Complex Formation of Class I Transplantation Antigens and a Viral Glycoprotein*

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Indirect immunoprecipitations of labeled glycoproteins from the adenovirus-transformed rat cell line A₂T₂C₄ and from adenovirus-infected HeLa cells revealed that the class I major histocompatibility antigens co-precipitated with the viral E19 protein. The degree of co-precipitation was highly dependent on the antiserum used. The identity of the co-precipitated components was verified by peptide mapping and radiochemical amino acid sequencing. Cell-free translation of mRNA for the E19 protein and the class I antigen heavy chains demonstrated that the E19 protein-class I antigen interaction is an inherent property of the participating components. In intact cells the virus protein and the transplantation antigens form large complexes, held together by weak, noncovalent interactions.

T-cells can only recognize foreign antigens in conjunction with major histocompatibility complex structures (1). Cytotoxic T-cells preferentially recognize foreign antigens in the context of class I molecules, HLA-A, B, and C antigens in man and H-2K, D, and L antigens in the mouse (2), while helper T-cells primarily react towards antigens presented together with class II molecules, HLA-DR antigens in man and Ia antigens in the mouse (3). The extensive genetic polymorphism of the class I and II antigens, as well as their structural similarity with immunoglobulins (4-7), raise the possibility that class I and II antigens may function as primitive cell surface antibodies (8). If this idea has any merit one may expect to find physical complexes of major histocompatibility complex antigens and foreign molecules on the cell surface. Several controversial reports have argued for the existence of such complexes (see Refs. 9-16).

We have shown that an early adenovirus glycoprotein, the E19 protein, forms complexes with class I antigens (14). In this article we extend this observation and demonstrate by identification at the structural level that the E19 protein forms complexes with class I antigens both in transformed and acutely infected cells. Moreover, we demonstrate that isolation of the complexes depends on a judicious choice of the antiserum used.

EXPERIMENTAL PROCEDURES AND RESULTS¹

Complex Formation between Class I Antigen Chains and the E19 Protein Following Cell-Free Translation—We examined whether a spontaneous association of class I antigen and E19 protein chains occurs. To this end, mRNAs coding for class I antigen heavy and light chains and the E19 protein were isolated from Raji cells and infected HeLa cells, respectively, and translated *in vitro* in the presence of dog pancreas microsomes.

All three mRNA preparations were efficiently translated, and the immunoreactive chains were in each case completely confined to the microsomal vesicles. The mRNA preparations for the class I antigen heavy chains and the E19 protein were co-translated in the presence of varying amounts of microsomes. In the presence of high concentrations of microsomes, no co-precipitation could be demonstrated. However, on lowering the concentration of microsomes, antibodies against the heavy chain co-precipitated the E19 protein (Fig. 1). Antibodies against the E19 protein, on the other hand, did not coprecipitate significant amounts of the heavy chain (not shown, *cf.* Table I).

These data suggest that class I antigen heavy chains and the E19 protein may associate independently of other plasma membrane constituents.

Efficiency of Various Antisera to Co-Precipitate Class I Antigens and the E19 Protein—We examined the co-precipitation of class I antigens and the E19 protein using various antisera. To this end, [^{36}S]methionine-labeled glycoproteins of A₂T₂C₄ cells and adenovirus-infected HeLa cells were immunoprecipitated. Following sodium dodecyl sulfate-polyacrylamide gel electrophoresis, the amount of label associated with the constituent chains of the complex was measured. Table I summarizes the results. Although the degree of coprecipitation varied with the same antiserum in different experiments, the data of Table I are representative.

Table I shows that the two reagents against class I antigen heavy chains reacted similarly with material from the $A_2T_2C_4$ cells. Although the heavy chains were precipitated in different amounts the co-precipitations of the E19 protein and the β_2 -

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¹ Portions of this paper (including "Experimental Procedures," part of "Results," Figs. 1–6, and Table I) are presented in miniprint at the end of the paper. Miniprint is easily read with the aid of a standard magnifying glass. Full size photocopies are available from the Journal of Biological Chemistry, 9650 Rockville Pike, Bethesda, MD 20814. Request Document No. 83M-153, cite the authors, and include a check or money order for \$4.80 per set of photocopies. Full size photocopies are also included in the microfilm edition of the Journal that is available from Waverly Press. The abbreviations used are: TPCK, L-1-tosylamido-2-phenylethyl chloromethyl ketone; SDS sodium dodecyl sulfate; HPLC high pressure liquid chromatography; BPB, bromphenol blue; TCA, Trichloroacetic acid.

microglobulin, expressed in relative amounts, were low and similar. The antiserum against β_2 -microglobulin co-precipitated a significant amount of the heavy chain but only a fraction of the E19 protein. The antiserum against the virus protein precipitated approximately 10-fold more of this protein than did any of the co-precipitating antisera (Table I). Taken together, these results demonstrate that the degree of co-precipitation of the associated polypeptide chains vary with the antiserum.

Table I also summarizes the data obtained with infected HeLa cells. Also in this case, the relative amounts of the three precipitated chains vary. A monoclonal antibody raised against cell-surface expressed β_2 -microglobulin was most efficient in co-precipitating heavy chains and the E19 protein. In fact, this antibody precipitated more of the virus protein than did the antiserum raised against the E19 protein.

Common to all precipitations was the finding that labeled β_2 -microglobulin appeared to be present in smaller amounts in the E19 protein-producing cells than in the control cells (*cf.* Fig. 3). This may signify that the synthesis of β_2 -microglobulin or that the size of the endogenous pool of β_2 -microglobulin changes when the E19 protein is expressed. Alternatively, the affinity of β_2 -microglobulin for the heavy chain may decrease on complex formation (see "Discussion").

DISCUSSION

The present study confirms and extends previous observations that class I antigens and an early adenovirus-coded glycoprotein, the E19 protein, form complexes (14, 16). Thus, in this article we demonstrate that monoclonal antibodies directed against class I antigen chains co-precipitate the E19 protein both from adenovirus-transformed and -infected cells, thereby eliminating the possibility that the previously demonstrated co-precipitations were the result of extraneous antibodies present in the rabbit antisera used.

Since the isolation of class I antigen-virus protein complexes in general has been hard to document, it seemed of importance to ascertain at the structural level that the immunological co-precipitations involved class I antigens and the E19 protein. Thus, the 40,000-Da chains precipitated by antisera against class I antigens and co-precipitated by an antiserum against the E19 protein were shown to be identical by peptide mapping. Likewise, radiochemical amino acid sequence analyses of the 19,000-Da component co-precipitated by class I antigen antisera revealed that it is identical with the E19 protein of the adenovirus E3 region (17, 18).

The immunological co-precipitations suggested that the protein complexes only consisted of class I antigens and the E19 protein. As an initial attempt, we wished to examine whether the complex formation was dependent on other plasma membrane or cytoplasmic components. Moreover, we also wished to determine whether both or only one of the class I antigen chains was needed for the complex formation. To this end, the mRNAs coding for the E19 protein and the class I antigen chains were translated in vitro in the presence of varying concentrations of microsomal vesicles. Complex formation occurred at low but not at high concentrations of the vesicles. In the latter case, the polypeptide chains most probably were sequestered in separate vesicles. Although the immunoprecipitations were carried out subsequent to the solubilization of the vesicles, which should have brought the various polypeptide chains into contact, this was obviously not sufficient to generate complexes. From these observations it seems reasonable to conclude that complex formation may be dependent on a high local concentration of the associating proteins. In addition, the spatial orientation of the interacting

components may also be of importance, but complex formation does not seem to be greatly dependent on extraneous components, *e.g.* cytoskeletal elements.

During the course of this study, it was noted that different antisera with the same nominal specificity varied in their efficiency to precipitate the class I antigen, E19 protein complexes. This notion was substantiated by quantitatively examining the ability of several antisera to precipitate the protein complexes both from adenovirus-transformed and -infected cells. The most likely interpretation of the coprecipitation data is that some of the antibodies, particularly those against the heavy chains and the E19 protein, respectively, may bind to structures directly involved in the complex formation (19). In the extreme, such antibodies should either be nonreactive or dissociate the protein complexes.

Despite the fact that antibodies against β_2 -microglobulin co-precipitated heavy chains and the E19 protein quite efficiently, the protein complexes isolated with these antibodies, as well as with antibodies against the heavy chains, contained less labeled β_2 -microglobulin than expected from precipitates of control cells. The interpretation of this observation is obscure. Thus, the intracellular pool of β_2 -microglobulin (20-22) may change during an adenovirus infection or the rate of synthesis of β_2 -microglobulin may be reduced in E19 proteinexpressing cells as compared to control cells. A more intriguing interpretation is, of course, the possibility that all heavy chains of the protein complex do not associate with β_2 -microglobulin. Provided that the complexes consist of many copies of the heavy chain (see below), only a fraction of those would have to be bound to β_2 -microglobulin to ascertain the co-precipitations observed. Thus, a conformational change of the heavy chain, induced by the interaction with the virus protein, may diminish the affinity for β_2 -microglobulin.

It is obvious that the apparent molecular weight and chain composition of the protein complexes are difficult to determine since antibody binding as well as dilution caused by solubilizing the cells may dissociate the complexes. For this reason, we covalently cross-linked the proteins prior to the immunoprecipitations to minimize dissociations. Complexes isolated by this procedure were so large that we could not estimate their apparent molecular weights. Despite the fact that several molecules must make up the complexes, de-crosslinking did not reveal the presence of components other than the class I antigen subunits and the E19 protein.

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SUPPLEMENTARY INFORMATION TO:

COMPLEX-FORMATION OF CLASS I TRANSPLANTATION ANTIGENS AND A VIRAL GLYCOPROTEIN Bv

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EXPERIMENTAL PROCEDURES

Extension into involution in the adenovirus-transformed rat fibroblast line $A_3 T_{C_4}$, derived from Hooded Litter rat embryos (23), as well as Hooded Litter rates more than the set of the set o

serum-containing medium was added to the infected cells. Antibodies. The rabbit antiserum raised against highly purified $H_2^{\rm of}$ antigens was the same as described earlier (25). Antiserum against highly purified urinary rat β_2 -microglobulin, kindly supplied by Drs antisers araised against hubbalh. The rabbit antisers araised against hubbalh. respectively, were the same as aralier described (26). A monoclonal antibody against human β_2 --microglobulin (R.9.11.4) was obtained from Dr J. Rosenlund (Pharmacia Fine Chemicals, Sween). A rat monoclonal antibody against rat class I antigen heavy chains was produced using conventional fusion and cloning protocols (see ref. 27). A monoclonal antibody of similar specificity was the kind gift of Dr D. Smilek. monoclonal D. Smilek.

Radioactive labeling of cells $A_2T_2C_4$ cells in log-phase were incubated for 6 hours in methionine-, lysine-, or phenylalamine-free DREM supplemented with 4 mM glutamine, 5% dialysed fetal calf serum, 1% normal DMEM and the appropriate radioactive amino acid. Adeno-virus-infected HeLa cells were radioactively labeled in the same medium between 3 and 7 hours after the initiation of the infection.

medium between 3 and 7 nours after the initiation of the infection. Immunoprecipitation. Radioactively labeled cells were solubilized in 0.01 H Tris-HCl buffer, pH 7.4, containing 0.15 H NaCl, 1% Triton X-100, 1 M PMSF and 1% Trasylol. After 30 min at 0° nuclei and cell debris were removed by centrifugation at 100,000 xg for 30 minutes at +4°C. The supernatures were enriched for glycoproteins on Leng <u>Culinaris</u> hemagglutinin - Sepharose 4B columns (28), Glycoproteins buffer, Immunoprecipitation on the d'obter when using the monoclonal antibody R9.11.4, a rabbit anti-rat immunoglobulin serum was used as a second antibody to ascertain binding to the bacteria.

a second antibody to ascertain binding to the bacteria. The resulting immunoprecipitates were collected using the Staphylo-cocci. The pelleted bacteria were subsequently washed 4 to 5 times unto ice-cold 0.02 M Tris-Hcl buffer, pH 7.4, containing 0.15 mm and 0.2% Triton 1000 at 95°C for 3 minutes in the SDS-polyacrylamide el electrophoresis sample buffer which consisted of 0.10 M Tris-Hcl buffer, pH 8.6, containing 3% SDS, 30% sucrose, 10 mM DTT and trace amounts of BFB. When the bacteria had been removed by centrifuga-tion, iodoacetamide was added to a final concentration of 50 mM, when immuoprecipitations were performed with in vitro translation products, protein A-Sepharose CL 48 (Pharmacia Fine Chemicals, Uppsala, Sweden) was used as the insoluble matrix rather than the bacteria.

bacteria. Tryptic peptide mapping. Spleen cells from Hooded Lister rats werg labeled with H-phenylalanine, and A₇C_c cells were labeled with C-phenylalanine. Immunoprecipitation5 of labeled glycoproteins from the cells were performed with various antisera and the polypeptide chains of interest were fractionated on cylindrical SDS-polyacryl-amide gels, which after completed electrophoresis were segmented into 2-mm slices. The proteins were eluted and localized by their content of radioactivity. Proteins to be compared by peptide mapping were washed twice with a diethyl ether-thanol (lit: V/V) and then dissolved in 100 µl of 0.2 M ammonium bicarbonate, pH 8.1, containing at Murea. To the clear solution 5 µg of PfC-trypsin were added in 100 µl of 0.1 M ammonium bicarbonate. After 90 min another 5 µg portion of TPCK trypsin was added. The digestion was terminated by heating at 95°C for 3 min after a total incubation period of 4 hours. Peptides were collected at 1 min Intervals. Madioactivity in the laute was measured in a Packard Tri-Carb scintillation counter with a double-isotope program. Quench-corrections were made by the external standard channel ratio method.

with a double-isotope program. Quench-corrections were made by the external standard channel ratio method. Radiochemical mains acid sequence determination. Radiochemical amino acid sequence determination with the standard channel ratio method. Radiochemical mains acid sequence determination. Radiochemical amino acid sequence determination with the standard channel ratio with method. Radiochemical acid sequence determination. Radiochemical amino de standard channel ratio with method with a sequent were segmented and minoed by a Gilson automatic gel slicer after completion of the electro-phoretic separation. When the segments containing the relevant protein had been identified by radioactivity measurements on aliquots from each segment, the protein was letted by soaking the appropriate segments overnight in 20 MM of Tris-HCl buffer, pH 8.0, containing 0.3% SDS. The radioactive protein was reduced and alkylated in a 0.2 M Tris-HCl-buffer, pH 8.0, containing 0.3% SDS. prior to the precipitation of the protein with lec-cold TCA at a final concentration of 20%. The precipitate, collected by centri-fugation, was washed twice in a disthyleted to automatic amino acid sequencing in a Beckman 890 C sequence. After drying, a wash cycle, omitting the addition of the cleavage acid, was carried out. The fast protein Quadrol Program with 0.5 M Quadrol was used in all indiazoilnones were dried under a stream of containing 0.1% ethamethiol at 80°C for 10 minutes. The phenyltho-chaining 0.1% Retracted with two 0.7 ml-portions of ethylacetate, dried under N, and subjected to radioactivity measurement in a Packard Tri-Cab Liquid Schuller 100 containing the sequence of the duder a stream of containing 0.1% ethamethiol at 80°C for 10 minutes. The phenyltho-chaining 0.1% Retracted with two 0.7 ml-portions of ethylacetate, dried under N, and subjected to radioactivity measurement in a Packard Tri-Cab Liquid Schuller 100 contactivity measurement in a Packard Tri-Cab Liquid Schuller 100 contactivity measurement in a Packard Tri-Cab Li

Isolation of mRMA. Microsomes were isolated (21) from exponentially growing Raji cells and from infected HeLa cells harvested at 9 hours after the initiation of an adenovirus-infection. RMA was extracted from the microsomal fraction with phenol-chloroform-isoamyl alcohol (5^{2} :241: V/v) and the mRMA was enriched by oligo-dT-cellulose

chromatography. The mRNA was further purified on a 10 to 30% linear aqueous sucrose gradient by centrifugation for 11 hours at 39,000 rpm in a Beckman 3W 40 rotor at 15°C. Fractions containing mRNA corresponding to human class I antigen heavy chains, 8,-micro-globulin and the E19 protein were identified by cell-free frams-lation (see below) and immunoprecipitation. The mRNA fractions were stored at -20°C until used.

stored at -70° C until used. **Cell-free translation**. Translation of mRNA in vitro was performed in a rabbit reticulocyte lysate system according to Pelham and Jackson (29). Dog pancreas microsomes, kindly supplied by Dr. B. Dobberstein were added to a concentration of 1 A₂₀ unifme Theorem and the system according to the system incubated at 30°C or 20°C and 20°C and

Crosslinking. Glycoprotein fractions from radioactively labeled cells in 0.01 M sodium phosphate buffer, pH 7.4, containing 0.147_M NaCl, 0.003 M KCl and 0.2% Triton X-100 were incubated with 2x10 M DTSP for 30 minutes at room temperature. The crosslinking reaction was terminated by the addition of lysine to a final concentration of 2 mM, Separation of the proteins from the crosslinking reagent was performed on a small Sephadex G-200 column (Pharmacia Fine Chemicals AB, Uppsala, Sweden). Immunoprecipitations of crosslinked proteins were performed as described above. However, the following changes were introduced to avoid reducing the crosslinkier elution of immune complexes from the bacteria was accomplished without heating and the sample buffer did not contain DT. De-crosslinking was accomplished by reduction with DTT and boiling.

Obter methods. SDS-polyacrylamide gel electrophoresis was carried out as described by Blobel and Dobberstein (30) on 10 to 15% gradient slab gels. Cylindrical gels, using a 12% acrylamide concentration, were run according to Laemmii (31). Slab gels were fixed in 10% TCA for 15 minutes and then treated with Enhancer (New England Nuclear, Boston, Nass.) for 60 minutes. Subsequenty, the gels were soaked in water complished as described by Bonner and Laskey (22) on dried gels. Kodak XAR films were used throughout.

RESULTS

Table I

R NS

240

Reaction	vity of	various	antibodi	es with	35S-methionine-labele	d glycoproteins :	ron
A.T.C.	cells	normal	rat splee	n cells,	adenovirus-infected	and mock-infected	HeLa
cells							

Antiserum ²	Amount precipi- tated from A2TaC/cells			Ratio ³	Amount precipi- tated from spleen cells		Ratio ³
	EIS	H	B2H	E19:H: 87M	H	B.H	H: 62H
		cpm		-		cpm	
R anti-HR	630	8.000	1.300	6:100:16	5.400	3.200	100:60
MC anti-HR	280	1.500	160	8:100:4	1.500	660	100:43
R anti-82MR	730	3.000	5.900	20:100:213	3.300	4.600	100:148
R anti-E19	6.300	1.800	220	403:100:7	240	100	-
R NS	180	280	110	-	290	140	-
	Amount	precipi-			Amount	precipi-	
	tated i	rom in-			tated	from nor	
	fected E19	HeLs cel H	^{1.6} В ₂ М	El9:H:B2H	H H	B2H cpm	H:B2H
		cpm					
R anti-HH	5.000	11.000	1.200	45:100:10	7.600	1.800	100:24
R anti-82MH	6.000	6.800	1.500	91:100:21	4.200	2.100	100:52
MC anti-62MH	14.400	9.800	1.700	152:100:17	9.800	2.500	100:25
R anti-E19	10.400	2.600	220	477:100:3	300	120	-

Aliquots of the glycoprotein fractions of the labeled cells were separately immunoprecipitated with the various antisers. The immunoprecipitates were subjected to SOS-polyacrylands gel electrophoresis. The anounts of radioactivity in the class I antigen heavy (H) and light (B_M) chains and in the E19 protein were estimated by subjecting 1.0 mm slices of the gels to a liquid scintilation counter.

470 150

counter. ²Dre antiera used were: Rabbit antiserum agsinst murine class I antigen heavy chaina (R anti-HR), monoclonal antibodies against rat class I antigen heavy chaina (NC anti-HR), rabbit antiserum against rat dl, M(R anti-AgMR), rabbit antiserum against the E19 protein (R antis-E19), rabbit antiserum against human class I antigen heavy chains (R anti-HN), rabbit antiserum against human anti-g_MN), R NS denotes normal rabbit serum.

anti-3,981). R NS denotes normal rabbit serum. ³The ratios were calculated by setting the radioactivity of class I antigen heavy chains to loo in all precipitates. The radioactivities in the E19 protein and $\beta_{\rm N}$ peaks respectively, were expressed in percentages of the radioactivity of class² I antigen heavy chains peaks. All values have been corrected for back-ground.

2 1 HE MAN E19 .

370 100

Figure 1 Compresipitation of class I antigen heavy chains and the E19 protein in vitro Sucrose gradient-fractionated mRNAs specifying the E19 protein, and the HLA-R, B and C antigen heavy chains respectively, were mixed and subjec-ted to cell-free translation in vitro in the presence of dog pancreas in the presence of dog pancreas many set of the set of the set of the translation products present in the microsomes were immunoprecipitated with rabbit antiserum against human class I antigens (lame 2). The immuno-precipitates were subjected to SDS-polyacrylamide gel electrophoresis and radioactive bands were detected by fluorography.

Transplantation antigens and a virus encoded protein form a ternary complex in adenovirus-transformed $A_2 \underline{\Gamma}_2 \underline{C}_4$ cells and in acutely adenovirus-infected HeLa cells

 $\overline{adenovirus-infected Hela cells} \\ \hline \\ \hline \\ The adenovirus-transformed rat fibroblast line A_5-C, has integrated about 80% of the adenovirus genome, and several of the early provide the second several of the second several of the second several severa$



HeLa cells are permissive for human adenovirus-2, i.e. the virus that was used to establish the A.T.C. cell line. Exploring infected and mock-infected HeLa cells fore labeled with "S-methio-nine and solubilized glycoproteins were subjected to immunoprecipi-tation. A rabbit anti-human class I antigen serum precipitated a 19,000 daiton chain together with the heavy and light transplanta-tion antigen chains from the infected cells (Fig. 3, lane 1) but not from the mock-infected cells (Fig. 3 lane 4). Both rabbit antiserum and monoclonal antibodies against human 8,-microglobulin precipi-tated the same set of molecules as the antiferum against the class I antigens (Fig. 3, lanes 2, 3, 5 and 6). Thus, it may be concluded that antisera directed against both the heavy and the light chains of the class I molecules co-precipitate a 19,000 dalton virus protein.

The 19,000 dalton virus-coded polypeptide chain could also be precipitated by an antisem raised against the purified virus glycoprotein both from A75.C cells (14) and from adenovirus -infected but not mock-infécted HeLa cells. In both cases class I antigens were co-precipitated (not shown).



Figure 3 Co-precipitation of class I antigens and the E19 protein in ademoviru-but not mock-infected Mela cells. Fluorography of an SSS-polyacryl-anide slab-gel showing jamunopre-cipitates obtained from S-methio-nine-labeled, adenovirus-infected (lanes 1-3) or mock-infected (lanes 4-6) Mela cells. The rabbit sera used were directed against HA, 8 against directed against HA, 9 against of S, A S-at conclusion (lanes 2-3) and S, A S-at conclusion (lanes 3-3) and S-at conclusion (lanes 3-3) and S) was also used.

identification of the constituent chains of the class I antigen-virus protein complex derived from $A_2T_2C_4$ cells The polypeptides precipitated from $A_2T_2C_4$ cells by a rabbit anti class I antigen serum were compared to finas I antigens of ayngeneic spieen cells. The immunoprecipitates, containing H- and C-labeled phenylalanine, respectively. were separately resolved by SDS polyacrylamide gel electrophoresis. The 44 000 dalton chains were recovered from the gels, mixed, digested with trypsin and subjected to reverse phase HPLC. Fig. 4 shows that the two 44 000 dalton chains were identical as regards their phenylalanine-containing, tryptic peptides.

tryptic peptides. In a separate experiment the tryptic peptides of the 44,000 dalton chain, isolated by co-precipitation with the E19 protein from A.T.C. colls, were shown to be identical to the tryptic peptides of the class I antigen heavy chains of A.T.C. cells (not shown). Likewise, the 44,000 dalton chain co-precipitated with the E19 protein from adenovirus-infected HeLa cells displayed a peptide pattern indistinguishable from that of class I antigen heavy chains of the mock-infected cells.

The complete nucleotide sequence of the E19 gene (31) in conjunction with limited radiochemical protein sequence information on the signal sequence of the E19 protein (32) have established the entire amino acid sequence of the protein. We examined whether the E19 protein of $A_{T,C}^{-2}$ cells, which co-precipitated with class I antigens, is 10eht[cal to the E19 gene product, $A_{T,C}^{-2}$ cells were separately labeled with "H-19sine and "H-phenylalanine" and the E19

protein was isolated by immunoprecipitation of the class I antigens. Following SDS-polyacrylamide gel electrophoresis the E19 protein was recovered from the gel and subjected to automatic amino acid sequence determination. The identification of phenylalamines in positions 6 and 15 and of lysines in positions 2, 3 and 7 (Fig. 5) is in agreement with the amino acid sequence predicted from the nucleotide sequence.



Figure 4 Figure 4 Comparison of the 44,000 dalton chain co-precipitated with the E19 protein and class I molecules of spleen cells fliph-pressure liquid chromatography on a Bondapac C18 column of tryptic digests of 44,000 dalton material from M-phenylalanine-labeled Mooded Lister spleen (C-phenylalanine-labeled X-C_c cells, respectively). The glycoprotein fractions of the labeled cells were separately isolated by affinity chromato graphy on <u>Lens</u> column for the spleen the separately isolated by affinity chromato with an antiserum against class I antigens. The spleen the superschleted to SDS-polycarylanid ge leiceophores of 44,000 were recovered, mixed and subjected to tryptic diggetion. Details are given under Experimental Procedures. A K K Y E F K E F A C N Y T F K S Phe



Residue number

Pigure 5 Residue number The 19,000 daiton polypeptide is encoded in the denovirus-2 EcoRI-D region The 19,000 daiton polypeptide was isolated by Lemunoprecipitation of material for the 10 polypeptide was isolated by Lemunoprecipitation of material the 10 polypeptide was isolated by Lemunoprecipitation of material for the 10 polypeptide was isolated by Lemunoprecipitation of material the 10 polypeptide was explicitly of the 10 polypeptide was and the 10 polypeptide was explicitly of the 10 polypeptide was explicitly of the determination was performed as described under Experimental Procedures. The NN determination was performed as described under Experimental Procedures. The NN determination be added to code for an adenovirus glycoprotein with a molecular wight of 19,000 (31).

In a control experiment the E19 protein of $A_3T_3C_4$ cells was isolated with the antiserum raised against the E19 protein and subjected to amino acid sequence determination. The result was identical to that documented in Fig. 5.

These data firmly identify the 44 000 and 19 000 dalton polypeptides forming complexes in $A_2 T C_2$ cells as heavy chains of class I antigens and the E19 proferio di denovirus-2, respectively.

Large class I antigen-E19 protein complexes are revealed by covalent crosslinking

<u>crosslinking</u> Since antibodies seem to affect the stoichiometry of the class I antigen chains and the E19 protein in the complexes (see Table 1) we used the covalent crosslinker DTSP to reduce dissociation during the immunoprecipitations. To there the the set of the spectrum of the errors linked, immunoprecipitated and separated by SDS polyacrylamide gel electrophoresis. Crosslinked proteins of $A_{1,T_{c}}$ cells (Fig. 6B) and infected HeLa cells (Fig. 6E) precipitated by antisera against class I antigen heavy chains remained at the top of the gels while immunoprecipitates of non-crosslinked proteins gave the expected electrophoresis. GS bolyacrylamide gel electrophoresis (Fig. 6C) and re-examined by SDS polyacrylamide gel electrophoresis (Fig. 6C) and F). Only class I antigen chains and the E19 protein were resolved after de-crosslinking with a slight change in their relative propotions

These observations strongly suggest that adenovirus-infected and transformed cells contain fragile class I antigen-E19 protein complexes of large sizes. Moreover, the data support the notion that these complexes exclusively consist of class I antigen chains and the E19 protein.



Figure 5 Evaluate tensolinking of class I agtign-859 protein The glycoprotein fractions of S-methionine labeled A_T_C_ cells (A-C) and adenovirus-infected Hela cells (D-F) were separately treated with the cleavable crosslinker DFS. Immuporcipitations were carried out with rabbit antisera specific for murine (A-C) and human (D-F) class I antigen heavy chains, respectively, and the precipitated molecules were separated by SDS-polyacyllanide gel electrophoresis. A and D display immunoprecipitates obtained prior to the crosslinking of the immunoprecipitates. The arrows denote the migration positions of the marker proteins where molecular weights are given in kilodal-tons.



Complex formation of class I transplantation antigens and a viral glycoprotein.

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