikeda et al., 1976*). It acts *in vivo* in *cis* fashion specifically on the replicative form DNA of bacteriophage ϕ X174 and introduces a nick into the viral strand. The 3'-OH end of this nick serves as primer for a "rolling circle" type DNA synthesis. Since the gene A product is required

for both the RF to RF replication and the subsequent single-stranded synthesis of bacteriophage ϕ X174 DNA in vitro it appears that it may have additional functions (Eisenberg et al., 1977). The analogous protein for M13 reproduction is the gene 2 product of this phage (Fidanián and Ray, 1972; Lin and Pratt, 1972).

In vitro, many DNA polymerases have been shown to accept oligoribonucleotides as primers (Wells et al., 1972; Chang and Bollum, 1972; Keller, 1972; Tambllyn and Wells, 1975; Plevani and Chang, 1977; Chargaff, 1976). A number of experiments provided evidence that priming of DNA synthesis by RNA might also occur in vivo (Brutlag et al., 1971; Crippa and Tocchini-Valentini, 1971; Ficq and Brachet, 1971). This priming mechanism was attractive because the primer RNA could be synthesized by an RNA polymerase, since RNA polymerases, in contrast to DNA polymerases, are able to initiate ribonucleotide chains de novo on a duplex template (Maitra and Hurwitz, 1965). A brief transcriptional event therefore would be adequate to provide the system with a primer that in turn could be extended by a DNA polymerase. The question has often been raised as to why RNA primers may be of particular advantage over DNA primers. It appears plausible that the answers to this question is related to the ultra-high fidelity that is required for the copying of the DNA and the error-free preservation of the genetic information. As has been stressed in the context of the fidelity requirement in a review article by Alberts and Sternglanz (1977), the initiation of DNA chains bears the highest risk of introducing mistakes. An RNA primer is likely to be more easily recognized as a foreign piece of nucleic acid and erased than a DNA primer. With its removal any error that may have occurred at this step is automatically corrected. Since the formulation of the RNA primer hypothesis several years ago, considerable evidence has been accumulated that indeed RNA priming seems to be one major way of providing the necessary primers for DNA synthesis. To prove the participation of RNA, different approaches have been used in a variety of systems. The purpose of this review is to summarize these approaches and to discuss the significance of the results obtained for the assessment of the role of RNA priming of DNA synthesis. I am aware that this review covers only a very special aspect of DNA replication. Therefore, for a broader view of DNA synthesis and for earlier literature references the reader is referred to a monograph by A. Kornberg (1974) and several recent reviews by Gefter (1975), Geider (1976), and Jovin (1976). Articles on RNA priming of DNA replication have also been published by Kornberg (1976) and by McMacken et al. (1977).

II. Existence of Several Initiation Mechanisms for DNA Synthesis Involving RNA Primers

Biochemical and genetic evidence in the *Escherichia coli* system suggests that a distinction can be made between two RNA-primed initiation mechanisms: one that initiates DNA synthesis starting at the origin of replication, and another, which seems to be employed during the discontinuous propagation of the DNA

chains, and initiates the synthesis of nascent DNA fragments. Still other initiation mechanisms involving RNA primers may be at work in bacteriophage DNA replication. The main types of DNA synthesis for which RNA priming is very probable shall be discussed now.

A. DNA Synthesis Starting from an Origin of Replication

New rounds of replication of the *E. coli* chromosome start at a unique origin of replication, which has been mapped in the vicinity of the *ilv* operon (Bird et al., 1972; McKenna and Masters, 1972; Hohlfeld and Vielmetter, 1973; Louarn et al., 1974). Its position is at about 82 min on the revised genetic map of *E. coli* (Bachmann et al., 1976). Initiation of DNA synthesis at this origin is more directly inhibited by rifampicin, a specific inhibitor of DNA-dependent RNA polymerase than by chloramphenicol (Silverstein and Billen, 1971; Messer, 1972). Therefore, the inhibition by rifampicin seems to be due not to the indirect prevention of protein synthesis but to the inhibition of the synthesis of a necessary RNA. One interpretation of these results has been that a functional RNA polymerase transcribes an RNA that may serve as a core for the assembly of the replication proteins (Lark, 1972a). Whether this interpretation is true or whether the RNA would actually serve as a primer for extension by DNA polymerase is not yet clear. The latter possibility may be true if it turns out that an RNA that can be isolated covalently linked to high-molecular-weight DNA, is the primer RNA for the initiation of DNA synthesis at the origin. Because of its presumed function, this RNA has been termed oriRNA (Messer et al., 1975).

Extrachromosomal elements in *E. coli*, such as plasmids and bacteriophages, to the extent that they depend on the replication machinery of the host, may also make use of this initiation mechanism. The colicinogenic factor Col E1 may be an example. Its replication starts at a unique origin in vivo (Inselburg, 1974; Lovett et al., 1974) as well as in an in vitro system (Tomizawa et al., 1974), and is inhibited by rifampicin, but not by chloramphenicol (Clewell et al., 1972; Tomizawa et al., 1975). Inhibition of the initiation of replication by rifampicin has been reported for other plasmids as well (see below). By fulfilling the criteria of uniqueness of the origin and inhibition by rifampicin, the replication of bacteriophage λ DNA resembles the DNA synthesis in the host starting from the origin of replication. λ -DNA replication starts at a unique site (Schnös and Inman, 1970) that has been mapped between genes *c II* and *O* (Stevens et al., 1971). As shown by genetic analysis, transcription appears to be a necessary prerequisite for the initiation of lambda DNA replication in vivo (Dove et al., 1971) and in an in vitro system (Klein and Powling, 1972). However, it is puzzling that the replication of wild-type λ DNA is inhibited by rifampicin while the replication of a λ -derived plasmid λ dv is not (Hobom and Hobom, 1973). Although this circular dimeric molecule contains two copies of the ori sites, an initiation mechanisms for DNA synthesis different from that used for the wild-type λ DNA seems to be employed for its replication.

B. Discontinuous DNA Synthesis

Once DNA synthesis has started at the origin, further synthesis appears to proceed by a discontinuous mechanism (*Okazaki et al.*, 1973). In contrast to the start of new rounds of replication at the origin, discontinuous synthesis is not inhibited by rifampicin (*Lark*, 1972a).

Deoxyribonucleotides are polymerized by all known DNA polymerases in the 5' to 3' direction into a new DNA strand. Therefore, in principle, one strand of the double helix, the leading strand, could be synthesized continuously while the other, the lagging strand, would require frequent chain starts. However, it appears as if both strands are synthesized discontinuously (*Okazaki et al.*, 1973; *Sternglanz et al.*, 1976) and multiple starts of short DNA pieces, called nascent DNA or Okazaki fragments, occur in both strands. Evidence was first obtained in *E. coli* that the Okazaki fragments are primed by RNA (*Sugino et al.*, 1972). The experimental approaches to show the possible involvement of RNA will be discussed in detail later, but, whichever RNA polymerase may synthesize these RNA primers, it must be different from the well-known RNA polymerase, since as stated above, discontinuous replication is not affected by rifampicin. In *E. coli* the *dnaG* protein is a likely candidate for a primer synthetase. From a study using a temperature-sensitive *dnaG* mutant it has been implicated in the synthesis of the primers for the Okazaki fragments (*Lark*, 1972a), and it has been shown to act as a rifampicin-resistant RNA polymerase in vitro, providing the primer RNA for the conversion of G4 single-stranded viral DNA into the double-stranded replicative form (*Bouché et al.*, 1975b).

The concept of discontinuous replication requires that three problems be solved: (1) RNA serving as primer has to be removed after it has fulfilled its purpose; (2) the gap left after the removal of the RNA has to be filled in with deoxyribonucleotides; and (3) the ends have to be joined in order to form the continuous strands that constitute natural DNA. In the *E. coli* system there is good evidence that DNA polymerase I is responsible (*Olivera and Bonhoeffer*, 1974; *Lehman and Uyemura*, 1976) for both the excision of primer RNA and the filling of the gap. The 5' to 3' nuclease activity of DNA polymerase I can function to remove the primer RNA, and the polymerase activity can fill the gap. Mutants with defects in the 5'→3' nuclease function accumulate 10 S pieces to an abnormally high degree (*Konrad and Lehman*, 1974), which is a strong indication that this enzymatic activity is indispensable for the conversion of Okazaki pieces into larger DNA.

The final joining of the pieces may be accomplished through the action of polynucleotide ligase. This is strongly indicated by the finding that a thermosensitive *E. coli* mutant defective in ligase activity accumulates Okazaki pieces upon a shift to the nonpermissive temperature (*Konrad et al.*, 1974).

Recently, however, a different mechanism has been discovered that can give rise to the transient formation of short fragments (*Tye et al.*, 1977). DNA polymerases can incorporate in vitro dUTP, the natural precursor of dTTP, into DNA (*Bessman et al.*, 1958). However, uracil is not normally found in DNA. This is because in normal cells the level of dUTP is kept very low

by the enzyme dUTPase, and, in addition, cells have excision–repair systems that detect and remove foreign bases from DNA. It was observed in mutants of *E. coli*, originally called *sof*, that radioactive pulse-labeling of the cellular DNA yielded nascent fragments 5–10 times smaller than normal Okazaki fragments (Konrad and Lehman, 1975). *sof* mutants have been found to be identical to *dut* mutants, which are deficient in dUTPase (Tye et al., 1977). Therefore, these mutant cells contain a higher than normal ratio of dUTP to dTTP, and more dUTP than usual appears to be incorporated into their DNA. The uracil residues are quickly removed, possibly by an excision–repair mechanism like that proposed by Lindahl (1976). However, during the repair there are temporary breaks introduced into the DNA that may yield small fragments in pulse-labeling experiments. In view of these results it cannot be excluded that, also in *dut*⁺ cells, a significant proportion of the Okazaki fragments comes from excision–repair and not necessarily from de novo priming events, and that perhaps all of the Okazaki fragments from the leading strand and at least some of the fragments from the lagging strand may arise from the repair reaction.

In eukaryotic cells all DNA, including viral DNA, appears to be synthesized discontinuously (for reviews see Taylor, 1974; Edenberg and Huberman, 1975; Winnacker, 1975). Nascent fragments isolated from nuclei of polyoma-infected cells are smaller than the bacterial Okazaki pieces, about 4 S in size, and they are primed by an RNA for which the name initiator RNA (iRNA) has been proposed (Reichard et al., 1974). However, it has not yet been possible to find out which of the several RNA polymerases present in eukaryotic cells functions in the primer synthesis.

C. Replication of Bacteriophage DNA

1. Bacteriophages Containing Double-Stranded DNA

In contrast to the difficulties encountered in studying the replication of such a large DNA as the *E. coli* chromosome, bacteriophages offer obvious advantages as model systems. By studying the replication of phages like T4, T7 or λ one could hope to gain knowledge about replication mechanisms that may provide clues also applicable to the replication of the host chromosome. Replication starts in vivo at a unique origin on the chromosomes of the bacteriophages T4 (Mosig, 1970), T7 (Dressler et al., 1972), λ (Schnös and Inman, 1970), and P2 (Schnös and Inman, 1971). Short DNA intermediates, taken as an indication for the discontinuous mode of chain propagation, have been reported for T4 (Sugino and Okazaki, 1972), for T7 (Miller, 1972), and for P2 (Kurosawa and Okazaki, 1975). An indication for the RNA priming of T4 replication, obtained by density shift experiments (Buckley et al., 1972; Speyer et al., 1972), should be regarded with reservation (see below). However, RNA primers have also been suggested for the discontinuous replication of phages T4 and P2 on the basis of evidence obtained with the polynucleotide kinase and the spleen exonuclease methods (Okazaki et al., 1975b).

In vitro replication systems reconstituted from purified proteins for T4 replication (Morris et al., 1975; Alberts et al., 1977) and for T7 replication (Masker

and Richardson, 1976; Scherzinger and Klotz, 1975) did not yield conclusive evidence for RNA priming. However, a requirement for all four ribonucleoside triphosphates for optimal T4 replication as well as for T7 replication may indicate that RNA synthesis precedes DNA synthesis.

In addition to rifampicin inhibition mentioned above, evidence for RNA priming of λ DNA replication has been obtained through the functional analysis of short λ DNA fragments cloned into Col E1 plasmid vectors. That analysis revealed that λ replication requires RNA transcription that runs into the segment carrying the t_0 terminator (=oop-RNA terminator). λ -specific, gene O and P-dependent, replication (in temperature-sensitive pol A⁻ cells at the nonpermissive temperature) does not occur when this transcription is blocked either by deletion of the promoter part or by insertion of an extra terminator piece (carrying the λt_{R1} signal) between the promoter and the t_0 terminator. Inversion of the t_0 terminator fragment with respect to the promoter fragment will also abolish the λ -specific replication. However, when a DNA fragment containing both the promoter and the t_0 terminator is inserted inversely with respect to the rest of the plasmid, λ -specific replication does occur (Lusty, M. and Hobom, G., 1977 personal communication).

2. Bacteriophages Containing Single-Stranded DNA

In prokaryotic systems the most convincing evidence for RNA priming of DNA synthesis has come from work on the replication of single-stranded DNA containing bacteriophages such as the filamentous phages M13 and its relatives fd and fl, and the spherical phages ϕ X174 and the related phages G4 and S13. The biology of the filamentous phages has been reviewed by Marvin and Hohn (1969), and their replication by Ray (1977). The biology of the spherical phages has been reviewed by Sinsheimer (1968), and their reproduction recently by Denhardt (1977). For both phage classes the reproductive cycle comprises three stages: At first the circular single-stranded viral strand is injected into the host and immediately used as a template for the synthesis of a complementary strand (SS \rightarrow RF II conversion). The product, named parental replicative form II (RF II), contains the circular, intact viral strand and, annealed to it, an almost complete complementary strand. Yet, a small gap between the 5' and the 3' end remains in the complementary strand. In vitro, this gap can be filled in by DNA polymerase I and the adjacent ends can be joined by ligase. The same mechanism probably works in vivo, too. The resulting double-stranded circular molecule, having two covalently closed DNA strands, is called replicative form I (RF I). During the second stage the duplex RF is multiplied (RF \rightarrow RF). The final stage is the production of progeny single strands, for which a rolling circle type mechanism has been proposed. The duplex RF, which has been nicked in its viral strand by a phage-coded specific endonuclease, serves as primer template for the synthesis of viral strands (RF \rightarrow SS).

Although the overall scheme of reproduction is similar for both the filamentous and the spherical phages, both classes differ in the replication mechanisms of the single stages. Thus far, the SS to RF conversion of M13 viral DNA is the most clear-cut example for RNA priming of DNA synthesis. The reaction

is inhibited by rifampicin in vivo (*Brutlag et al., 1971*) and in vitro (*Wickner, W. et al., 1972*). No inhibition is observed in a rifampicin-resistant RNA polymerase mutant. All four ribonucleoside triphosphates are required for optimal in vitro conversion and are supposedly incorporated into the primer RNA (*Wickner, W. et al., 1972*). In contrast, the SS→RF conversion of ϕ X174 and that of the related phage G4, are not inhibited by rifampicin (*Schekman et al., 1972, 1974*). Yet, RNA priming of the reaction is suggested by several lines of evidence. First, label transfer from [α - 32 P] deoxynucleotides to ribonucleotides has been reported for ϕ X174 (*Schekman et al., 1972*), and a piece of RNA covalently linked to the 3' end of the complementary strand of G4-RF II synthesized in vitro has been isolated. The *dnaG* protein, characterized as a rifampicin-resistant RNA polymerase, is responsible for the synthesis of this primer RNA in vitro on DNA unwinding protein-covered G4 viral strands (*Bouché et al., 1975b*). A comparison of the in vitro replication of phages M13, ϕ X174, and G4 and of their roles, as probes for the investigation of the replication machinery of *E. coli* has been published by *A. Kornberg (1977)*.

D. DNA Replication in Small Animal Viruses

The replication of the double-stranded DNA of small animal viruses such as polyoma and SV40 initiates at fixed origins of replication (*Crawford et al., 1974; Nathans and Danna, 1972*) by a yet unknown mechanism. The chain propagation of both strands follows a discontinuous mode of DNA synthesis (*Fareed and Salzman, 1972; Pigiet et al., 1973*). Studies of the discontinuous replication of polyoma DNA in vitro indicated strongly that the majority of the 4 S DNA chains are initiated by RNA (*Magnusson et al., 1973; Hunter and Francke, 1974*). Nascent fragments during SV40 replication are initiated by RNA as well (*Kaufmann et al., 1977*).

E. DNA Synthesis by Reverse Transcriptase

Synthesis of the proviral DNA of a number of RNA tumor viruses by reverse transcriptase may be primed by transfer RNA molecules tightly associated with the RNA genomes inside the virion. It was first shown for Rous sarcoma virus that a 4 S RNA that remains complexed with the viral RNA after disruption of the virion by detergent serves as a primer for DNA synthesis by reverse transcriptase in vitro (*Dahlberg et al., 1974*). This 4 S RNA was identified as cellular tryptophanyl-tRNA (*Harada et al., 1975*). Although tRNA^{Trp} seems to be a unique genome-associated primer for the avian myeloblastosis virus (AMV) other tRNAs have been found to serve as primers for other viruses. For example, one particular isoaccepting species of tRNA^{Pro} seems to function as a primer for Moloney murine leukemia virus (*Peters et al., 1977*) and tRNA^{Pro} has also been found to be the primer 4 S RNA for AKR, Friend, and Rauscher murine leukemia viruses, for simian sarcoma virus, and for feline leukemia virus (*Waters, 1975; Waters and Mullin, 1976*). The role of tRNA species as primers for the transcription into DNA of RNA tumor virus genomes in vitro

has been reviewed recently by *Taylor (1977)*, *Dahlberg (1977)*, and *Waters and Mullin (1977)*.

III. Evidence for RNA Priming of DNA Synthesis

A. Direct Evidence for RNA Priming

To obtain direct evidence that RNA is serving as the primer for DNA synthesis one approach often used is to demonstrate a covalent linkage between the RNA and the DNA. However, mere demonstration of covalent linkage may not be sufficient to make a primer function plausible. It must be shown, in addition, that the RNA is linked to the 5' end of the DNA. The following methods have been employed for demonstrating covalent RNA-DNA linkage:

1. Comigration under Denaturing Conditions of RNA and DNA Labeled with Different Isotopes

The RNA that primes *in vitro* synthesis of the complementary strand of bacteriophage G4-DNA was shown to cosediment with the newly synthesized DNA in sucrose gradients made up in pure formamide (*Bouché et al., 1975b*). Formamide at high concentrations disrupts hydrogen bonds that may hold together RNA-DNA hybrids and DNA-DNA hybrids (*McConaughy et al., 1969; Casey and Davidson, 1977*). Therefore, the cosedimentation of the primer RNA labeled with ^{32}P together with the newly synthesized DNA, which was labeled with ^3H , indicated covalent linkage between RNA and DNA. A single cleavage site in the synthesized G4 replicative form II DNA for the restriction endonuclease Eco RI served as a reference point to show that the RNA fragment was covalently bound to the DNA at the 5' end. Similarly, it was shown that, under denaturing conditions, RNA which was synthesized by DNA-dependent RNA polymerase of *E. coli* on ϕX174 viral strands served as the primer for covalent extension by DNA polymerase II from human KB cells, and sedimented together with the newly synthesized DNA in a sucrose gradient containing a mixture of deuterium oxide and dimethylsulfoxide, which supposedly disrupts hydrogen-bonded RNA-DNA hybrids, as well (*Keller, 1972*).

2. Density Shift in Isopycnic Centrifugation Experiments

Evidence for covalent linkage between RNA and DNA in nascent fragments isolated from *E. coli* has been derived from the observation that in cesium sulfate isopycnic gradients the buoyant density of nascent DNA pieces labeled by a very brief pulse with $[^3\text{H}]$ thymidine is greater than that of the bulk of the DNA. Furthermore, some $[^3\text{H}]$ uridine-labeled RNA bands in the DNA region in such gradients (*Sugino et al., 1972; Okazaki et al., 1973; Hirose et al., 1973*). Similarly, in Ehrlich ascites tumor cells (*Sato et al., 1972*), in human lymphocytes (*Fox et al., 1973*), in chinese hamster ovary cells (*Taylor, J.H. et al., 1975*), the slime mold *Physarum polycephalum* (*Waqar and Huberman,*

1973), in HeLa cells (*Blinkerd and Toliver, 1974; Olgiati et al., 1976*), and in polyoma (*Magnusson et al., 1973; Hunter and Francke, 1974; Sadoff and Cheevers, 1973*), an increased density of nascent fragments was observed. However, others were unable to detect a higher density of nascent DNA isolated from mouse myeloma cells (*Berger and Huang, 1974*) or mouse P-815 cells (*Gautschi and Clarkson, 1975*), and upon reexamination of the nascent DNA isolated from *E. coli* in the laboratory, where the density shifts originally were observed and interpreted as covalent RNA-DNA linkages, these shifts could not be reproduced (*Ogawa et al., 1977*). Therefore, evidence for covalent linkage between RNA and DNA based on density shift experiments should be considered weak, unless the possibility of the reassociation of RNA and DNA during centrifugation is rigorously eliminated, for instance, by denaturation, and centrifugation of the nascent fragments in the presence of a sufficiently high concentration of formaldehyde to prevent reassociation (*McGhee and von Hippel, 1977*). It has been shown that without such treatment reannealing can occur very readily and simulate a covalent attachment of RNA to DNA (*Mendelsohn et al., 1975; Pearson et al., 1976; Probst et al., 1974; Reichard et al., 1974*).

3. Label Transfer Experiments

Covalent linkage between RNA and DNA has been inferred from the phosphate transfer from deoxyribonucleotides to ribonucleotides at the RNA-DNA junction. For these experiments usually a variation of the nearest neighbor analysis technique is employed, which was originally described for DNA by *Josse et al. (1961)*. At the junction between RNA and DNA a radioactively labeled phosphorus is introduced by incorporation of an [α - ^{32}P] dNTP as the first deoxyribonucleotide of the DNA chain. This radioactive phosphate group is transferred to the last ribonucleotide of the primer RNA either in the 2' or 3' position upon alkaline hydrolysis and allows the unambiguous identification of the donor deoxynucleotide and the acceptor ribonucleotide. Using this approach ribo-deoxyribo linkage has been shown in nascent fragments isolated from toluenized *E. coli* cells (*Sugino and Okazaki, 1973*), in lysates of various mammalian cell lines (*Waqar and Huberman, 1975; Waqar et al., 1975*), and in nascent DNA isolated from nuclei of the slime mold *Physarum polycephalum* injected with radioactive precursors (*Waqar and Huberman, 1975a*). RNA-DNA linkages have also been demonstrated by label transfer experiments in small fragments synthesized in vitro on polyoma virus DNA, (*Magnusson et al., 1973*) and on SV40 DNA (*Anderson et al., 1977*).

For the nascent fragments of permeabilized *E. coli* a predominant ^{32}P transfer from dCTP to UMP or from dGTP to UMP was originally reported (*Sugino and Okazaki, 1973*). Reexamination of these experiments, though, could not confirm these results (*Okazaki et al., 1975b*). Instead, in *E. coli* nascent fragments also, all sixteen possible combinations seem to occur (*Ogawa et al., 1977*) with roughly equal frequency, which would agree with results obtained in nascent fragments isolated from *E. coli* lysates (*Ramareddy et al., 1975*), from the slime

mold *Physarum polycephalum* (Waqar and Huberman, 1975a), and human lymphocytes (Tseng and Goulian, 1975). For polyoma a slight preference of transfer from dC has been reported (Magnusson et al., 1973; Hunter and Francke, 1974). However, repetition of these experiments with an improved technique did not confirm that transfer from one deoxynucleotide is more frequent than from the three others in polyoma nascent fragments, either by label transfer experiments or by polynucleotide kinase labeling of the 3'-terminal deoxynucleotide after removal of the primer RNA by alkali (Pigiet et al., 1974). Specific transfer of label from [α - 32 P] dNMP to 2' (3') rAMP was observed at the primer RNA-DNA junction present in the in vitro-synthesized complementary strand of bacteriophage M13 DNA (Schekman et al., 1972). Also, transfer occurred more frequently to rG and rA than to rU and rC in the RNA-DNA junction of the in vitro-synthesized complementary strand of ϕ X174 bacteriophage DNA (Schekman et al., 1972). Label transfer may appear a convincing way of demonstrating an RNA-DNA junction. However, the use of deoxyribonucleoside triphosphates of very high specific radioactivity, which may be necessary to detect the relatively rare label transfer, for instance, once every 2000 bases in nascent fragments of *E. coli* or only once every 6000 bases during the synthesis of the M13 RF II, includes the risk of picking up artifacts arising, e.g., from misincorporation of ribonucleotides into DNA. Furthermore, as pointed out by Hartman and Werner (1977), some of the label added as [α - 32 P] deoxyadenosine triphosphate could end up in RNA precursors because of nucleotide turnover during the incubation period, and RNA synthesized from these precursors may yield 2',3' ribonucleotides after alkaline hydrolysis indistinguishable from those that arise from direct label transfer.

4. Evidence Derived from Phosphorylation of Terminal Nucleotides

An elegant method for demonstrating linkage of RNA to the 5' end of DNA has been devised using polynucleotide kinase (Hirose et al., 1973). 5'-OH ends of nascent DNA are blocked by primer RNA and are therefore inaccessible to enzymatic phosphorylation by T4 polynucleotide kinase. They become accessible, though, after the ribonucleotides have been removed by alkali treatment and can then be phosphorylated with radioactive phosphorus from [γ - 32 P]ATP. By this method, the ends can be tagged and counted. The method is very sensitive but has the disadvantage that the reaction conditions have to be chosen carefully in order to minimize the exchange of phosphate between ATP and 5'-phosphoryl-terminated DNA fragments, a reaction that is also catalyzed by the kinase (van de Sande et al., 1973). The exchange reaction can be largely suppressed if the incubation temperature during the kinase reaction is kept at 0° C (Okazaki et al., 1975a); however, even under these conditions, as much as 3% of any 5'-phosphoryl-terminated DNA may exchange its terminal phosphate (Ogawa et al., 1977). Therefore, if the amount of free DNA pieces is large relative to the amount of nascent, RNA-containing pieces, the exchange reaction can severely impair accurate measurement of the RNA-DNA linkages by the kinase method.

5. The Spleen Exonuclease Assay

An alternative method for assaying RNA-linked nascent DNA fragments has been developed using spleen exonuclease (*Okazaki et al.*, 1975b; *Kurosawa et al.*, 1975). Only DNA having a free 5'-OH terminus is degraded by spleen exonuclease. Nascent fragments containing an RNA primer would expose a free 5'-OH deoxyribonucleotide end after removal of the ribonucleotides. The presence of RNA covalently linked to DNA at its 5' end therefore would be indicated by the liberation of deoxyribonucleotides after alkali treatment of the nascent fragments. Interference from contaminating DNA fragments having free 5'-OH ends can be prevented by phosphorylation of these fragments with polynucleotide-kinase before the alkali treatment. The spleen exonuclease assay was used successfully to demonstrate the presence of RNA at the 5' end of nascent fragments isolated from *E. coli* cells (*Okazaki et al.*, 1975b).

6. Inclusion of Primer RNA in a DNA Strand by Joint Action of T4-DNA Polymerase and T4 Ligase

Evidence that RNA serves as primer for the *in vitro* synthesis of the complementary DNA strand of the replicative form II (RF II) of bacteriophages M13 and ϕ X174 has been obtained by an ingenious approach: When T4-DNA polymerase and T4 ligase were used to convert *in vitro* the replicative form II DNA of these phages (which has a gap in the complementary strand) into the covalently closed, duplex replicative form I (RF I), this RF I was found to be alkali sensitive (*Westergaard et al.*, 1973). RNA that served as primer was evidently preserved and incorporated into the complementary strand because the T4-DNA polymerase lacks a 5'→3' exonuclease function that appears to be needed for the excision of the primer RNA during the gap-filling process. The RNA is sealed covalently into the complementary strand by T4 ligase, which is able to join DNA and RNA segments (*Lehman*, 1974). In contrast, no covalently closed RF I was formed when *E. coli* ligase, which cannot join DNA and RNA, was used instead of T4 ligase. On the other hand, the RF I formed by the joint action of *E. coli* DNA polymerase I and *E. coli* ligase was alkali insensitive. *E. coli* DNA polymerase I with its 5'→3' exonucleolytic activity apparently removed the primer RNA while filling the gap, and thereby created the conditions necessary for the sealing of the strand by *E. coli* ligase, which can only join adjacent deoxynucleotide ends. Although this approach has not yet found widespread application in other systems, it has proved its potential with the demonstration of the RNA-DNA link in the *in vitro*-synthesized RF IIs of bacteriophages M13 and ϕ X174 (*Westergaard et al.*, 1973). The polymerase ligase method has recently been used to probe for ribonucleotides in M13 RF II isolated from *E. coli* RS 5052, a mutant strain deficient in the 5'→3' exonuclease function of DNA polymerase I. From the analysis it appears as if RF II made under these conditions contains ribonucleotides in both strands (*Dasgupta*, 1977).

B. Indirect Evidence for RNA Priming

1. Inhibition of DNA Synthesis by Drugs Known to Inhibit Transcription

a) Rifampicin

Rifampicin, a derivative of the natural antibiotic rifamycin SV, inhibits the growth of *E. coli* by blocking the activity of DNA-dependent RNA polymerase (Hartmann et al., 1967; Wehrli and Staehelin, 1971; Riva and Silvestri, 1972). The enzyme appears to be the only target of the drug (Tocchini-Valentini et al., 1968; Ezekiel and Hutchins, 1968). So far no other target for rifampicin has become known. Therefore, if it can be shown that DNA synthesis is affected by rifampicin directly and not indirectly via its effect on translation i.e. that the synthesis of a mRNA coding for a protein, which is required for DNA synthesis, is prevented, the inference may be justified that RNA polymerase or at least its β subunit, with which the drug interacts (Heil and Zillig, 1970), plays a role in the DNA synthesis being inhibited, presumably for the synthesis of a primer RNA. Usually the inhibition by rifampicin is contrasted to that of chloramphenicol to distinguish whether transcription is the crucial step or protein synthesis. Thus, it was shown that rifampicin, added at a time in the replication cycle when chloramphenicol was no longer inhibitory, would prevent the initiation of new rounds of replication from the origin in *E. coli* cells synchronized by amino acid starvation (Lark, 1972 b) or by the filtration technique (Messer, 1972). For a number of plasmids and phages, inhibition of replication by rifampicin has been suggestive evidence for the requirement of RNA synthesis. Thus, replication of F-episomes (Bazzicalupo and Tocchini-Valentini, 1972; Kline, 1972, 1973; Hiraga and Saitoh, 1975), the replication of Col E1 in vivo in the presence of chloramphenicol (Clewell et al., 1972) and in vitro in an *E. coli* extract (Sakakibara and Tomizawa, 1974a) or in plasmolyzed cells (Staudenbauer, 1975), and the reproduction of the small minicircular DNA in *E. coli* 15 (Messing et al., 1972) are inhibited by rifampicin. Conversion of the single-stranded DNA of bacteriophage M13 into double-stranded RF II is strongly inhibited by rifampicin in vivo in an *E. coli* wild-type strain but not in a rifampicin-resistant RNA polymerase mutant strain (Brutlag et al., 1971). The conversion is also inhibited in vitro (Wickner, W. et al., 1972). However, a wild-type extract inactivated by the addition of rifampicin will resume synthesis of the complementary strand when purified rifampicin-resistant RNA polymerase is added (Zechel, unpublished results).

A rifampicin-sensitive step seems to precede the synthesis of the complementary strand during the second stage of the M13 reproductive cycle, the RF to RF replication (Fidanián and Ray, 1974). Perhaps RNA polymerase provides a primer RNA during this step, too. The last stage of M13 reproduction, i.e. the synthesis of the viral strands, is also inhibited by rifampicin faster than by chloramphenicol, and on the basis of this differential inhibition, an involvement of RNA polymerase in the viral strand synthesis was suggested (Staudenbauer and Hofschneider, 1972). However, rifampicin appears to affect the viral-strand synthesis indirectly by inhibiting the expression of the gene

5 protein whose concentration inside the cell is crucial for viral-strand production (Fidanián and Ray, 1974).

Inhibition of phage λ DNA replication by rifampicin and, consequently, the involvement of RNA polymerase in its initiation has been mentioned above.

b) Streptolydigin

Streptolydigin, like rifampicin, binds to the β -subunit of RNA polymerase (Heil and Zillig, 1970). The binding is reversible and affects a different site than rifampicin (Ghysen and Pironio, 1972; Iwakura et al., 1973). While rifampicin inhibits initiation of transcription (diMauro et al., 1969), streptolydigin inhibits subsequent chain elongation of the RNA (Schleif, 1969; Cassani et al., 1971). Streptolydigin has been used as an alternative for rifampicin for probing that RNA polymerase plays a role in the initiation for new rounds of replication at the origin of the *E. coli* chromosome (Lark, 1972b) and in the conversion of M13 viral DNA to RF II in vitro (Schekman, et al., 1972). The replication of Col E1 DNA studied in the presence of chloramphenicol is also inhibited by streptolydigin but it was found to be at least 100 times less sensitive than cellular RNA synthesis. In contrast, the inhibition of DNA synthesis by rifampicin was approximately the same as the inhibition of cellular RNA synthesis (Clewell and Evenchik, 1973). The authors speculate that RNA polymerase may be modified for primer synthesis, which makes it less susceptible to inhibition by streptolydigin but not by rifampicin. However, the Col E1 DNA replication in cell-free extracts is fairly sensitive to streptolydigin while relatively high concentrations of the drug are necessary to inhibit the M13 SS to RF conversion. Therefore, the sensitivity to the drug may also be related to the properties of the template.

c) Actinomycin D

This drug is widely used as an inhibitor of transcription. However, it inhibits not only transcription but, although less effective, also replication because it acts by intercalating into duplex DNA and binding to deoxyguanosine (Sobell and Jain, 1972). Inhibition of the conversion of M13 or ϕ X174 viral strands in vitro by concentrations of actinomycin D, just high enough to inhibit transcription but still low enough not to affect replication substantially, was taken together with other evidence to be discussed below to argue that both reactions contain a transcriptional step, presumably the synthesis of an RNA primer (Schekman et al., 1972). The inhibitory effect of actinomycin D on the replication of Col E1 DNA in the presence of chloramphenicol, which was lower than that of rifampicin but comparable to that of streptolydigin, was interpreted as additional evidence for the RNA priming of this reaction (Clewell and Evenchik, 1973). Although actinomycin D is the only drug among those discussed that inhibits transcription by bacterial as well as animal polymerases, the possibility that it already interferes with replication at low concentrations makes it appear less suited for probing the role of transcription for priming of DNA synthesis.

2. Other Indirect Evidence

a) Requirement for a Functional RNA Polymerase in Bacterial Systems

The requirement for a functional RNA polymerase for the synthesis of M13 parental RF in vitro has been demonstrated not only through the inhibition by drugs but also by studies of an RNA polymerase mutant and anti-RNA polymerase antibodies. An extract prepared from a temperature-sensitive RNA polymerase mutant converted M13 viral strands to RF II at the permissive temperature but failed to do so at the nonpermissive temperature (Geider and Kornberg, 1974). From the fact that the conversion in vitro of fd, (or M13 DNA) but not that of ϕ X174 DNA, could be inhibited by antibodies raised against purified RNA polymerase, independent evidence was obtained that RNA polymerase is required for the conversion of fd single-strand, but is dispensible for ϕ X174 viral strand conversion (Wickner, R.B. et al., 1972).

3. Requirement of Four Ribonucleoside Triphosphates for Replication

A requirement of ribonucleoside triphosphates (rNTP) for replication has been observed in many systems and has been taken as an indication that RNA synthesis is coupled to DNA synthesis and may serve the purpose of providing the primer. Since cells are normally impermeable for the highly charged nucleoside triphosphates, these studies are restricted to in vitro systems either in cell extracts or in cells permeabilized for rNTPs by various treatments. In such crude systems it is usually only possible to observe a more or less pronounced stimulation of replication by rNTPs because, despite dialysis or gel filtration steps, there may be still enough rNTP present to meet the possibly extreme low-level requirement of primer RNA synthesis. An up to 20-fold stimulation of the replicative DNA synthesis by ATP (e.g. Moses and Richardson, 1970) is common to the nucleotide-permeable system used to study replication of *E. coli* phages λ or T4 (several systems are described in R.B. Wickner, 1974). Other nucleoside triphosphates can partially substitute for ATP (Vosberg and Hoffmann-Berling, 1971, Pisetsky et al., 1972). However, no evidence has been presented that the ATP requirement is connected to the synthesis of a primer. ATP may be needed just to provide energy for one or several energy-requiring reactions. For instance, ATP is required for the formation of an initiation complex between DNA polymerase III, copolymerase III, and the primer terminus (Wickner, W. and Kornberg, 1973). Several of the proteins involved in the replication process have been shown to possess ATPase activity, notably the *dnaB* protein (Wickner, S. et al., 1974), a replication factor from *E. coli* for ϕ X174 viral strand conversion called Y (Wickner, S. and Hurwitz, 1975c), the rep-protein, which exhibits a single-stranded DNA-dependent ATPase activity during its presumed function of melting duplex DNA in the replicative fork (Scott et al., 1977), and DNA gyrase, which introduces superhelical turns into circular DNA molecules (Gellert et al., 1976). Two other enzymes, termed DNA helicases, have recently been described, which bind to single-stranded DNA regions and unwind adjacent double-stranded regions. This process is dependent on the presence of ATP which is hydrolyzed during the

unwinding step. DNA helicase I may not be involved in DNA replication. DNA helicase II is probably identical with the rep-protein (*Abdel-Monem et al.*, 1976; 1977a, b).

A clear requirement for all four ribonucleoside triphosphates has been shown for the replication of Col E1 in plasmolyzed *E. coli* cells (*Staudenbauer*, 1975) and in a crude cell-free extract (*Sakakibara and Tomizawa*, 1974a). Since, the rifampicin sensitivity of Col E1 replication discussed above, the presence of oligoribonucleotide stretches in Col E1 DNA isolated from cultures grown for several generations in the presence of chloramphenicol (*Blair et al.*, 1972) and the association of RNA with a 6 S replication intermediate isolated in vitro (*Sakakibara and Tomizawa*, 1974b) indicate that RNA primers may initiate Col E1 replication, the requirement for ribonucleotides does fit the picture.

Up to 20-fold stimulation by ribonucleoside triphosphates has been observed for the replication of bacteriophage T7-DNA in vitro in extracts from T7 infected *E. coli* cells (*Strätling et al.*, 1973; *Hinkle and Richardson*, 1974). T7-DNA replication by purified enzymes is also stimulated but not dependent on ribonucleoside triphosphates (*Hinkle and Richardson*, 1975; *Scherzinger and Klotz*, 1975). However, recent studies suggest that the ribonucleoside triphosphates play a role as energy sources for the energy-requiring unwinding of the duplex DNA rather than being precursors for primer RNA synthesis (*Kolodner and Richardson*, 1977). The replication of T4-DNA in a cellophane-disc system prepared from T4-infected *E. coli* shows a threefold stimulation when ATP is added (*Imae and Okazaki*, 1976). With the bacteriophage T4-DNA replication apparatus reconstructed from the purified protein products of the phage T4 genes 41, 43, 44, 45, 62, 32, and the X protein, extensive DNA synthesis on duplex and on single-stranded templates can be achieved. However, initiation of DNA chains de novo on a single-stranded template is found only if ribonucleoside triphosphates are present (*Alberts et al.*, 1975; 1977; *Morris et al.*, 1975). In view of the fact that rifampicin-resistant T4 replication proceeds by a discontinuous mechanism (*Okazaki and Okazaki*, 1969), the ribonucleotides may be used for the synthesis of RNA primers for the Okazaki pieces.

An absolute requirement for all four ribonucleoside triphosphates has been found for the in vitro conversion of the viral SS to RF of the filamentous phages M13 and fd (*Wickner, W. et al.*, 1972; *Wickner, R.B. et al.*, 1972), a result very much in agreement with the notion that RNA polymerase synthesizes an RNA primer for this reaction.

A stimulation of G4-RF II synthesis in vitro by ATP and GTP has been observed (*Zechel et al.*, 1975), and incorporation of all four ribonucleoside triphosphates into an isolatable primer RNA has been described (*Bouché et al.*, 1975a). Nevertheless, the requirement of ribonucleoside triphosphates for the in vitro SS to RF conversion of the viral strand of ϕ X174 and its relatives is still controversial. There seems to be agreement over the principal need of ATP for optimal conversion. However, ATP appears to be involved in one or more reactions preceding the primer synthesis. Thus, it has been described that the formation of a replication intermediate from the ϕ X174 viral template and five proteins, which precedes the *dnaG* RNA polymerase action, requires ATP (*Wickner, S. and Hurwitz*, 1974; *Weiner et al.*, 1976). It has not been

established, in which step(s) the ATP is necessary, but one ATP-dependent reaction during the formation of this replication intermediate could be the association of the *dnaB* and the *dnaC* (D) proteins. Purified *dnaB* protein has been shown to associate with pure *dnaC* protein only in the presence of ATP (Wickner, S. and Hurwitz, 1975a, b).

A strong stimulation by GTP, UTP, and CTP of ϕ X174 RF II synthesis in vitro has been demonstrated by one group (Schekman et al., 1974) and the transfer of label from [α - 32 P] deoxyribonucleotides to all four ribonucleotides appears to support the RNA-primer hypothesis (Schekman et al., 1972). However, others have found that no other ribonucleoside triphosphates were necessary besides ATP for the conversion of ϕ X174 viral strands to the replicative form II in vitro (Wickner, R.B. et al., 1972; Wickner, S. and Hurwitz, 1974). In light of a recent report that the *dnaG* protein can synthesize in vitro an oligonucleotide primer on the DNAs from phages G4 or ST-1, two relatives of ϕ X174, using either deoxyribonucleoside triphosphates or ribonucleoside triphosphates (Wickner, S., 1977), it is conceivable that either substrate may be sufficient for the synthesis of a suitable primer for the conversion of ϕ X174 viral strands to RF II in vitro, and that ribonucleoside triphosphates other than ATP may not be necessary for the synthesis of a primer when deoxyribonucleoside triphosphates are present. The stimulation of primer formation by ADP is an observation that appears to deserve some further attention.

IV. The Structure of Primer RNAs

While direct and indirect evidence suggesting RNA as primer for DNA synthesis is convincing for several systems, notably the M13 and G4 SS to RF conversion in vitro, the polyoma nascent DNA synthesis in vitro, and the discontinuous synthesis in various eukaryotic systems, the isolation and characterization of the primer RNAs has turned out to be extremely difficult. One could conceive of a number of reasons why primer RNAs are so elusive. For example, their function as primer may require them to be very unstable. They are presumably one-way molecules ear-marked for rapid degradation. RNA primers in the nascent pieces, the intermediates during discontinuous replication, ought to be removed as quickly as possible after they have served their purpose. Otherwise they would become obstacles to the formation of a continuous DNA strand. Furthermore, primer RNAs may be very small RNA species, making it difficult to detect and identify them within the cellular RNA pool. Also, the average amount of some RNA primers, e.g. at the origin may be small because they are present only during certain stages of the reproductive cycle. This means that very sensitive methods are required for their detection. Nevertheless, with the refinement of the methods it has become possible to isolate a number of RNA species that are likely to be primer RNAs, and to obtain data with respect to their size and, in some cases, even to their sequences. In early attempts to estimate the size of the primer RNA on Okazaki pieces from *E. coli*, values of 50 to 100 nucleotides were reported. These estimates were based mainly on gel filtration studies combined with density centrifugation analyses

of the RNA-DNA copolymers isolated from *E. coli* after short pulses with radioactively labeled thymidine and/or uridine (Okazaki et al., 1973). However, others were unable to confirm the presence of RNA in nascent fragments isolated from the same *E. coli* strain, or even from *E. coli* mutants that accumulate nascent pieces (Eichler, Thorner and Lehman cited in Uyemura et al., 1976). These mutants were thought to provide better chances for the detection of the primer RNA because they are defective in the 5'→3' exonuclease function of DNA polymerase I, which is presumed to be responsible for the removal of the RNA from nascent pieces. Upon reexamination of the problem in the original laboratory with improved techniques, and this time including in the studies the conditionally lethal DNA polymerase mutants, the authors again concluded that RNA is present in the nascent pieces. However, in contrast to the earlier findings, the size of the primer oligoribonucleotides was estimated to range from mono- to trinucleotides (Ogawa et al., 1977).

Another partly characterized RNA that may be a primer is the ori-RNA, which is believed to initiate the DNA at the origin of replication. It has been estimated to be not more than 500 nucleotides long. This estimate is based on the analysis in polyacrylamide gels of the RNA part that remained after the DNA fraction of the oriRNA-DNA copolymers, isolated from [³H]uridine-pulse-labeled *E. coli* cells, had been digested with DNase (Messer et al., 1975).

Supercoiled circular Col E1 DNA containing a single stretch of RNA in either strand can be isolated after extensive replication in the presence of chloramphenicol, which prevents the replication of the host's DNA but does not interfere with Col E1 DNA replication (Blair et al., 1972). The ribonucleotide stretches occur with equal probability in either the light or the heavy strand of the Col E1 DNA (Williams et al., 1973). Analysis of the RNA showed that the light-strand RNA segment consists of 38 ribonucleotides. The base composition is 17 G, 5 A, 8 C, and 8 U, and the sequence of this RNA segment has been partially determined: 5'...p(rG)p(rG)p(rG)p(rG)p(rA)p(rC)...3'. The deoxyribonucleotide-ribonucleotide junction at the 5' end of this RNA segment is specifically ...p(dC)p(rG)... The RNA segment associated with the heavy strand consists of 15 ribonucleotides with a base composition of 5 G, 2 A, 4 C, and 4 U. The partial sequence of its 5' terminus reads 5'...p(rG)p(rA)p(rA)-p(rU)p(rG)...3' and its deoxyribonucleotide-ribonucleotide junction is uniquely...p(dA)p(rG)... (Helinski et al., 1975; Helinski, 1976). The RNA segments appear to be located at random, or at multiple unique sites. This has been concluded from the analysis of the distribution of gaps created by hydrolysis of the RNA segments with alkali with respect to the single Eco RI cleavage site (Sugino, Y. et al., 1975). The RNA segments, at least in the heavy strand, may be the remnants of the RNA primers of nascent fragments that have not been removed, possibly due to the conditions created by the inhibition of protein synthesis by chloramphenicol during their synthesis (Helinski, 1976). It is puzzling, though, that only a single RNA segment seems to persist per each circle and that the segments having such a distinct sequence are obviously located at many different sites in the heavy strand. If the RNA segment associated with the light strand is the whole or part of the primer RNA that initiated Col E1 DNA synthesis at the origin of replication, it should be comple-

mentary to the heavy-strand DNA at or near the origin of replication. Recently the sequence of the DNA around the origin of replication has been determined (Tomizawa et al., 1977; Bastia, 1977), but no sequence complementary to the light-strand RNA segment was found in this region. Therefore it seems as if the questions concerning the function of the RNA segments in Col E1 DNA synthesized in the presence of chloramphenicol and their possible role as primers for DNA synthesis are still open and have to await further studies to obtain clarification.

Much direct and indirect evidence strongly suggests RNA priming of the M13 or fd SS to RF conversion. The unambiguous identification of the primer RNA synthesized in vitro in crude cell extracts and with purified components has been confounded because other RNA was synthesized as well that was not covalently linked to DNA and therefore did not seem to serve primer functions. The size of RNA segments postulated to be covalently linked to newly synthesized DNA was estimated to be less than 50 nucleotides (Geider and Kornberg, 1974).

The structure of an RNA transcribed from the ori region of bacteriophage fd that is thought to be a primer RNA was recently determined by a different approach. It has been possible to isolate a hairpin-structured fragment of the viral DNA because it is protected against nuclease digestion by RNA polymerase, which specifically and strongly binds to it in the presence of DNA unwinding protein. This DNA region is an efficient promoter and appears to comprise the region where the primer RNA is being synthesized. This oriDNA, as it has been termed, consists of about 125 nucleotides and was found, by annealing it to restriction fragments produced by the endonuclease Hpa II, to map in the fragment H (Schaller et al., 1976). The origin of in vitro SS to RF conversion of M13 phage has been located in or near the same restriction fragment Hpa-H (Tabak et al., 1974). Through recent advances in DNA sequencing techniques (Maxam and Gilbert, 1977), it was possible to sequence the oriDNA (Gray et al., 1977). A corresponding RNA, called oriRNA, was synthesized on phage fd DNA complexed with *E. coli* DNA-binding protein by the action of *E. coli* RNA polymerase (Geider et al., 1978). This RNA has a length of about 30 nucleotides, and it gave a simple fingerprint after T1-nuclease digestion. The characterization of the digest products by fingerprinting and the analysis of the restriction pattern obtained after the RNA had been extended by DNA polymerase I yielded its localization in the origin region. The total sequence of the fd-oriRNA was deduced from the known DNA sequence in this region. The results suggest that the oriRNA starts at the end of a sequence that is protected by RNA polymerase. Six nucleotides upstream from the start point of the oriRNA, the DNA forms a hairpin structure. Half of this hairpin is transcribed, but then the RNA polymerase is presumably stopped by interfering DNA binding protein. Since binding of the DNA binding protein is not sequence specific, termination by this mechanism may cause the different 3'-OH ends of the isolated oriRNA.

RNA polymerase is also involved in the replication of λ DNA. In wild-type λ phage it presumably transcribes a small 4 S RNA, called oopRNA, from within the ori region of the λ DNA, which is believed to serve as primer

to initiate replication (*Hayes and Szybalski, 1973*). The sequence of the *oopRNA* has been determined by RNA sequencing (*Dahlberg and Blattner, 1973*) and has been confirmed through the corresponding DNA sequence (*Scherer et al., 1977*). It is 81 nucleotides long and is the only λ RNA known that starts with pppG... However, whether it serves as primer has not been established unequivocally. Experiments aimed to show that it is covalently linked to newly synthesized DNA did not yield conclusive evidence (*Hayes and Szybalski, 1975*).

The synthesis of an RNA primer for the initiation of complementary strand synthesis of the replicative form (RF II) of bacteriophage G4 has been studied in great detail. This reaction requires three purified proteins: the *dnaG* protein, the DNA-unwinding protein, and the DNA polymerase III holoenzyme complex (*Zechel et al., 1975*). The *dnaG* protein has been shown to act as a rifampicin-resistant RNA polymerase on the DNA-unwinding protein-covered G4-single-stranded DNA. In the presence of ATP, GTP, and UTP several short RNA transcripts were synthesized. These segments can be isolated together with the template in the voided fraction of a gel filtration column (*Bouché et al., 1975a*). Gel filtration analysis of the RNA transcripts after their removal from the template showed that they were fairly homogeneous in size, consisting of about 20 nucleotides (*Bouché et al., 1975b*). Only one of these transcripts, though, is used as a primer for extension by DNA polymerase III holoenzyme and can be isolated associated with the 5' end of the newly synthesized complementary DNA strand (*Bouché et al., 1975a*). This primer was sequenced and its provisional sequence, with some uncertainties in its 3' region, was reported to be pppA-G-U-A-G-G-G-A-C-G-G-C-G-G-C-U-U-U-C-G-C-C-G-U-C-C-A-U...DNA (*Rowen and Bouché, 1976; Bouché et al., 1978*). A G-C-rich region in the middle part of the sequence can be aligned to form a hairpin-like secondary structure. The complementary sequence in the viral DNA probably also exists in a hairpin-like structure and serves as a promoter-like signal to which the *dnaG* protein binds. The triphosphate group at the 5' end indicates that this primer RNA survives its isolation in intact form.

The synthesis of polyoma nascent fragments in isolated nuclei from infected mouse 3T6 cells has been reported to be primed by an oligoribonucleotide called initiator RNA (iRNA) whose size was estimated from gel electrophoresis to be a decanucleotide. The iRNA starts with either ATP or GTP and has an intact triphosphate group at its 5' end (*Eliasson et al., 1974; Reichard et al., 1974*). The sequence of the iRNA seems to be variable but its size seems to be constant. An iRNA, 9–11 ribonucleotides long, with a triphosphate group at the 5' end and two or three deoxynucleotide residues at the 3' end that are not removed by DNase has also been found covalently linked to the nascent pieces synthesized in an in vitro system from cultured human lymphocytes (*Tseng and Goulian, 1977*).

As mentioned earlier, certain cellular transfer RNAs in eukaryotic cells may serve a dual purpose: as isoaccepting tRNA and as primer for the DNA synthesis on the genomes of RNA tumor viruses.

RNA tumor viruses are replicated via a DNA intermediate, called a provirus, which is synthesized on the viral 70 S RNA genome (*Temin, 1974*). Proviral DNA can be synthesized in vitro either with the endogenous RNA dependent-

DNA polymerase (reverse transcriptase) present in the virion (*Temin and Mizutani, 1970; Baltimore, 1970*) or in reconstituted systems with isolated RNA and purified reverse transcriptase (*Faras et al., 1973b; Junghans et al., 1975; Haseltine et al., 1976*). In reconstituted systems, the enzyme isolated from Rous sarcoma virus accepts DNA- and RNA-DNA hybrids as templates for DNA synthesis and extends 3'-OH termini in a repair-like mode (*Duesberg et al., 1971; Hurwitz and Leis, 1972; Leis and Hurwitz, 1972*). The 70 S RNA complex extracted from purified virus has been found to be an excellent primer-template. This complex consists of two molecules of 35 S RNA (*King, 1976*) and several molecules of 4 S tRNA and 5 S rRNA (*Faras et al., 1973a*). The 35 S subunits are identical (*Beemon et al., 1974; Billeter et al., 1974; Quade et al., 1974*). When the RNAs were denatured by heat, and separated, the single species were found to be poor templates. However, they regained as much as 60% of the original template efficiency when allowed to reassociate (*Canaani and Duesberg, 1972*). Especially the reassociation of the 35 S species and the 4 S RNA seemed to be required, and it was concluded that a 4 S RNA hydrogen-bonded to the 35 S RNA may act as primer. The primer function of the 4 S RNA was shown by the isolation of that RNA covalently linked to newly synthesized DNA (*Verma et al., 1971*) and by demonstrating that [α - 32 P] label was transferred from dC to rC and from dA to rA, respectively (*Flügel et al., 1973*). Denaturation and degradation of the DNA by pancreatic DNase was shown to release an RNA species with the mobility in gels of tRNA (*Faras et al., 1973a*). In the case of AMV this 4 S RNA was identified as tryptophanyl tRNA (*Harada et al., 1975*). The tRNA^{Trp} found as primer RNA associated with the virions can be assumed to be identical with the normal cellular tRNA^{Trp} since in chicken cells there is only one isoaccepting tryptophanyl tRNA. The reason for its preferential use as primer for viruses of the avian sarcoma-leukosis group is not yet known. The association of the tRNA^{Trp} that can serve as primer seems to be very tight. Partial denaturation at 60 °C of the 70 S RNA complex, which would suffice to split the 35 S subunits and release all the loosely bound 5 S rRNAs and 4 S tRNA (including some tRNA^{Trp} that does not serve primer purposes), is apparently inadequate to remove the primer tRNA^{Trp}. The 35 S species isolated after the partial denaturation are still excellent template-primers in vitro. Upon further heating to 80 °C, though, release of about one molecule tRNA^{Trp} per 35 S RNA and a concomitant decrease in template efficiency were observed (*Dahlberg et al., 1974; Sawyer and Dahlberg, 1973; Canaani and Duesberg, 1972*).

Another line of evidence suggested that the primer tRNA^{Trp} associated with the 70 S viral RNA is identical with the cellular tRNA^{Trp}: The template activity of isolated inactive 35 S RNA could be almost completely restored when tRNA^{Trp} isolated from uninfected cells was reannealed to the template 35 S RNA (*Faras and Dibble, 1975; Sawyer et al., 1974; Taylor, J.M. et al., 1975*). The tRNA^{Trp} appears to bind at a distinct site near the 5' terminus of the 35 S RNA (*Taylor and Illmensee, 1975; Cashion et al., 1976; Shine et al., 1977*). There is evidence that only part of the tRNA^{Trp} may be involved in the actual binding to the template. Nucleotides 2-17, as numbered from the 3' end, are resistant to RNase attack in high salt, which may be an indication that they

are tightly base-paired with the template (Cordell et al., 1976; Eiden et al., 1976). For efficient primer function, the whole, intact tRNA does not seem to be required. The 3' half of the molecule, which can be obtained by controlled nucleolytic cleavage, still binds to the 35 S RNA at the 5'-terminal site and is recognized as primer terminus by the RNA-dependent DNA polymerase (Brown and Armentrout, 1977). Although, among the avian sarcoma leukosis virus group only tRNA^{Trp} seems to serve as primer, this tRNA^{Trp} needs not be from homologous sources. tRNA^{Trp} isolated from bovine liver has been shown to substitute for the avian-derived species and primes DNA synthesis on the 35 S avian RNA subunit (Baroudy et al., 1977). Whether bovine tRNA^{Trp} can functionally fully substitute for avian tRNA^{Trp}, though, is not completely clear, since the product of the DNA synthesis primed by the heterologous primer RNA has not been characterized.

V. Proteins Involved in RNA Primer Formation

A. RNA Polymerase of *E. coli*

As indicated by the rifampicin sensitivity of the DNA synthesis in several bacterial systems, the classical DNA-dependent RNA polymerase appears to be one of the enzymes that is involved in the synthesis of primer RNA. It is not yet clear how the primer-synthesis by RNA polymerase is regulated. Possibly, unique structures may exist, or may be shaped through the association of DNA-binding proteins on the DNA at or near the origin of replication as signals for RNA polymerase to bind and synthesize a primer RNA. One may expect similar structural elements in the DNA sequences around the origin of replication of, for instance, *E. coli*, bacteriophages, and plasmids whose replication depends on RNA polymerase, but these structural elements need not necessarily be similar to the promoter sequences known to be recognized by RNA polymerase for messenger RNA synthesis (Gilbert, 1976). RNA primers appear to be shorter than mRNA or even tRNA. Presumably, a termination signal for RNA polymerase follows shortly after the initiation signal. Whether termination requires accessory protein factors is not known, but for the regulation and timing of the primer-synthesis during the replicative cycle additional proteins are probably required. Analysis of temperature-sensitive mutants has shown that besides RNA polymerase at least the products of the genes *dnaA* and *dnaC* (Wechsler and Gros, 1971; Zyskind et al., 1977), of *dnaI* (Beyersmann et al., 1974), and *dna-252*, which is a *dnaB* mutant (Zyskind and Smith, 1977), may be involved in the initiation of DNA synthesis at the origin of *E. coli* replication. The *dnaH* mutation, which has been described by Sakai et al. (1974) to cause a defect in the initiation at the nonpermissive temperature, probably does not code for still another protein. It appears to be a double mutant whose defect in initiation is due to a lesion in the *dnaA* gene (Derstine and Dumas, 1976). The precise role of all these accessory proteins is unknown. However, available evidence seems to suggest that the *dnaA* gene product functions like a repressor regulating the initiation of new rounds of chromosome replication in *E. coli* (Messer et al., 1975). RNA polymerase is apparently also responsible for the

primer-synthesis in the conversion of viral strands of filamentous bacteriophages to the duplex replicative form II. Evidence obtained *in vivo* (Horiuchi and Zinder, 1976) and *in vitro* in cell-free extracts of *E. coli* (Tabak et al., 1974) suggests that the primer RNA is synthesized at a unique site on the genome of filamentous phages. Studies with purified components indicate that covering of the single-stranded template with DNA-unwinding protein is required to restrict the initiation of RNA synthesis by RNA polymerase to a single site (Geider and Kornberg, 1974). The presence of DNA-binding protein obviously directs RNA polymerase to start an RNA chain only at a unique initiation site on the viral DNA. RNA polymerase can initiate in the absence of DNA-binding protein at multiple sites on purified viral DNA from bacteriophage $\phi 1$ (Stavriano-poulos et al., 1972) or M13 (Geider et al., 1978). The unique site of the primer-synthesis appears to be part or all of the hairpin region in the viral DNA, which, probably because of its double-stranded structure, is not covered by single-strand (specific DNA-binding protein, and therefore remains accessible to RNA polymerase (Schaller et al., 1976). The origin for the synthesis of M13 progeny viral strands (Suggs and Ray, 1977) seems to be in the same region, but on the opposite strand. However, it remains to be seen whether this region, again, is a site where RNA polymerase initiates a primer RNA for viral DNA synthesis. Although the DNA-binding protein prevents RNA polymerase from forming primers adventitiously on M13 (fd) DNA, it does not do so on $\phi X174$ viral DNA. The *in vitro* system that primes M13 viral strand will also prime $\phi X174$ viral strands, and these primers can be utilized by DNA polymerase I or III for the synthesis of $\phi X174$ complementary DNA *in vitro*. This reaction may be a salvage pathway for the priming of $\phi X174$ DNA replication *in vivo* when the usual priming mechanism is inoperative. For instance, the $\phi X174$ replication in a *dnaC* mutant at the nonpermissive temperature may be primed by RNA polymerase (Dumas et al., 1975). However, in normal *E. coli* cells, the parental RF II synthesis of $\phi X174$ is, in crude extracts *in vivo* and *in vitro*, completely insensitive to rifampicin and therefore independent of RNA polymerase. To explain the distinction between both single-strand phage DNAs, it has been suggested that factors exist that allow primer-synthesis by RNA polymerase only on M13 (fd) DNA, but not on $\phi X174$ DNA. One such discriminatory factor has been described that forms a complex with the RNA polymerase. It appears to be a protein that is released from the enzyme by rifampicin (Wickner, W. and Kornberg, 1974), and its presence directs RNA polymerase to synthesize a primer RNA only on M13 DNA and to ignore $\phi X174$ DNA *in vitro*.

Two other factors described by Vicuna et al. (1977a, b) operate by a different mechanism. They appear to protect specifically the primer formed on fd DNA from being degraded by RNase H, a constituent of the *in vitro* assay mixture. RNA that may have been formed erroneously on $\phi X174$ DNA seems to be eliminated by the enzyme before it can serve as primer for DNA synthesis.

B. DNA Primases

The term DNA primase was first suggested for the T7 gene 4 protein (Scherzinger et al., 1977). It was probably meant to imply that this protein, although in

principle an RNA (or DNA) polymerase, is highly specialized for the synthesis of primers for DNA replication. This definition would also apply for the *dnaG* protein. The gene 41 protein of bacteriophage T4 (*Alberts et al.*, 1975) may also turn out to be a DNA primase.

1. T7 Gene 4 Protein

Genetic and biochemical analysis have shown that two proteins, the phage-induced DNA polymerase and the protein encoded by gene 4 of phage T7, play a major role in the replication of bacteriophage T7. The T7 DNA polymerase, as all other known DNA polymerases, is unable to initiate DNA chains *de novo*. However, in combination with gene 4 protein, extensive DNA synthesis was catalyzed *in vitro* by T7 DNA polymerase on the natural template, double-stranded T7 DNA (*Strätling et al.*, 1973; *Hinkle and Richardson*, 1974) as well as on a variety of other templates (*Scherzinger and Litfin*, 1974). Stimulation of DNA synthesis by the gene 4 protein seemed to suggest a function of this protein in the initiation of DNA strands (*Hinkle and Richardson*, 1974; *Scherzinger and Klotz*, 1975), and the stimulation of the reaction by ribonucleoside triphosphates seemed to indicate that an RNA might be synthesized to serve as primer. Neither enzyme alone showed RNA polymerase activity, yet, together, purified gene 4 protein and T7 DNA polymerase synthesize *in vitro*, in a ribonucleoside triphosphate-dependent reaction on single-stranded ϕ X174 DNA, an RNA-DNA copolymer whose RNA part consists of a tetranucleotide of the sequence pppApCpCpA-(DNA).. (*Scherzinger et al.*, 1977a, b). However, the appearance of the primer by which DNA synthesis on duplex T7 DNA is initiated, and whether it is an RNA, are not yet known. The ribonucleoside triphosphates that stimulate the replication of T7 DNA two to fourfold may also be required for another function that has recently been suggested for the T7 gene 4 protein (*Scherzinger et al.*, 1977a; *Kolodner and Richardson*, 1977). The T7 gene 4 protein has been shown to be a single-strand DNA-dependent nucleoside 5'-triphosphatase, and it appears also to hydrolyze triphosphates during the replication of the duplex T7 DNA template. It was proposed that the hydrolysis serves to provide the energy for the necessary unwinding of the DNA strands. With respect to this function, the T7 gene 4 protein may be comparable to the rep-protein of *E. coli* (*Scott et al.*, 1977).

Highly purified T7 gene 4 protein preparations consist of a mixture of two polypeptides with molecular weights of 57,000 and 66,000 (*Hinkle and Richardson*, 1975; *Scherzinger et al.*, 1977a). Both polypeptides seem to be the product of the T7 gene 4 because both are absent in cells infected with T7 gene 4 amber mutants. Since the tryptic peptide maps of the two polypeptides labeled with radioactive ^{125}I are almost identical, the small polypeptide could be a proteolytic cleavage product of the larger one. Looking at DNA polymerase I of *E. coli* as an example of the fact that proteolytic cleavage of a multifunctional protein can lead to the separation of enzymatic activities (*Kornberg*, 1974), one might wonder whether the two polypeptides found in the T7 gene 4 protein preparations may also differ in functional capabilities.

2. The *dnaG* Protein

Synthesis of the parental replicative form of the bacteriophages ϕ X174 and G4, a close relative of ϕ X174 (Godson, 1974), is not inhibited by rifampicin, nor is the initiation of the nascent fragments during the replication of the *E. coli* chromosomal DNA inhibited by the drug. Yet, evidence, which has been discussed above, suggests that in all three cases DNA synthesis is primed by RNA. The synthesis of such a primer RNA clearly would require a rifampicin-resistant RNA polymerase. In vitro studies of the parental RF II synthesis of bacteriophage G4 have yielded evidence that the *dnaG* protein may possess the rifampicin-resistant RNA polymerase activity that is required for the synthesis of the G4 RNA primer. The *dnaG* protein catalyzes the polymerization of all four ribonucleoside triphosphates on G4 viral strands covered with DNA-binding protein. This RNA synthesis is not affected by rifampicin. Although in the in vitro reaction several short oligoribonucleotides are generated, apparently only one serves as primer for the synthesis of the complementary DNA strand (Bouché et al., 1975b). The others are presumably degraded, or removed during the elongation of the DNA chain by a strand displacement reaction. The *dnaG* protein was originally characterized by a temperature-sensitive mutant of *E. coli*, which, upon transfer to the nonpermissive temperature, would cease DNA synthesis almost immediately. On the basis of this result it was proposed that the *dnaG* gene product is involved in DNA chain elongation (for review see Gross, 1972). Closer examination of this phenomenon in *E. coli* cells led Lark (1972a) to conclude that the *dnaG* protein may participate in the priming of the Okazaki pieces. Studies of phage growth in *dnaG* ts mutants at the nonpermissive temperature have shown that a functional *dnaG* gene product is also required during the initial stages of the reproductive cycle of ϕ X174 (Mc Fadden and Denhardt, 1974) and Ha₂, a ϕ X174 mutant able to grow on *E. coli* K12 (Truffaut and Manheimer, 1975). The *dnaG* function is not required, for the parental RF formation from the infecting M13 viral strand, but it seems necessary for the RF to RF synthesis step (Ray et al., 1975). Surprisingly, the parental RF formation of phage G4, which was shown to be dependent on the *dnaG* protein in vitro, did not appear to be impaired in vivo at the nonpermissive temperature in two *dnaG* ts mutants (Derstine et al., 1976). However, the subsequent step, the RF to RF replication, would not take place in these mutants at the nonpermissive temperature. To reconcile the discrepancy between in vitro and in vivo results the authors speculate that the *dnaG* protein coded by the alleles they used in their experiments may have a partial lesion that would affect its function during RF to RF synthesis but not its function during the priming of the parental RF synthesis.

A functional *dnaG* protein also seems to be necessary in several other systems. Thus, the synthesis of the putative primer RNA (oopRNA) for bacteriophage λ replication depends on a functional *dnaG* protein. Besides the *dnaG* protein, the *dnaB* protein, RNA polymerase, and the products of the λ genes O and P are required (Hayes and Szybalski, 1975). The replication of plasmid Col E1 DNA was shown to be dependent on the *dnaG* function (Collins et al., 1975). The bacteriophage P2 also requires a functional *dnaG* gene product

for its replication, but the satellite phage P4 seems to be replicated by a different mechanism. Its reproduction is normal in *dnaG* ts mutants at the nonpermissive temperature (Bowden et al., 1975). Perhaps the rifampicin-resistant RNA polymerase activity induced by P4 can substitute for the *dnaG* function for the primer synthesis (Barrett et al., 1972).

The *dnaG* gene has been mapped between the *tol C* and the *uxa C* marker genes (Chen and Carl, 1975) corresponding to a location at about 60 min on the recalibrated *E. coli* linkage map (Bachmann et al., 1976). The availability of the *dnaG* ts mutants has greatly facilitated the isolation of the *dnaG* protein. They provided the basis for the development of a complementation assay that was used to monitor the purification procedure. Three laboratories reported the isolation of the *dnaG* protein (Klein et al., 1973; Wickner, S. et al., 1973; Bouché et al., 1975b; Rowen and Kornberg, 1978a). All three procedures yield a protein of approximately 60,000 daltons. According to sedimentation studies and gel electrophoresis under native and denaturing conditions, it appears to exist in solution as a monomeric molecule. When the protein is purified from *dnaG* ts cells, it is more thermolabile than the wild-type enzyme, which is strong evidence that the purified protein is indeed the *dnaG* gene product. As mentioned earlier, the *dnaG* protein exhibits rifampicin-resistant RNA polymerase activity on DNA-binding protein-covered G4 viral strands if all four ribonucleoside triphosphates are present. It does not accept M13 viral strand in the presence of DNA unwinding protein (Schekman et al., 1974). The resolution of the parental RF formation of ϕ X174 in vitro into a two-stage reaction showed that the *dnaG* protein is not required during the first stage when the viral DNA template is converted into a so-called activated form. The *dnaG* protein is required, presumably for the synthesis of the primer on this activated form DNA, during the second stage (Ray et al., 1976). This activated form DNA is probably identical to an isolatable "replication intermediate" that is formed upon incubation of five proteins—protein i, protein n, DNA-unwinding protein, *dnaB* protein, and *dnaC* protein—with ATP and ϕ X174 viral DNA (Weiner et al., 1976). In the replication intermediate the *dnaB* protein has been suggested to function as a "mobile promoter" serving as a recognition signal for the *dnaG* protein (McMacken et al., 1977). When *dnaG* protein is incubated with the replication intermediate and the four ribonucleoside triphosphates, multiple short RNA transcripts, each approximately 20 nucleotides long, are synthesized (McMacken and Weiner, 1976). Recently, however, it was found that the *dnaG* protein not only has RNA polymerase activity forming oligonucleotides from ribonucleoside triphosphates but it also seems to have DNA polymerase activity, and can also incorporate deoxyribonucleoside triphosphates into short oligodeoxyribonucleotide chains on the G4 template in vitro (Kornberg, 1977). Even a hybrid ribonucleotide-deoxyribonucleotide transcript is formed if both ribonucleotide triphosphates and deoxyribonucleotide triphosphates are present in the reaction mixture (Rowen and Kornberg, 1978b). Either nucleotide can serve as primer for chain elongation by DNA polymerase II or III in combination with *dnaZ* protein and DNA elongation factors I and III. The product is an almost full size complementary strand (Wickner, S., 1977). It remains to be seen which of the priming modes is physiologically relevant.

Perhaps both RNA and DNA priming by the *dnaG* protein, can occur in parallel inside the cell. Then the *dnaG* protein would be the first example of a DNA polymerase capable of initiating a new chain.

Besides the *dnaG* protein several other rifampicin-resistant RNA polymerases have been described. Most of them are either products of bacteriophage genes, like the RNA polymerase of T7 (Chamberlin et al., 1970) and T3 (Dunn et al., 1971; Maitra, 1971), or at least they are induced after infection, as is the case with the *Bacillus subtilis* phage PBS2 (Clark et al., 1974) or the *Pseudomonas putida* phage gh-1 (Towle et al., 1975). A rifampicin-resistant RNA polymerase has also been found associated with the virion of the coliphage N4 (Pesce et al., 1976). However, whether these RNA polymerases play a role in primer synthesis during phage DNA replication remains to be shown.

Another rifampicin-resistant RNA polymerase activity present in cytoplasmic membranes and DNA protein complexes isolated from uninfected *E. coli* cells has been purified and tested for its possible involvement in primer-RNA synthesis for DNA replication, but no positive evidence was obtained (Ohasa and Tsugita, 1976). This enzyme is structurally very different from the *dnaG* protein. The properties of the enzyme isolated from a *dnaG* ts mutant are not different from those of the enzyme isolated from wild-type cells. It does not substitute for the *dnaG* protein in priming G4 complementary strand synthesis in vitro nor does it complement *dnaG* ts mutant extracts in vitro. Therefore it is apparently not related to the *dnaG* protein.

VI. Excision of the RNA Primer

The necessarily transient nature of RNA primers calls for enzymatic mechanisms for the excision of the primer RNA. In *E. coli* the 5'→3' exonucleolytic activity of DNA polymerase(s) seems to be the most likely candidate for this job, although the specificity of ribonuclease H for the RNA part of an RNA-DNA hybrid may also be perfectly suited for the removal of an RNA primer.

A. The 5'→3' Exonuclease Activity of DNA Polymerase I

DNA polymerase I of *E. coli* has, besides its polymerase activity also a 5'→3' exonuclease activity capable of degrading polyribonucleotides and polydeoxyribonucleotides (Kornberg, 1974; Lehman and Uyemura, 1976). In vitro, this nuclease function was shown to remove the oligoribonucleotide primers from the 5' end of a growing DNA chain (Roychoudhury and Kössel, 1973). Both functions of DNA polymerase I are required in a concerted action together with *E. coli* ligase to convert the in vitro-synthesized M13 replicative form II into the covalently closed double-stranded replicative form I. The polymerase is believed to fill in the gap in the complementary strand of the RF II while the 5'→3' nuclease excises the RNA primer. The two adjacent DNA ends can then be joined by *E. coli* ligase (Geider and Kornberg, 1974). Interestingly, the DNA polymerase III holoenzyme, which is present for the synthesis of

the complementary strand of RF II, is obviously unable to fill the gap and/or excise the RNA-priming fragment, although it too has a 5'→3' exonuclease associated with it (*Livingston and Richardson, 1975*). It is not clear whether the 5'→3' exonuclease of DNA polymerase I is also responsible for the primer excision in vivo. Col E1 DNA isolated from a thermosensitive pol A⁻ mutant after a shift to the nonpermissive temperature is sensitive to alkali and pancreatic RNase. It has been suggested that this may be due to the lack of an excising nuclease function (*Goebel and Schrempf, 1973*). However, this evidence seems rather indirect. More direct evidence comes from the studies on a conditional lethal mutant of *E. coli* defective only in the 5'→3' exonuclease function of DNA polymerase I. These cells accumulate small nascent DNA fragments at the nonpermissive temperature. Since the polymerase I activity is normal under these conditions, the accumulation of short fragments seems to be due to the missing nuclease function, which may be required to remove RNA primers from those fragments (*Konrad and Lehman, 1974*). Without excision of the RNA *E. coli* ligase cannot seal the nicks between fragments because *E. coli* ligase is unable to join RNA and DNA.

B. Ribonuclease H

RNase H was first isolated from calf thymus (*Hausen and Stein, 1970*), but it has also been found in *E. coli* (*Henry et al., 1973; Miller et al., 1973; Berkower et al., 1973*), in yeast (*Wyers et al., 1973*), and associated with the RNA-dependent DNA polymerase of RNA tumor viruses (*Mölling et al., 1971*).

RNase H specifically degrades the RNA moiety of RNA-DNA hybrids and therefore seems especially suited for the excision of RNA primers. The RNase H activity found as an unseparable constituent of the viral reverse transcriptase (*Keller and Crouch, 1972; Baltimore and Smoler, 1972; Leis et al., 1973*) may be conceived to have an obvious function in the degradation of the tRNA primer and eventually of the whole viral RNA to allow synthesis of a complete double-stranded proviral DNA.

Whether the cellular RNase H is engaged in the excision of RNA primers remains to be demonstrated. In *E. coli* it is probably not. One could argue that, in *E. coli*, RNase H cannot substitute for the 5'→3' nuclease function of DNA polymerase I. If it were able to substitute, one should expect to see no accumulation of Okazaki fragments in the 5'→3' nuclease-deficient mutant of *Konrad and Lehman (1974)* at the nonpermissive temperature, because RNase H, which was probably not defective in this mutant, could have removed the primer RNA thought to be obstructive for the joining of the fragments.

VII. Conclusions

There can be no doubt that, in a number of cases, RNA serves as a primer for DNA synthesis. Ample demonstration in vitro that RNA can be a primer for DNA chain initiation by DNA polymerase from prokaryotic as well as

eukaryotic organisms may justify the conclusion that RNA priming may also be one way in which DNA synthesis is initiated *in vivo*. The inhibition of the replication in bacterial systems *in vivo* by rifampicin is one major argument for this conclusion. Primer-synthesis by RNA polymerase, which is affected by the drug, may be especially advantageous for the initiation of DNA synthesis at specific sites, for example at the origin of replication. RNA polymerase of *E. coli* is, in contrast to DNA polymerase, able to recognize specific signals on DNA. It can, in addition, be directed by factors to respond to such signals at a certain time during the replicative cycle. Therefore, the initiation of new rounds of DNA replication can be effectively controlled via regulation of primer-RNA synthesis by RNA polymerase. It can be hoped that cloned fragments of the *E. coli* genome containing the origin of replication, like the one described by Marsh and Worcel (1977), will facilitate the studies on the regulation of the DNA chain initiation at the origin of replication and will also facilitate the determination of the components that are involved in this step.

For the more basic questions about the mechanisms of primer-RNA synthesis and its degradation, the parental RF II formation of the filamentous bacteriophages M13, fd, f1 still appears to provide the most promising system because of its relative simplicity and its advanced characterization. It also may offer the best possibilities at present to correlate *in vitro* and *in vivo* data. Insofar as the initiation site for the primer synthesis appears to be identical *in vivo* and *in vitro* there is a high probability that results on the primer-RNA synthesis obtained *in vitro* indeed reflect the *in vivo* situation. Furthermore, because the part of the sequence of the fd genome containing the replication origin is known (Gray et al., 1977), and because it was possible to pinpoint exactly the base sequence where RNA polymerase initiates and terminates the primer RNA *in vitro* it may also become possible to elucidate the fate of that primer inside the cell.

Another reason to claim that RNA is priming DNA synthesis *in vivo* is the observation that RNA fragments, covalently linked to short nascent DNA (Okazaki pieces), could be isolated from pulse-labeled *E. coli* cells. However, the apparent difficulties involved in repeating these experiments together with the discovery of an excision-repair mechanism that was shown to produce fragments similar in size to Okazaki fragments without involving RNA primers (Tye et al., 1977) make this argument crumble. Aside from these findings it looks as if nascent DNA pieces during discontinuous chain elongation could be, but *need not* be initiated by RNA. The recently discovered ability of the *dnaG* protein to synthesize *in vitro* oligonucleotide primers on G4 DNA either from ribonucleoside triphosphates and/or deoxyribonucleoside triphosphates makes it necessary to consider the possibility of Okazaki pieces without RNA primers in bacterial systems *in vivo*.

Good evidence for RNA priming of discontinuous replication has been obtained in eukaryotic *in vitro* systems. However, due to the complexity of these systems almost nothing is known about the enzymes involved in the primer-RNA synthesis. The primers isolated from *in vitro* replication systems from animal cells were found to be six to ten ribonucleotides long. They have apparently no specific sequence. In contrast to earlier reports, the lack of

sequence specificity has been recently confirmed for bacterial RNA primers of discontinuous replication. The question then arises as to how these primer RNAs are initiated and how they are terminated. Perhaps the suggestion by *Reichard et al.* (1974) is correct that the length of the primer is the signal for its termination and that its sequence is unimportant. But what is the signal for its start? No experimental proof has yet been provided for the theory put forward by *Okazaki et al.* (1973), i.e., that signals for the initiation may exist at regular intervals on the DNA. Based on observations made during bacteriophage fd SS to RF conversion *in vitro*, *Gefter and Sherman* (1977) suggest that self-complementary sequences may play an important role as signals for the initiation of Okazaki fragments. It appears as if one key to the solution of the recognition problem lies in the DNA sequence. Therefore it can be hoped that the examination of known and forthcoming DNA sequences will provide some clues as to whether such signals exist and what their structure might be.

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Speculations on the Role of Major Transplantation Antigens in Cell-Mediated Immunity Against Intracellular Parasites

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I. Introduction	113
II. <i>H-2</i> Restriction of Antigen-Specific T Cells	115
A. Experimental Models and Cellular Parameters	115
1. Cytotoxic T Cells	115
2. Noncytolytic T Cells	116
3. Immune Responsiveness	117
B. Models of T Cell Recognition	117
III. Experiments to Analyze Mechanisms of T Cells Recognition	118
1. F ₁ Experiments	118
2. The Chimera Experiments	118
3. Experiments with Mutant Mice	120
4. Similarity of Idiotype of T and B Cell Receptors for Antigens	120
5. Minor Alloantigens as T Cell Targets	120
6. Relative Susceptibility of Infected Targets to Alloreactive T Cells	120
7. Anti <i>H-2</i> Antisera Block Antigen Specific Interactions	121
8. Evidence for Complex Antigen Formation	121
9. Derepression—Repression of <i>H-2</i> Antigens	122
10. Crossreactivity of Syngeneic Antigen-Specific Cytotoxic T Cells with Unrelated Antigens or with Alloantigen	122
11. The TNP Model	123
IV. <i>H-2</i> Antigens as Receptors for Differentiation Signals	124
A. Introduction	124
B. Allorecognition	124
C. Evidence for the Function of <i>H-2</i> Coded Antigen as Receptors of Differentiation Signals	126
1. <i>K</i> and <i>D</i> as Receptors for Lytic Signals	126
2. <i>H-2I</i> Coded Structures as Receptors for Nonlytic Differentiation Signals	128
V. Concluding Remarks	129
References	130

Abbreviations: Ag-B=Major rat histocompatibility; CMI=Cell-mediated immunity; DTH=Delayed-type hypersensitivity; H=Major histocompatibility; H-2=Major murine histocompatibility; HL-A=Major human histocompatibility; Ir=Immune response; P=Parental; T=Thymus derived.

I. Introduction

In three major fields of immunology—“academic” immunology, immunology of infectious diseases, and transplantation immunology—exciting features in

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common have been discovered over the past few years. As early as the 1950's, possible links between the transplantation reaction and cell-mediated immunity to cell-bound antigens or intracellular parasites were postulated. For instance, Mitchison speculated that cellular immune recognition of antigen in delayed-type hypersensitivity (DTH) reactions probably occurred only when the antigen involved (e.g., tuberculin or chemical allergens) were present on the cell-membrane, thus resembling a foreign transplantation antigen (*Mitchison, 1954*). *Lawrence*, stimulated by *Thomas'* surveillance hypothesis (*Thomas, 1959*), proposed that immune lymphocytes recognize not only foreign antigens on cell surfaces, since cell-mediated immunity originally evolved against intracellular parasites, but also recognized a self-component (*Lawrence, 1959, 1974*). This self-plus-X hypothesis was a very lucid speculation that foresaw many of the principles discovered since. All these discoveries now lead to the conclusion that thymus-derived lymphocytes (T-cells) seem to express a double specificity for foreign antigenic determinants and for cell-surface self determinants (For reviews see *Paul and Benacerraf, 1977*; *Munro and Bright, 1976*; *Doherty et al., 1976*; *Shearer et al., 1976*; *Forman, 1976*; *Zinkernagel and Doherty, 1977a*; *Koszinowski et al., 1977a*; *Schrader et al., 1977*; *Katz, 1977*; *Langman, 1978*).

The facts that substantiate early speculations about the involvement of self cell-surface markers in cell-mediated immunity (CMI) are as follows: *McDevitt* described mice and *Benacerraf* guinea pigs in which immune responses to certain antigens were regulated by genes coding within the major histocompatibility (H) gene complex (*Benacerraf and McDevitt, 1972*). Then *Lilly et al.* showed that, in some mouse strains, the susceptibility to induction of viral leukemogenesis segregated with the murine H gene complex (*H-2*) (*Lilly et al., 1964*; *Lilly, 1968*; *Lilly and Pincus, 1973*). Subsequently, similar evidence linked disease susceptibility with certain human H (*H-2*) types in humans. (In reviews *Dausset, 1972*; *Amos et al., 1973*; *Morris, 1974*; *Zinkernagel and Doherty, 1976a*; *Vladutiu and Rose, 1972*.) About at the same time *Bryere and Williams (1964)* and *Svet-Moldavsky* and collaborators (*Svet-Moldavsky et al., 1968*) reported that skin from inbred mice that were congenitally infected with oncogenic virus was rejected by syngeneic nonvirus carrier mice, just as allogeneic skin is usually rejected. This phenomenon of heterogenization was also observed by *Lindenmann* and coworkers, who found that virus-infected tumor cells, but not uninfected cells, immunized hosts against subsequent tumor growth (*Lindenmann and Klein, 1967*). After the discovery that T-B cells collaborate in the immune response, (*Claman et al., 1966*; *Miller and Mitchell, 1968*; *Mitchell and Miller, 1968*; *Mitchison, 1971a, b*) *Katz et al. (1971)* found that the need for carrier-specific T cells could be fulfilled by unprimed allogeneic T cells. This "allogeneic effect" preempted some of the subsequent findings by *Kindred and Shreffler (1972)* and *Katz* and collaborators that helper T cells had to be *H-2* compatible with B cells to cooperate efficiently (*Katz et al., 1973*; *Katz and Benacerraf, 1975*; *Katz, 1977*). These results explained the finding of *Miller et al.* some 4 years earlier that allogeneic T and B cells cooperated poorly (*Miller and Mitchell, 1968*; *Mitchell and Miller, 1968*). Independently, *Rosenthal* and *Shevach* reported that antigen-specific T cell proliferation was not only antigen-specific but also depended upon responding T cells and stimulating antigen-pulsed macrophages

being histocompatible (*Rosenthal and Shevach, 1973; Shevach and Rosenthal, 1973*). Both examples of T cell interactions in mice were subsequently shown to be specific for *H-2I* region coded structures (or the guinea pig equivalent thereof). Since both these T cell-effector functions were under *Ir*-gene control, these examples appeared to offer possible explanations for the mode of action of *Ir* genes as regulators of T cell-B cell or T cell-B cell-macrophage interactions (For reviews see *Katz and Benacerraf, 1975; Munro and Bright, 1976; Zinkernagel and Doherty, 1977b*).

The latest decisive finding in conceptualizing the actual role and function of the major histocompatibility gene complex was the *H-2* restriction of the cytotoxic activity of virus-specific T cells (*Zinkernagel and Doherty, 1974a, b*). This *H-2* restriction also applies to trinitrophenyl (TNP) and other hapten or minor alloantigen-specific cytotoxic T cells (*Shearer, 1974; Bevan, 1975a; Gordon et al., 1975*). All these examples that established the crucial role of the major histocompatibility gene complex in "syngeneic" reactions, beside its well-established role in allogeneic confrontations (reviewed in *Cerottini and Brunner, 1974*), have been reviewed extensively (*Katz and Benacerraf, 1974; Doherty et al., 1976b; Shearer et al., 1976; Forman, 1976; Zinkernagel and Doherty, 1977a, Langman, 1978*).

The recent preoccupation of immunologists with *H-2* and *H-2* restriction reflects the feeling that essential information on the elusive T cell receptor is hidden in this phenomenon. In mice, all T cell functions that have been tested are *H-2* restricted. Thus, the histocompatibility restriction over immune reactions appears to be a general phenomenon in mice and probably is universal in higher vertebrates. For example, and not surprisingly, virus-specific cytotoxicity in rats is strain-restricted and probably restricted by the rat major histocompatibility gene complex (Ag-B) (*Zinkernagel et al., 1977a; Marshak et al., 1977*). Strong evidence exists that the H-restriction is also operative in chickens as best documented by the elegant experiments of the *Toivanens* (*Toivanen et al., 1974*) who showed that germinal centers in bursectomized chickens could be reconstituted only by transplanting B locus-compatible bursa cells. *Wainberg* and coworkers (*Wainberg et al., 1974*) have also suggested that B locus restriction may be valid for virus-specific cytotoxic T cells in chickens. In humans, *van Rood* and coworkers (*Goulmy et al., 1976*) uncovered the first indication that the *HL-A* restriction may govern cytotoxicity against cells bearing the male H-Y antigen.

This paper is not a comprehensive review, but aims rather at discussing the open questions of T cell recognition and the possible functions of antigens coded by the major histocompatibility gene complex from biologic, teleologic and evolutionary points of view.

II. *H-2* Restriction of Antigen-Specific T Cells

A. Experimental Models and Cellular Parameters

1. *Cytotoxic T Cells*. First, *Lundstedt* (1969) and subsequently *Oldstone* and *Dixon* (1970) observed that virus-immune lymphocytes specifically inhibited the

growth of or destroyed virus-infected syngeneic target cells by direct contact. This observation was analyzed in more detail by *Marker and Volker* (1973), *Cole* and coworkers, *Blanden and Gardner* and many others (*Cole and Nathanson*, 1975; *Blanden*, 1974; *Doherty and Zinkernagel*, 1974). The characteristics of these highly active virus-immune cytotoxic lymphocytes can be summarized as follows: They are thymus-derived lymphocytes whose cytotoxic function does not involve antibodies. These T cells are virus-specific; they kill by direct contact only in a one hit kinetic pattern. They are demonstrable about 3–5 days after the initiation of infection, peak in quantity at 6–9 days and disappear rapidly thereafter (summarized in *Zinkernagel and Doherty*, 1977a). In all these respects, virus-immune cytotoxic T cells have the same characteristics as cytotoxic T cells directed against foreign major transplantation antigens. (For a review see *Cerottini and Brunner*, 1974; *Zinkernagel and Doherty*, 1977b; *Zinkernagel*, 1977.)

These striking similarities became convincing evidence of the relationship between the transplantation reaction and CMI to intracellular parasites when it was found that virus-specific cytotoxic T cells lysed syngeneic virus-infected target cells but were 30–300 times less efficient in destroying allogeneic target cells infected with the same virus (*Zinkernagel and Doherty*, 1974a, b, *Doherty and Zinkernagel*, 1975a). Analysis of this restricted virus-specific killing of infected target cells revealed that the restriction mapped to the major murine histocompatibility gene complex (*H-2*), and more precisely to the *K* and *D* but not to the *I* region of *H-2* (*Blanden et al.*, 1975a; *Koszinowski et al.*, 1977a). Thus alloreactive and syngeneic virus-specific cytotoxic T cells reacted specifically and probably with the same kind of cell surface structures.

Exactly these same *K* and *D* regions of *H-2* were also found to restrict; first, cytotoxic T cells that were generated *in vitro* against trinitrophenylated syngeneic spleen cells (*Shearer et al.*, 1975) and, second, cytotoxic T cells that were primed *in vivo* and restimulated *in vitro* against minor histocompatibility antigens (*Bevan*, 1975b; *Gordon et al.*, 1975). The basic findings, the experimental conditions, and the characterization of the genetic requirements for cytotoxic interactions, as well as the cellular parameters and their kinetics of generation and activities have been reviewed extensively. Therefore, only selected experiments that appear to hint at some properties of the still-elusive T cell-receptor(s) and mechanisms of T cell recognition are reviewed in the following section.

2. *Noncytolytic T Cells*. Similar phenomena of T cells that are doubly specific for an antigen plus a self-marker on the target cell were discovered in circumstances marked by notable dissimilarities. In 1972, *Kindred and Shreffler* reported that *H-2* -incompatible T cells could not serve as reconstituting T helper cells in nude mice (*Kindred and Shreffler*, 1972). This observation was analyzed in great detail by *Katz, Benacerraf* and collaborators, *in vivo* and *in vitro* using conventional hapten-carrier antigens (*Katz et al.*, 1973a, b; *Katz et al.*, 1975). These results can be summarized as follows: T cells collaborate with B cells much more efficiently if the donor of the primed helper T cells and the B cells share the *I* region of *H-2*. Independently, *Rosenthal and Shevach*, who assayed guinea pig cells, demonstrated that antigen-specific proliferation of T cells was triggered much more efficiently by antigen-pulsed macrophages of histocompat-

ible donors than of incompatible ones (*Shevach and Rosenthal, 1973; Rosenthal and Shevach, 1973*). *Schwartz and Paul (1976)* obtained similar results in the murine system. The adoptive transfer of delayed-type hypersensitivity (DTH) to conventional antigens such as fowl- γ -globulin is *H-2I* restricted in mice (*Miller et al., 1975*) and DTH to chemically reactive antigens or viruses also maps to *K* and *D* (*Miller et al., 1976*). *Erb and Feldman (1975)* studied T cell-macrophage interaction in triggering T helper cells. These investigators found antigen-specific macrophage factors that were *H-2I* restricted in their capacity to sensitize T helper-cell activity.

3. *Immune Responsiveness.* The *H-2* gene complex, besides restricting T cell activities also harbors regulatory genes (immune response genes, *Ir*) as described first by *Benacerraf and McDevitt (1972)*. Although originally it was found that *Ir* genes influenced only levels of immunoglobulin production against weak antigens, more recently it has become obvious that similar phenomena can be shown for the levels of generation of syngeneic cytotoxic T cells *Schmitt-Verhulst and Shearer, 1975, 1976; Simpson and Gordon, 1977; von Boehmer, 1977*). In some instances, two genes seem to be involved in determining responsiveness, one mapping to *I-A* the other probably to the right of *I-C* (*Dorf and Benacerraf, 1975; Debre et al., 1976; Munro and Taussig, 1975; Shearer et al., 1976; Simpson and Gordon, 1977; von Boehmer, 1977*). The relationship between *H-2* restriction and the two complementing *Ir* genes in *H-2* is unclear as yet. However, future interpretation offer some insight into how T cell recognition occurs, independent of whether these genes code for the T cell receptor(s) (*Benacerraf and McDevitt, 1972*), whether such genes define "alterable" self-markers (*Paul and Benacerraf, 1977*), whether they code for cell-interaction structures, (*Katz and Benacerraf, 1975*) or just for cell-surface markers that have only indirect regulatory function themselves (*Zinkernagel, 1977*).

B. Models of T Cell Recognition

Several models for T cell recognition have been proposed; they fall into one of two groups. First, the dual recognition models and, second, the single recognition models (*Katz et al., 1973b; Zinkernagel and Doherty, 1974b; Doherty and Zinkernagel, 1975b; Schrader et al., 1975; Bevan, 1975b; Shearer et al., 1975; Blanden et al., 1976; Zinkernagel and Doherty, 1977b*).

Although the distinction between the two models is in many ways artificial, it has allowed great diversity in experimental designs, approaches and questions. The dual recognition model states that T cells have two receptors, one for the antigen X and one for a self-marker, and these receptors see two distinct antigenic entities.

The single recognition model postulates that T cells have a single receptor that recognizes some sort of a neoantigen formed either by the complex of self-markers with an antigen, by antigen-specific modification of the self-marker or by host-specific modification of the antigen. The single antigen (altered self) recognition model does not permit one to distinguish between these possibilities and a situation in which self-recognition and antigen X recognition are either linked or are independently clonally expressed (*Doherty et al., 1976a; Zinker-*

nagel and *Doherty*, 1975). Since both of these latter propositions (linkage or independent clonal expression) are dual recognition models in molecular terms, but appear phenotypically and functionally as one receptor unit, substantial confusion exists in discussing these models. The term *altered self* was originally conceived as a functional concept, but we now prefer to use the term *neoantigen* or new antigenic determinant to define the *single antigenic entity*; *self* or *self-marker* are the antigenic determinants involved in self-recognition and *antigen X* is the conventional type of antigenic determinant. The latter two form the two separate antigenic specificities recognized by a dual receptor.

The various models have been discussed, reviewed and analyzed extensively. Unfortunately, to date there is no clear cut evidence that could exclude or prove one or the other or even a third new model.

III. Experiments to Analyze Mechanisms of T Cells Recognition

1. *F₁ Experiments.* *F₁* heterozygote and *H-2* recombinant mice infected with virus, sensitized against TNP or against minor alloantigens, generate cytotoxic T cells that are specific for one only of the *K* or *D* markers plus antigen. This has been shown in two ways. First *F₁* immune cytotoxic T cells proliferate preferentially in the parental one (*P₁*) recipients that express the foreign antigen to increase cytotoxicity against antigen expressing targets of that same *P₁* haplotype (*Zinkernagel* and *Doherty*, 1974b, 1975; *Bevan*, 1976). Second, *F₁* T cells that lyse infected *P₁* target cells can be inhibited competitively only by excess added antigen expressing targets of the same *P₁* haplotype but not by targets of the other parent, *P₂* (*Zinkernagel* and *Doherty*, 1975; *Shearer* et al., 1975; *Bevan*, 1976).

These results were initially interpreted to support the single neoantigen-single T cell receptor idea. However, although allelic and genic exclusion of self-recognition was thought to be unlikely (*Zinkernagel* and *Doherty*, 1975) this may in fact be a viable alternative. Thus, these *F₁* experiments may be interpreted to reflect that T cells express two receptors that are both clonally expressed; the specificity of self-recognition is regulated by allelic and or genic exclusion mechanisms (*Langman*, 1978; *Zinkernagel* and *Doherty*, 1977a, b; *Zinkernagel*, 1976a).

2. *The Chimera Experiments.* Several research groups have shown that T cells, differentiated either in chimeras formed by zygote-fusion or in parent (*P*) → *F₁* irradiation chimeras, could cooperate with B cells or could lyse haptentated or virus-infected target cells of the tolerated haplotype from the other parent (*Bechtol* et al., 1974; *Sprent* et al., 1975; *Pfizenmayer* et al., 1976; *Zinkernagel*, 1976a; *von Boehmer* and *Haas*, 1976). This may indicate that these T cells tolerate the other parental haplotype but not the neoantigen formed between it and the haptenic or viral antigens; therefore, the modified alloantigen can be recognized or lysed. However, one can also postulate that such T cells have learned to recognize the tolerated alloantigen as self and handle it as a self-marker as originally proposed by *Katz* and *Benacerraf* (1976) (*Katz*, 1977; *Zinkernagel*, 1976a).

More recent experiments demonstrated that $(H-2^a \times H-2^b)F_1 \rightarrow P(H-2^a)$ irradiation bone marrow chimeras generated cytotoxic activity in association with $H-2^a$ only (Bevan, 1977c; Zinkernagel et al., 1978a, b, c). In contrast, when such chimeras were formed by using adult spleen cells $(H-2^a \times H-2^b)F_1 \rightarrow P(H-2^a)$ then cytotoxic T cells were generated for both $H-2$ haplotypes. These experiments suggested that the host determined which $H-2$ specificity lymphopoietic stem-cells could learn to recognize; however, immunocompetent T cells do not change the specificity for self- $H-2$ under similar conditions. The crucial role of the thymus in dictating the specificity for $H-2$ of T cells was documented in the following experiment. Adult thymectomized, lethally irradiated and reconstituted mice of $(H-2^a \times H-2^b)F_1$ type were transplanted with irradiated thymus lobes of $H-2^a$ origin. Three months later such thymus chimeras were able to generate significant cytotoxicity against infected target cells of $H-2^a$ type only. Thus, the radiation-resistant portion of the thymus, i.e., probably the thymic epithelial cells, select the specificity of T cells for $H-2$ structures expressed on these thymus cells.

These results can be explained along the lines of a single receptor model for a neoantigenic determinant (NAD). Accordingly, precursor T cells may gain their maturity by differentiating receptors for foreign antigens (NAD) in the thymus as proposed by Jerne (1971). Thus, in a mouse of $H-2^a$ type, T cells with specificity for a will proliferate during ontogeny in the thymus upon contact with self $H-2^a$ structures; some of these proliferating T lymphocytes will mutate to express a receptor not any longer specific for a but for "slightly different from a ". Through a "filter mechanism", T cells with specificity for a will not be able to leave the thymus and would be pushed to proliferate further, or alternatively are inactivated. Only T cells having a mutated recognition specificity for "different from a " will be released from the thymus. This could explain the preference of T cells of $(H-2^a \times H-2^b)F_1 \rightarrow A$ chimeras for "altered a ". Since these chimeric T cells cannot react to "altered b " we must introduce the rule that the specificity spectrum anti-X that can be generated in a thymus a cannot overlap with that generated in a thymus b . When applied to a model of single receptor specificity for neoantigenic determinant this rule is unpredicted and seems unlikely but cannot be formally excluded as yet. In the light of the data presented here, which requires the T cell's receptor quality for anti-self- $H-2$ structures to be specifically learned, i.e., selected for and expressed independently of the receptor quality for anti-X, the dual recognition model provides a simple interpretation. To argue that one receptor has two independent recognition sites is tantamount to accepting two independent recognition sites, i.e., dual recognition. The distinction between models with one and two receptors may, therefore, be reduced to deciding whether signals generated by antigen binding to the anti-self- $H-2$ structure and anti-X sites are transmitted intracellularly via one or two molecules.

3. *Experiments with Mutant Mice.* Apparently, there is an inverse relationship between skin graft rejection and the self-recognition capacity of mutant and wildtype mice when tested reciprocally. $H-2$ mutant mice were selected by skin graft testing by Bailey, Egorov and Kohn (Reviewed in Klein, 1975). The mutant mice's TNP or virus-immune T cells were tested for the capacity to lyse

TNP modified or with virus-infected target cells of the wildtype (*Forman and Klein, 1977; Zinkernagel, 1976b; Doherty et al., 1976a; Blanden et al., 1976*). Against TNP-sensitized targets, killer T cells from wildtype mice cross reacted widely with TNP-mutant cells and vice versa. In contrast, virus-specific cytotoxic T cells from some mutant mice (e.g., the H2I strain) failed to cross react to various extents. These results can be explained by either theory of T cell recognition (*Zinkernagel and Doherty, 1976b*). However, the fact that the cross-reactivity patterns of wildtype and mutant mice are similar for various viruses seems to be most compatible with the dual recognition model (*Zinkernagel and Klein, 1977; Zinkernagel and Doherty, 1977a*). The complete cross reaction of mutant and wildtype H-2-restricted TNP-specific cytotoxicity contrasts sharply with the results obtained with virus-specific cytotoxic T cells suggesting that the recognition mechanisms may be different in the two experimental models (*Zinkernagel and Klein, 1977*).

4. *Similarity of Idiotype of T and B Cell Receptors for Antigens.* Many findings indicate that the idiotypic specificity of the antigen receptor on B cells and T cells is very similar (*Ramseier and Lindenmann, 1969, 1972, 1977; Binz and Wigzell, 1975, 1977; Eichmann and Rajewski, 1975; Rajewsky and Eichmann, 1977*). If so, then it seems unlikely that the T and B cell receptors differ vastly. This concept fits best with the idea that the antigen receptor on T cells is probably a separate entity, distinct from the self-interaction mechanism (*Doherty et al., 1976b; Janeway et al., 1976; Katz, 1977*).

Most of the following experiments address the problem of the antigenic entity recognized by T cells; i.e., whether evidence for neoantigens such as a complex of self and X, modified self, or modified X can be demonstrated.

5. *Minor Alloantigens as T Cell Targets.* Cytotoxic T cells that are specific for minor alloantigens (*Bevan, 1975a, b, 1976, 1977a; Gordon et al., 1975, 1976; Simpson and Gordon, 1977*) are restricted by H-2K or D. Although the idea that a complex of self plus minor alloantigen constitutes the single neoantigen is favored by some investigators, it is more readily envisaged that the two cell-surface molecules of self and alloantigen constitute distinct antigenic entities.

6. *Relative Susceptibility of Infected Targets to Alloreactive T Cells.* Virus-infected cells or cells expressing minor alloantigens seem to be as susceptible to lysis by alloreactive T cells as "normal" target cells (*Koszinowski and Ertl, 1975a, b; Gardner et al., 1975; Zinkernagel and Doherty, 1977a, b*). Possibly, cell surface structures that are targets for alloreactive killing (at least some) remain unmodified. If so, either virus infection or minor alloantigen fail to "modify" all self-markers, or the target for alloreactivity is different from the relevant self-marker. However, most evidence suggests that the target for alloreactivity and for self-recognition are identical or very similar and closely linked. Any quantitative effects that suggest modification of self-markers by virus infection can be explained by the shutdown of host-cell protein synthesis after virus infection (*Hecht and Summers, 1972; Koszinowski and Ertl, 1975a, b*). Since we know neither the quantitative antigenic requirements for cytotoxic T cells to act nor the relative frequency of antigens on the target cells, these data cannot argue strongly for or against any of the models.

7. *Anti H-2 Antisera Block Antigen Specific Interactions.* Rosenthal and Shevach were the first to use anti-H-2 antiserum to block antigen-specific T cell proliferation of guinea pigs (Rosenthal and Shevach, 1973; Shevach and Rosenthal, 1973). Subsequently, the same sort of blocking was shown for virus-specific or hapten-specific cytotoxic T cell interactions (Germain et al., 1975; Schrader et al., 1975). These results were complemented only incompletely by the demonstration that killing of the appropriate target cells was sometimes blocked by antiviral or antihapten antibodies (Gardner et al., 1974b; Koszinowski and Ertl, 1975a, b; Burakoff et al., 1976a). This pattern may be interpreted to indicate that H-2 structures form part of the antigenic determinant to which killer cells respond, but simple steric hindrance obviously can not be excluded as the cause of such blocking. This is true even in a linked dual recognition model since the two postulated antigenic entities probably could not lie very far apart. Serologic evidence for a neoantigen in the virus or minor alloantigen systems is lacking. Therefore, positive proof of a serologically definable neoantigen that can block cytotoxicity would certainly support a single neoantigen hypothesis.

8. *Evidence for Complex Antigen Formation.* Schrader and Edelman have attempted to show that virally induced cell-surface antigens co-cap with H-2K and D determinants on the cell surface (Schrader et al., 1975). This result has been interpreted to support the concept that viral antigen and K or D form a complex. The analysis is however subject to the complication that many of the alloantisera are contaminated with anti-C-type viral antibodies. Although the authors made great efforts to prove that this was not the case with their reagents, a degree of uncertainty remains (Henning et al., 1976). The study of Formann et al. (1977) is probably the best evidence that, at least in the TNP model, a neoantigen is the crucial determinant for cytotoxic T cells. More recently, Geib et al. (1977) demonstrated that the H-Y-alloantigen and K and D determinants did not co-cap which would be compatible with the idea that most of the self-markers and H-Ys are not complexed. This is certainly no proof for dual recognition, since one can argue that only a few complexed self-H-Y are sufficient to be detectable by T cells even though not apparent in an insensitive test such as co-capping. There is a strong precedence that T killer cells need only few target antigens, since even after complete capping of H-2 antigens with anti-H-2 sera, sufficient H-2 determinant remained for alloreactive killer cells to be active (Stulting et al., 1976).

More recently, several groups (Schrader and Edelman, 1977, Koszinowski et al., 1977b) have shown that (noninfectious) viral antigens (Sendai-virus) can, when adsorbed to target cells, render them susceptible to T cell-mediated lysis. This interesting observation demonstrates that the relevant antigen can come from outside the cell and has not necessarily to come from within. Furthermore, in this experimental situation molecular modification of K or D products by virally induced processes or, alternatively, host-specific modification of viral antigen within the host cell apparently does not occur. However, since Sendai has a great potential for fusion, one cannot fully exclude the possibility that such processes occur during the fusion process on the cell membrane. Nevertheless, these

experiments and similar results obtained with vesicular stomatitis virus (*Zinkernagel*, unpublished) and vaccinia virus (*S. Hapel*, personal communication) suggest that viral antigen may be recognized directly as such on infected cells. Whether this actually is interpreted to favor the complex antigen idea implying a simple T cell receptor or the concept of two distinct antigenic entities (self plus X) that are recognized by two observed receptors, seems arbitrary. *Bubbers* and *Lilly* (1977) demonstrated that Friend leukemia virus grown in *H-2^b* cells incorporated serologically detectable *D^b* specificities but not *K^b*. This correlates selectively with the fact that virus-specific killer T cells are generated against the *D^b*-end preferentially. This might suggest that *K* and *D* associate with viral antigens, but does not directly answer the question of the nature of the antigenic moiety seen by T cells.

9. *Derepression—Repression of H-2 Antigens.* The appearance of neoantigens after virus infection of target cells have been described repeatedly (*Boyse and Old*, 1969; *Invernizzi and Parmiani*, 1975; *Garrido et al.*, 1976). Although most examples were found with tumor-associated viruses, one report (*Garrido and Festenstein*, 1976) showed that unexpected alloantigens can be detected by serological means after infection with vaccinia virus. These phenomena were interpreted to suggest that *H-2* antigen expression is not allelic but rather a function of regulator genes controlling expression of multigenically coded *H-2* antigens (*Bodmer*, 1973). If viruses can deregulate expression of *H-2* antigens, such derepressed specificities may in fact constitute the target antigens. Attempts to find such repression-derepression of alloantigens or self-markers by infecting cells with several viruses have failed when, instead of serologic methods, susceptibility to alloreactive T cells was used as an assay method (*Zinkernagel et al.*, 1977b). This would suggest that repression-derepression of *H-2* genes could not readily explain the phenomena of *H-2*-restricted virus-specific T cell cytotoxicity.

10. *Cross reactivity of Syngeneic Antigen-Specific Cytotoxic T Cells with Unrelated Antigens or with Alloantigen.* The unique neoantigen idea is best applicable to alloantigens. If antialloantigen activity is mediated by a single recognition structure the chance that syngeneic cytotoxicity against antigen X is also specific for an alloantigen B might be considerable. This is particularly to be expected if the T cell receptor is somehow restricted in favor of allorecognition. In the TNP model such cross reactivity has been found extensively; this point has been discussed in an earlier section (*Lemonnier et al.*, 1977; *Shearer et al.*, 1976). More recently however, *Bevan* has shown that one can select cytotoxic T cells directed against minor alloantigens to find a subpopulation that kills not only *H-2*-compatible targets expressing this minor alloantigen but also kills one particular foreign *H-2* type not expressing the specific, minor alloantigens (*Bevan*, 1977b). This finding is different from the TNP findings, in that the frequency of alloreactive cross reaction is much smaller. Although both findings can be used to support the neoantigen idea (*Matzinger and Bevan*, 1977; *Bevan*, 1977b), one can also explain the latter results with a dual recognition model. If allorecognition differs from antigenrecognition for reasons discussed in other sections in that, on target cells the excitable cell-differentiation trigger is hit

directly by the recognition arm that is used for antigen X recognition in syngeneic sensitizations, then a certain frequency of alloreactive cells is predicted. The fact that TNP-sensitization creates a large activity against alloantigens, where as cytotoxic T cells generated against minor alloantigens lyse only few allogeneic targets is compatible with the view that the rough chemical modification creates many different modifications of *K* and *D*. Similarly, there are so many minor alloantigens that the chance of coming within a binding affinity range against foreign alloantigens that is still low, but high enough to trigger *K* or *D* products of cells for efficient lysis to occur, is a real possibility.

11. *The TNP Model.* The results of the TNP model where T cells are sensitized *in vitro* against TNP coupled to syngeneic target cells indicate that these cytotoxic T cells react to a neoantigen (Shearer, 1974; Shearer et al., 1976; Burakoff et al., 1976a, b; Lemonnier et al., 1977). The reason for this contention is as follows: First, TNP-modified target cells are lysed only when conditions are used in which TNP is demonstrably coupled to the target cells' *H-2K* or *D* products (Forman et al., 1977a). Second, killer T cells that are activated against syngeneic TNP-modified cells are cross reactive against unmodified, i.e., normal, allogeneic target cells (Lemonnier et al., 1977; Shearer et al., 1976). This relatively high degree of cross reactivity is unique to the models using chemically coupled antigens since at least in the virus models no cross reactivity between *H-2^b* or *H-2^d*-restricted virus-specific T cells has been discovered that would exceed a level of 3% and in most experiments is at or below the 1% level (Doherty and Zinkernagel, 1976; Zinkernagel et al., 1977b). Third, Sprent, Wilson and coworkers (Wilson et al., 1977) have shown that lymphocytes that have been made unresponsive against an alloantigen by *in vitro* filtering of parental A lymphocytes through irradiated A × B F₁ recipients with collection of filtered T cells from the thoracic duct 3–18 h after transfer, could not react against B but could be sensitized against TNP-modified B in mixed lymphocyte cultures. More recently, Forman et al. (1977b) showed that mice *H-2^a* that were rendered tolerant by injection of (*H-2^a* × *H-2^b*)F₁ lymphoid cells at birth could generate cytotoxic T cells against both TNP-*H-2^a* as well as TNP-*H-2^b* targets when stimulated appropriately *in vitro*. Both results are not compatible with a dual recognition model and support for TNP the single neoantigen recognition model. The data from Thomas and Shevach (1977) agree but the preliminary data from Schmitt-Verhulst and Shearer do not (personal communication). Using both BUDR plus light to eliminate alloreactive lymphocytes, the latter investigators failed to sensitize lymphocytes specifically against TNP-modified targets possessing the tolerated H-2 haplotype. This result is supported by experiments with chimeras similar to those mentioned in section 3 (Zinkernagel, et al., 1978c). Lymphocytes from irradiation chimeras of the type (*H-2^a* × *H-2^b*) F₁ → (*H-2^a* × *H-2^c*)F₁ were stimulated with TNP-modified spleen cells from (*H-2^b* × *H-2^c*)F₁ and then tested for cytotoxic activity; only TNP *H-2^c* targets could be lysed, but not TNP-*H-2^b*. Fourth, if TNP is coupled to target-cell surfaces by means of a spacer instead of directly, killer cells that had been sensitized against TNP coupled directly to syngeneic stimulator cells do not lyse TNP-spacer-modified targets. This result is compatible with the presence of a neoantigen,

but could also indicate that the two linked T cell-recognition arms can span only very small distances (*Rehn et al.*, 1976).

These data are in support of the view that TNP-self behaves at least in part like an alloantigen and that the rules of alloreactivity may apply directly to this model.

IV. *H-2* Antigens as Receptors for Differentiation Signals

A. Introduction

Why have *H-2* antigens evolved? Many speculations exist (*Thomas*, 1959; *Snell*, 1968; *Burnet*, 1971, 1973; *Jerne*, 1971; *Bodmer*, 1972; *Amos et al.*, 1973; *Shreffler and David*, 1975; *Klein*, 1975; *Klein*, 1976). There is some consensus that these cell-surface markers probably evolved before immune systems, e.g., self-recognition has been shown in plants and in coelenteratae (*Hildemann*, 1974; *Theodor*, 1970; *Burnet*, 1971). In fact, some of the striking characteristics of major transplantation antigens are already found in these systems. For example, except for sexual propagation, the contact of two foreign members of colonial tunicates or coelenterates results in necrosis of interacting cells. As in higher vertebrates, related foreigners are recognized much more readily than vastly distinct foreigners. Also as best exemplified in the fecundation process in plants, such self-recognition phenomena may initiate or block differentiation processes.

From this point of view, the *H-2*-restriction of T cell activities resembles these very ancient recognition processes. Particularly if the dual recognition model is applicable, the postulated self-recognition event may well be a very primitive recognition and/or cell-interaction mechanism very much like that found in plants and colony-forming marine animals (*Zinkernagel et al.*, 1977c; *Katz*, 1977). As mentioned earlier, it is unclear, whether self-recognition in a dual recognition model operates via a complementing interaction or a like-like self interaction. If the first alternative is true one could postulate that immune recognition derives directly from this ancient mechanism of self-recognition. If the second alternative applies, immune recognition may have evolved quite independently. The postulates that self-recognition moieties may be coded within *H-2* or outside of *H-2* and that the variable regions of immunoglobulins are not linked to *H-2* leave all possibilities open as yet.

B. Allorecognition

Several hypotheses dealing with self-recognition, allorecognition and immune recognition of any antigenic determinants have been formulated (e.g., *Jerne*,

1971; Doherty et al., 1976b; Janeway et al., 1976; Zinkernagel and Doherty, 1977b). The main question is whether there is a genetic functional restriction and thus interdependence (and of what degree) between the H-antigens and the *V*-gene region products of the germ line or whether these two gene systems and their products are completely independent.

The argument in favor of some sort of relationship between the two gene systems stems from the puzzling finding of the high frequency of lymphocytes that can "react" immunologically with a species' major transplantation antigenic system (Simonson, 1962, 1974; Jerne, 1971; Elkins, 1971; Lafferty and Cunningham, 1975; Bodmer, 1972). This phenomenon is still unexplained but remains a constant challenge. A simplistic view, which tries to avoid genetic linkage of the *H* and the *V*-gene systems, is that this apparent preoccupation of *V*-gene products with H-antigens is purely "phenotypic", i.e., due to the unique properties of the H-2 antigens recognized but not to some genetic linkage. The unique property of these cell-surface markers that distinguishes them from most other antigens is that *H*-markers are receptors for signals that regulate differentiation and generation of immune effector cells. The greater efficiency with which these processes are triggered directly in the essentially abnormal allogeneic confrontations as compared to the antigen-induced "syngeneic" reaction may thus be explained by the fact that these receptors and the recognized antigen are *identical*. Because of this "abnormalcy", allogeneic stimulator cells provide an immunological trigger to the responder cells (Lafferty and Cunningham, 1975).

Furthermore, the chance that syngeneic associative recognition can trigger antigen-specific differentiation is much smaller, because of the low frequency of the antigen-specific receptor. Actually, the same small number of receptors may exist for alloantigen if they were conventional as an antigens; however, the conditions for triggering alloreactive cells, as compared with conventional antigens, may be different because of the stimulatory capacity of the allogeneic target cells. Also, at the effector level of a cytotoxic T cell directed against alloantigens, a binding activity of one hundredth of that needed for conventional antigens may be sufficient to lyse the target because the immunologic receptor hits the weak spot on the target cell directly. A very striking example of such abnormal "induction" of immunologic responses is the allogeneic effect. Here, B cells that are confronted with antigen are triggered to differentiate to plaque-forming cells not by syngeneic helper T cells but by alloreactive T cells that probably can trigger the very same differentiation signal-receptors on B cells in an "abnormal" fashion (Katz, 1972). In brief, we reason that the very involvement of *H*-2 antigens in syngeneic reactions is the reason for the tremendous triggering potential of alloantigens on lymphoid cells because they not only present antigens but also simultaneously stimulate the responding lymphocytes in an abnormal way via the *H*-2-coded receptors for immunologic differentiation; this applies to the induction as well as to the effector level. Therefore, the unusually great number of alloreactive lymphocytes can be explained by the unique stimulatory capacity as well as unique nature of the target antigen and there is no absolute need to postulate a linkage between the respective sets of *V* and *H* genes.

C. Evidence for the Function of *H-2* Coded Antigen as Receptors of Differentiation Signals

The *H-2* gene complex is located on the 17th chromosome. This chromosome also contains other important gene complexes that are thought to be involved in differentiation processes also. For example the *T/t* locus codes for gene products that regulate differentiation processes very early during embryogenesis as summarized excellently by *Hammerberg* and *Klein* (1975) *Klein* (1975), *Artzt* and *Bennet* (1975) and *Jacob* (1977). Another locus (*Tla*) codes for the TL (thymus leukemia) antigens first discovered by *Boyse* and *Old* in 1963 (*Boyse* and *Old*, 1969). The TL alloantigen system consists of a group of antigens that can be detected on normal thymocytes at various stages of differentiation or on leukemia cells. Apparently, both gene complexes code for structural as well as regulatory genes, as is true for the *H-2* gene complex. As mentioned earlier, it is unclear as yet what their exact mutual relationship is. Furthermore *H-2* is linked to both the *T/t* locus and the *Tla* locus. A strong linkage disequilibrium exists between *T/t* and *H-2*, and the expression of their respective gene products is mutually dependent during differentiation. Similarly, the expressions of TL antigen and of some *H-2* products are linked. An additional relationship exists between *H-2* and TL antigens in that their respective expressions may be modified by infection with tumor-associated viruses. *Boyse* and *Old* suggested that C-type RNA leukemia viral genes themselves may be integrated at the *Tla* locus and the expression of viral antigen may be coregulated with differentiation processes of thymocytes (*Boyse* and *Old*, 1969). Similarly, several investigators (*Invernizzi* and *Parmiana*, 1975; *Garrido* and *Festenstein*, 1976, *Garrido* et al., 1976) found that in certain cell lines infected with tumor-associated viruses, the phenotypic expression of serologically detectable *H-2* antigens changed; in cells infected with acute viruses (*Zinkernagel* and *Klein*, 1977b), such changes could not be detected by alloreactive cytotoxic T cells. To what extent parts of these genetic loci and complexes including *H-2* can be regarded as integrated viral information or the respective gene products as "footprints" of viruses is unclear at the moment; however, the hypothesis of viral integration is attractive and may explain at least some aspects of the functional immunologic association between acute viruses and some products of *H-2* (*Huebner* and *Todaro*, 1969; *Todaro*, 1975; *Del Villano* et al., 1975; *Zinkernagel*, 1977). Such a hypothesis could also explain why tumor-associated viruses, but not acute viruses, may be able to disturb such well-established symbioses and escape immune surveillance (this term is used in a much broader sense as proposed by *Thomas* and *Burnett* to include all immunoreactivity to self-plus-foreign not only to tumor antigens), because they successfully use and exploit self-recognition markers for this purpose.

1. *K* and *D* as Receptors for Lytic Signals. T cells that are specific for the serologically defined products of *H-2K* or *H-2D*, be it in allogeneic confrontation of the transplantation reaction or in syngeneic reactions against viruses, destroy the target cell. Cell lysis seems to be caused by dysregulation of the osmolar balance between extracellular and intracellular compartments. Whether this occurs by shut off of one of the ion pumps to establish ion gradients

or by actual overshooting activity of such pumps is unclear. One may suggest that *K* and *D* products are linked to regulators of the osmolar balance or are actively involved themselves. How these various regulators, ion-pumps and *K* or *D* structure, are actually linked is unclear; also, whether there exists a system such as the actin-myosin network that interconnects similar structures and coordinates processes is pure speculation (*Singer, 1977*).

From a teleologic point of view, target cell destruction as a means of protecting the host from potential harm may be functional in the following examples: Elimination of cells that have escaped normal controls over the rate of multiplication and anatomic restriction ("tumor cells"); here the cell itself is the target of destruction. Alternatively, a cell may be the target of destruction if it harbors parasites that hide inside the cell wall. However, this latter mechanism seems to exist only to eliminate intracellular parasites, which themselves destroy cells when growing in them. Acute viruses seem to be an excellent example of such parasites, since many of them shut down host protein synthesis and thus kill the host cell functionally. However, during infection, these viruses induce cell-surface changes very rapidly and the host cell may thus be susceptible to immunologic attack (*Ada et al., 1976; Koszinowski et al., 1977b*). In fact, virus-specific cytolytic T cells have been shown to lyse target cells well before assembly of viral progeny, at least in the case of vaccinia virus. Once viral progeny do assemble, host-cell lysis no longer affects the newly formed viruses, and the infected host can overcome viral invasion by cytotoxic T cells only after infection of surrounding cells by these progeny. However, noncytolytic viruses (such as lymphocytic choriomeningitis virus—LCMV) that do not halt host-cell functions, no longer release viral progeny after host cells die. Thus, viruses can be efficiently eliminated by target-cell lysis if it occurs during the eclipse phase of the virus infection, i.e., after penetration and uncoating and before reassembly of infectious progeny. It has to be kept in mind that many other antiviral immune mechanisms exist, such as neutralizing antibodies, immune interferon, etc. A second fact favors the idea that *K* and *D* products are receptors of T cell-mediated cell destruction. This fact is the ubiquitous distribution of *K* and *D* structures. So far, *K* and *D* cell-surface markers have been demonstrated on all nucleated cells, although the quantities vary (*Klein, 1975*). For example, neurons possess about a 1000 times less *H-2K* or *D* structures than lymphocytes. Since, viruses can actively infect phagocytic as well as nonphagocytic cells, the potential of different viruses to infect particular kinds of cells would require that the immune system use an ubiquitous self-marker if cell destruction is one of its means of eliminating virus. Thus *K* and *D* structures appear to fit both these requirements: receptors for lytic signals and ubiquitous distribution.

Why have viruses not escaped immune surveillance? Obviously viruses can adapt many times more quickly than their host, because of the vast difference in generation time. One explanation may be that virus life cycles and host defense mechanisms have established an overall optimal steady state condition. If cytopathic viruses lysed too many cells too quickly, hosts would die before they could efficiently propagate the virus. Similarly, too potent an immune response would result in virus elimination without propagation. The actual

kinetics of both virus spread in a host and throughout a population on one hand and of the immune response on the other hand is a compromise for mutual survival.

During the last few years, several groups of investigators have shown that under certain experimental conditions that include *in vivo* priming and *in vitro* secondary restimulation, it is possible to sensitize cytotoxic T cells that are specific for *H-2* region determinants (Wagner et al., 1975; Nabholz et al., 1975). More recently it was found that *I* region determinant-directed killing was not *K* or *D* restricted (Klein et al., 1977; Billings et al., 1977). These results may indicate that the functional roles of *K* and *D* versus *I*-coded structures may be less absolute than thought so far. However, it is interesting that virus specific cytotoxic T cell activity that was generated *in vivo* is, as far as can be detected in ⁵¹Cr-release assays or in adoptive transfer assays, exclusively directed against *K* and *D* (Blanden et al., 1975a; Shearer et al., 1976; Blanden et al., 1975b; Kees and Blanden, 1976; Doherty et al., 1976a; Zinkernagel and Welsh, 1976). Thus, the efficiency with which *K*, *D*-specific cytotoxic syngenic T cells are generated *in vivo* as compared to *I*-directed killer T cells is of the order of at least 100 fold better; consequently the biologic role of *I*-specific cytotoxicity is unclear as yet.

2. *H-2I* Coded Structures as Receptors for Nonlytic Differentiation Signals.

Except for the examples mentioned, in general, *H-2I*-specific T cell functions seem to be nonlytic. Thus, T cells involved in T-B cell cooperation (Kindred and Shreffler, 1972; Katz et al., 1973a, b; Katz and Benacerraf, 1975; Katz, 1977), in mediation of delayed-type hypersensitivity (DTH) (Miller et al., 1975; Miller et al., 1976), in proliferative responses (Rosenthal and Shevach, 1973; Paul et al., 1977), in the production of lymphokines such as migration inhibition factor (MIF), or in protection against intracellular bacteria such as *Listeria monocytogenes* (Zinkernagel et al., 1977c) all produce the differentiation of cell-specific special functions that lead to "neutralization" (i.e., destruction, and/or biologic inactivation) of foreign, potentially harmful antigens. Such neutralization may occur via several mechanisms, e.g., by antibodies alone or combined with complement or by release of chemotactic substances that attract phagocytic cells, which when activated digest engulfed antigens more efficiently. The mechanism of cell-mediated protection against intracellular bacteria such as *L. monocytogenes* may be an excellent representative for antigens that are handled via *I*-coded self-markers. Mackaness and his school have elaborated the immune mechanisms that lead to the protection against intracellular bacteria (Mackaness, 1962, 1964, 1969; Blanden et al., 1969). T cells are specifically triggered to release lymphokines that activate macrophages to nonspecifically increased bactericidal capacity (Lane and Unanue, 1972; Blanden and Langman, 1972; North, 1973).

It is obvious that lysis of the phagocytic cells would not result in inactivation or destruction of these intracellular parasites; similarly toxins that have become cell associated are not neutralized by the cell's destruction. In neither case do bacteria nor toxins lose their ability to replicate or act as toxins when entering cells. Furthermore, these bacterial antigens are, distinct from viruses

(or tumor antigens) not “active” and associate predominantly, if not exclusively, with phagocytic cells to become immunogenic for T cells.

Therefore, again from a teleologic point of view, the self-markers that are involved in handling these “inactive” or inert antigens immunologically, should fulfill two conditions; one, they should be expressed selectively on cells that phagocytize these antigens or are otherwise involved in disposing of them immunologically (macrophages, B cells, T cells, etc.), and two, they should represent receptors for signals that trigger differentiation of cell-specific functions whereby inert antigens are effectively neutralized. On macrophages such a differentiative step could lead to the activation of enzyme systems that improve their phagocytic and digestive capacity; on B cells the signal may initiate immunoglobulin production and/or the switch from IgM to IgG production; on T cells it may induce proliferation, etc.

Thus, *I*-coded structures may be partially cell-specific, cell-surface structures that function as receptors for final differentiation signals.

V. Concluding Remarks

All T cell-mediated functions that have been tested so far in mice obey the rule of *H-2* restriction. This restriction fundamentally distinguishes the recognition mechanism of T cells from that of B cells or of the B cell product, antibodies. The *H-2* restriction apparently generalizes the rule of associative recognition that was first established for T helper cells in the hapten-carrier system, i.e., self-determinants fulfill a carrier task. The fact that B cells do not recognize self-plus-X, but respond to X exclusively—obviously an easily excitable system—explains why deviations arise so often. The encounter of autoantibodies of various kinds in normal but also in many pathologic situations is in great contrast to the fact that no T cell activities have been detected that are directed against normal cell-surface antigens. In general, all so called cell-mediated autoimmune phenomena are most likely T cell activities against self-plus-X, X probably often being viral antigens; some examples are autoaggressive hepatitis in humans or the T cell-mediated immunopathology caused by lymphocytic choriomeningitis virus (Reviewed in *Cole and Nathanson, 1975*). Thus, associative self-plus-X recognition is a most efficient self-control device for cell-mediated immunologic lymphocyte interactions. Such an extremely restricting mechanism is much more efficiently regulated via two linked receptors than via a single T cell receptor because single receptors are subject only to clonal selection but are not also regulated by genic and/or allelic exclusion mechanism, as dual receptors would be.

Such complex regulation allows self-recognition to be expressed during differentiation. As has been proposed, when these self-recognizers are no longer expressed in the anti-X repertoire by allelic and/or genic exclusion then autoaggression in the strict sense cannot arise (*Langman, 1977*).

However, since we do not know whether self-recognition and recognition of X involve the same basic receptors, this proposal is only a speculation.

For example, other hypotheses evoke different mechanisms for self-recognition (namely glycosyltransferase-type interactions (*Rothenberg, 1976; Blanden et al., 1976a*) than for recognition of X. In this case, regulation of autoimmune receptors arising against self in the anti-X compartment would be as likely for T cells as for B cells.

From this point of view, the model advocating dual receptors, which may be linked and are subject to allelic and/or genic exclusion, would be the more appealing characterization of T cell recognition. Unfortunately, positive proof of either dual receptors or of a single receptor for a complex antigen for altered self or for self-plus-antigen X is still lacking, as becomes obvious from the experiments that have been reviewed here.

Irrespective of whether single or dual recognition is the more probable mechanism of T cell interaction, the experimental results discussed here suggest that histocompatibility and immunity are interrelated and that major histocompatibility antigens function as receptors for partially cell-specific immunologic differentiation signals.

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