Table 1. Formation (affinity) constants.

Ion	Bicine		TES, log K_{1B}
	log K_{1B}	log K_{2B}	
H^+	8.39 ± 0.01		7.60 ± 0.01
Cu(II)	8.07 ± 0.01	5.40 ± 0.02*	3.90 ± 0.02†
Co(II)	5.30 ± 0.01	3.38 ± 0.02	2.07 ± 0.02
Zn(II)	5.37 ± 0.01	2.67 ± 0.03	2.08 ± 0.02
Mn(II)	3.02 ± 0.01		‡
Ca(II)	2.66 ± 0.01		~ 0

*See Eqs. 10 and 11. †See Eqs. 12 and 13. ‡Hydrolysis and precipitation are concomitant with any complex formation.

The values for K_{1a} and K_{OH} are $10^{-12.36 \pm 0.02}$ and $10^{-10.42 \pm 0.02}$, respectively. On the other hand, TES forms much weaker metal complexes with metal ions (no complex formation with Ca^{2+}) than bicine. However, the 1:1 Cu(II)–TES chelate undergoes hydrolysis (Eq. 12) and subsequent dimerization (K_D) (Eq. 13) in the neutral *p*H range (*5*)

$$Cu(TES)^+ \overset{K_{OH}}{\rightleftharpoons} Cu(TES)OH + H^+ \quad (12)$$

$$2Cu(TES)OH \overset{K_D}{\rightleftharpoons} Cu_2(TES)_2(OH)_2 \quad (13)$$

The values for K_{OH} and K_D are $10^{-6.62 \pm 0.02}$ and $10^{+2.30 \pm 0.04}$, respectively. It is obvious from the above reactions that not only do "Good's" buffers complex metal ions but also that the metal complexes formed have a rich solution chemistry. These latter reactions further buffer H^+ concentration (Eqs. 10 through 12) and strengthen the metal complexes formed (Eq. 13).

Although the constants listed in Table 1 are on the whole small compared to those of metal ions for active sites of apoenzymes (10^{10} to 10^{20}), they are of sufficient strength to lead workers to erroneous conclusions in systems of low metal-binding capabilities, for example, fluorescence quenchers, spin labels, and paramagnetic shift reagents. Furthermore, the "Good's" buffer ADA forms a very stable chelate with Cu(II) ($K_1 = 10^{10.57}$)[2], rivaling that of apoenzymes, and Ca(II) ($K_1 = 10^{4.01}$)[2]. The latter constant is high enough to cause the extraction of labile Ca(II) from enzymes or other biochemicals, thereby altering the structure of the protein with concomitant loss of activity.

The users of "Good's" buffers should no longer assume, as is generally believed, that they do not complex metal ions below or at physiological *p*H values. Studies on the following "Good's" buffers, ACES {2-[(2-amino-2-oxoethyl)amino]ethanesulfonic acid}, ADA, BES, bicine, and TES indicate that all complex metal ions. The general tendency to bind M(II) is in the order ADA > bicine > ACES > BES ~ TES. The last three of these buffers, however, do not bind Ca(II). Those doing studies in the presence of these buffers and metal ions should take into account the metal complexes formed and their possible deleterious effects on the interpretation of data collected in their presence. Routinely used buffers other than those developed by Good *et al.* (*1*) have also been shown to complex metal ions, most notable tris, [tris(hydroxymethyl)methylamine] (*6*).

ROBERT NAKON
C. R. KRISHNAMOORTHY
Department of Chemistry,
West Virginia University,
Morgantown 26506

References and Notes

1. N. E. Good *et al.*, *Biochemistry* **5**, 467 (1966).
2. R. Nakon, *Anal. Biochem.* **95**, 527 (1979); J. M. Pope, P. R. Stevens, M. T. Angotti, R. Nakon, *ibid.* **103**, 214 (1980).
3. Potentiometric formation curves were obtained at 25.00° ± 0.05°C and 0.1*M* (KNO_3) ionic strength on a Corning Digital 130 research model *p*H meter. Metal ion concentrations were ~ 0.025*M*.
4. Visible spectra (not shown) of 2:1 bicine–Cu(II) solutions from **a** = 0 to **a** = 2.0 (**a** is the number of moles of base per mole of complexing agent) evince a monotonic shift in maximum wavelength (λ_{max}) and extinction coefficient (ϵ_{max}) from **a** = 0.0 to 1.0, indicating the formation of [Cu(bicine)$_2$]. The λ_{max} value at **a** = 1.0 is 610 nm, in good accord with the value for a variety of other bis(aminoacidate)copper(II) chelates ($\lambda_{max} \simeq 605$ nm [R. Nakon, E. Beadle, Jr., R. J. Angelici, *J. Am. Chem. Soc.* **96**, 719 (1974)]. From **a** = 1.0 to 2.0, λ_{max} shifts monotonically to lower energy (λ_{max} = 724 nm at **a** = 2.0); this behavior indicates the loss of an aminoacidate ligand (Eq. 10). The λ_{max} and ϵ_{max} values of 1:1 and 2:1 bicine–Cu(II) solutions at **a** = 3.0 and 2.0, respectively, are 724 nm and 64 M^{-1} cm^{-1}, an indication that both solutions contain the same species, [Cu(H_{-1} bicine)OH^-]. The electron spin resonance spectra of 1:1 and 2:1 bicine—Cu(II) solutions at **a** = 3.0 and 2.0, respectively, are identical; similarly, at **a** = 1.0 and 0.5, respectively, identical spectra were observed. However, the 2:1 spectrum at **a** = 1.0 was never seen in any 1:1 spectrum from **a** = 0.0 to 3.0. The species at **a** = 3.0 (2.0) is [Cu(H_{-1} bicine)OH^-], at **a** = 1.0 (0.5) is [Cu(bicine)$^+$], but at **a** = 1.0 (2:1 system) is [Cu(bicine)$_2$].
5. Visible spectral data of 1:1 TES–Cu(II) solutions show no large blue shift until *p*H > 11, an indication that there are no alcohol deprotonation reactions in the acidic or neutral *p*H regions.
6. J. L. Hall, J. A. Swisher, D. G. Brannon, T. M. Linden, *Inorg. Chem.* **1**, 409 (1962); K. S. Bai and A. E. Martell, *J. Inorg. Nucl. Chem.* **31**, 1697 (1969).

2 March 1983; revised 9 May 1983

Nucleotide Sequence of a Light Chain Gene of the Mouse I-A Subregion: $A\beta^d$

Abstract. *Ia (I region–associated) antigens are cell-surface glycoproteins involved in the regulation of immune responsiveness. They are composed of one heavy (α) and one light (β) polypeptide chain. We have sequenced the gene encoding the $A\beta^d$ chain of the BALB/c mouse. The presence of six exons is predicted by comparison with the complementary DNA sequences of human β chains and with partial protein sequence data for the $A\beta^d$ polypeptide. Sequence comparisons have been made to other proteins involved in immune responses and the consequent implications for the evolutionary relationships of these genes are discussed.*

The major histocompatibility complex (MHC) of the mouse is a cluster of genes encoding at least three different classes of proteins involved in immune responses (*1*). Class I molecules, the classic transplantation antigens, and class II molecules are cell-surface, membrane-bound glycoproteins. Class III molecules are serum protein components of the complement pathway. While class I proteins are found on essentially all cells, class II representatives appear limited mainly to the surface of B cells and to antigen-presenting cells such as macrophages. Class II proteins are required for antigen presentation and lymphocyte interactions involved in the activation and differentiation of antibody-producing cells or B cells (*2*). Murine class II genes are located in the I (immune response) region of the MHC and are consequently referred to as I region–associated or Ia antigens (*3*).

Two types of Ia antigen have been defined in mice, I-A and I-E. Both are composed of two noncovalently linked polypeptides, a heavy chain (α) of about 34,000 daltons and a light chain (β) of about 28,000 daltons (molecular size). In the past 2 years, advances in protein microsequencing and recombinant DNA technologies have led to a definition of the primary structure of various human and murine class II molecules (*4–14*). Both α and β polypeptides may be divided into two external domains of approxi-

mately 90 residues each (termed α_1 and α_2 for the α chain or β_1 and β_2 for the β chain), a transmembrane region about 30 residues long, and a cytoplasmic tail of about 15 residues.

We have determined the complete nucleotide sequence of the class II $A\beta^d$ gene. This structure, together with class I and class II genes that have been analyzed, permit us to discuss several interesting evolutionary features about the supergene family including the MHC and antibody genes.

An $A\beta$ gene was isolated from a cosmid library constructed from BALB/c (d haplotype) sperm DNA by screening with a complementary DNA (cDNA) probe of a human I-A region homolog, DC-β (*15*). We have sequenced 5.8 kilobases (kb) of cosmid clone 34.2 overlapping the region of DC-β hybridization. The sequencing strategy and gene organization are shown in Fig. 1 and the DNA sequence in Fig. 2. The predicted amino-terminal protein sequence is identical to that previously defined for the BALB/c $A\beta^d$ protein (*4, 5*).

The coding sequence of $A\beta^d$ is distributed among six exons. All exons have the appropriate donor and acceptor RNA splice sites. The first exon encodes a 27-residue-long putative signal peptide with 25 consecutive hydrophobic or neutral amino acids. It is identifiable because it begins with a methionine and the first four amino acids of the mature protein. The length of the $A\beta^d$ messenger RNA, 1.4 kb, and the lack of hybridization of probe 1 (Fig. 1) with BALB/c poly(A)$^+$ (polyadenylated) messenger RNA (mRNA) (see below) limits the extent of the 5′ untranslated region to less than 150 bp upstream of the initiation codon. Consistent with this, the canonical promoter-associated sequence CCAAT (C, cytosine; A, adenine; T, thymine) is found about 135 bp 5′ to the methionine codon. However, no recognizable candidate for the Hogness-Goldberg TATA box can be found within the 200-bp stretch 5′ of this codon. The $E\alpha^k$ gene also lacks a canonical TATA box (*13*), although it does have an AT-rich area missing from $A\beta^d$. It remains to be seen whether the partial or complete absence of such sequences will be a common feature of murine class II genes and, if so, whether this will have any significance for their regulation.

The other five exons were defined on the basis of similarity with two human cDNA sequences: DC-β (*11*) and DR-β (*12*). The two external domains are encoded by exons 2 and 3. Each contains a pair of cysteines, presumably involved in intradomain disulfide bridges. The predicted β_1 domain amino acid sequence contains one potential glycosylation site (Asn-Glu-Thr) beginning at residue 19. This site is also conserved in both human sequences. The fourth exon encodes three different structural elements: a hydrophilic-connecting peptide (amino acids 190 to 199), a hydrophobic or uncharged transmembrane segment (200 to 220), and a hydrophilic cytoplasmic tail (221 to 226). The transmembrane element is apparently anchored in the cell membrane by three basic residues (Arg-His-Arg) on the cytoplasmic side. Exon 6 encodes the last four amino acids of the cytoplasmic tail. A poly(A) addition signal (AATAAA) is found 280 nucleotides 3′ to the termination codon. The predicted 3′ untranslated sequence is found by computer analysis to be weakly, but recognizably similar to that of the DC-β cDNA.

The cytoplasmic region of the DR-β cDNA is eight codons longer than that of the DC-β cDNA. Alignment of all three β sequences suggests that the size difference is internal and not simply a 3′ truncation of the DC-β coding sequence relative to that of the DR-β cDNA. This relative insertion is located between exon 4 and exon 6 and led us to suspect there may be an additional cytoplasmic exon in the intervening sequence. A search of this intron revealed only one 24-base sequence bounded by the appropriate RNA donor and acceptor splice signals with an open reading frame in phase with the adjacent exons that shares similarity with the extra sequence of the DR-β clone. A restriction fragment including this sequence (probe 3, Fig. 1) was hybridized to BALB/c spleen poly(A)$^+$ mRNA on a nitrocellulose filter (Northern blot) (*16*) yielding a band at 1.4 kb, which is the same size as the $A\beta^d$ mRNA. The same mRNA did hybridize to another coding sequence (probe 2) but did not hybridize to a noncoding region (probe 1). We therefore include exon 5 as part of the expressed mouse gene sequence and assume that the DC-β gene

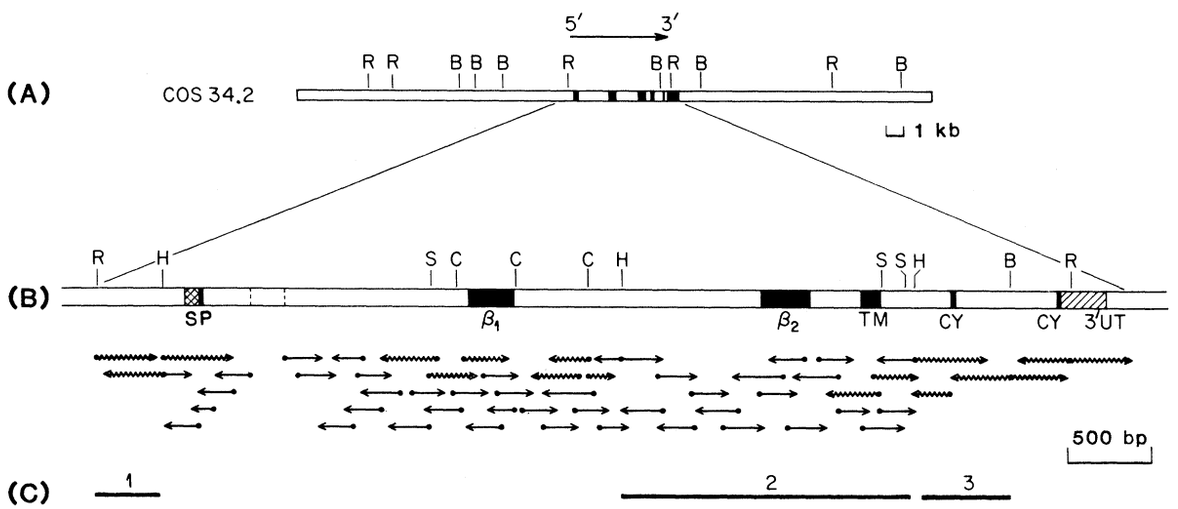
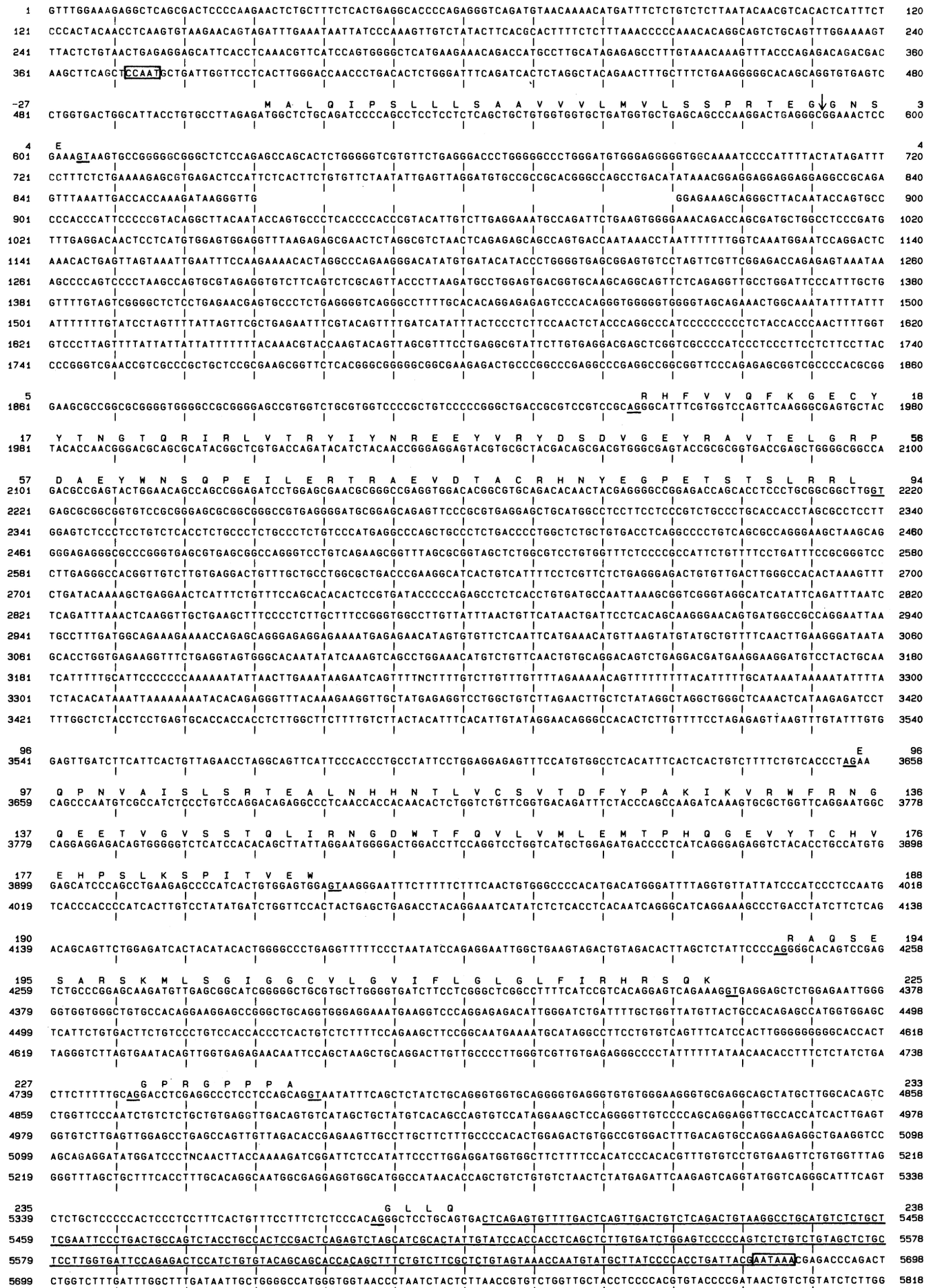


Fig. 1. The organization and sequencing strategy for the $A\beta^d$ gene. (A) Partial restriction map of the cosmid clone 34.2. Filled areas indicate exons. The arrow above shows the direction of transcription. Restriction enzyme names have been abbreviated as *R* (Eco RI) and *B* (Bam HI). (B) Structure and sequence strategy for the $A\beta^d$ gene. Arrows beneath indicate the sequencing strategy. Straight arrows give the sequence obtained by the dideoxy chain termination method (*20*). The two Hind III fragments were subcloned into the Sma I site of M13mp8 (*21*) in both orientations. Each subclone was used to generate a series of overlapping subclones by a deoxyribonuclease I deletion technique (*22*). Wavy arrows indicate the direction and length of sequences obtained by the chemical degradation method (*23*). *SP* refers to the signal peptide, β_1 and β_2 to the two external domains, *TM* the transmembrane portion of the protein, *CY* the cytoplasmic part, and *3′UT* the 3′ untranslated region of the mRNA. The region between the two dotted lines shown in the gene map has not been sequenced. Abbreviations for restriction enzymes not listed in (A) are *H* (Hind III), *S* (Sac I), and *C* (Sac II). (C) Different probes used in the Northern blot analysis (*16*).



has lost this exon subsequent to the divergence of humans and mice (*17*).

Similarity comparisons were made between defined regions of mouse and human Ia polypeptides. The greater similarity of $A\beta^d$ to DC-β (76 percent) than to DR-β (65 to 68 percent) supports the model that DC-β is the human homolog of the mouse I-Aβ molecule (*18*). The relative similarities between the equivalent domains of $A\beta^d$ and DC-β indicate that the first domain is the more divergent of the two external domains (66 and 86 percent, respectively). The high degree of similarity between the connecting peptides (90 percent) and transmembrane regions (86 percent) of human and mouse sequences is rather surprising in view of their presumably general functions. Conservation between similar regions of I-E–like α chains, class I molecules, and immunoglobulins is much less. This level of conservation leads us to suspect that the connecting and transmembrane regions may be involved in the interaction with the α chain or some other membrane protein rather than serving just as hydrophobic anchorage. The size difference between the $A\beta^d$ and DC-β cytoplasmic regions implies that significant variation of this region may have less severe selective consequences than it would for other regions of the gene.

Computer analysis reveals no significant similarity between the β_1 and β_2 domains of $A\beta^d$ nor between β_1 and any domain of any other gene involved in immune responses. However, the β_2 domain is significantly similar to the α_2 domains of class II proteins, the third external domain (α_3) of class I heavy chains, β_2-microglobulin, and immunoglobulin constant-region domains. A computer-aided alignment was made between most of the known representatives of these "Ig-like" domains. The alignment (data not shown) shows a striking conservation of functionally similar residues responsible in immunoglobulins for the β-pleated sheet regions of a tertiary structure referred to as the antibody fold (*19*). The alignment shows that the class I, class II, and β_2-microglobulin sequences are roughly comparable in their similarities to each other as well as comparably less similar to immunoglobulin sequences, establishing two evolutionary subgroups.

The organizations of the $A\beta^d$ gene, a class II α gene, a class I heavy chain, and β_2-microglobulin are shown in Fig. 3. The most striking comparison to be made from Fig. 3 is between class II α genes and β_2-microglobulin. Note particularly (i) the distances between the signal peptide and the Ig-like domain, (ii) that the first few amino acids of each mature protein are encoded with the signal peptide by the first exon, and (iii) the rare occurrence of an intervening sequence in the 3′ nontranslated region of both genes. The $A\beta^d$ gene shares the first two features but not the third one. Also, like the class I genes and not the class II α genes, the cytoplasmic coding sequence of $A\beta^d$ occurs on multiple exons.

These organizational comparisons support the suggestion (*14*) that class II α chains and β_2-microglobulin are more directly related evolutionarily than are class II α and β chains. It also was suggested that class I and class II genes might not be paralogous evolutionarily, but are each the result of de novo gene construction through the process of "exon shuffling." However, the structure of the $A\beta^d$ gene as presented here is not as dissimilar to class I genes as is the Eα gene. Moreover, though not significantly similar over their entire length, the first external domains of class I heavy chains (α_1) and the β_1 domains of class II β chains do share a highly conserved peptide sequence about residue 40 (Val-Arg-Phe-Asp-Ser-Asp). $A\beta^d$ differs by one conservative substitution (Phe to Tyr). The shorter α_1 domains of class II α chains possess a similar and completely conserved sequence, Phe-Asp-Gly-Asp, about residue 30, but have no better than random similarity beyond this with the α_1 domains of class I or β_1 domains of class II. The conservation of sequence across all examples of class I and class II molecules and the structural similarities of the genes support a direct evolutionary connection between class I and class II genes, particularly those of class II β chains.

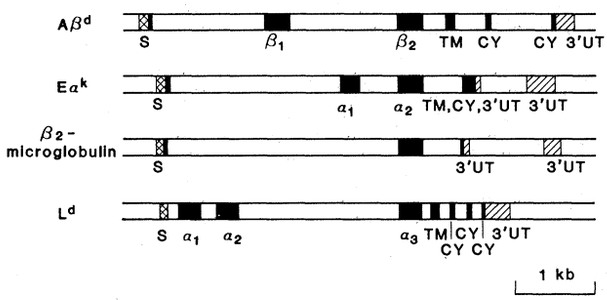


Fig. 3. Comparison of the intron-exon organization of class I, class II, and β_2-microglobulin (*24*). The $A\beta^d$ is representative of a class II β chain, the $E\alpha^k$ (*13*) of a class II α chain, and L^d of a transplantation antigen heavy chain (*25*). Solid, filled areas encode residues present in the mature proteins, crossed areas show the portions encoding the signal peptides, and hatched boxes represent the 3′ untranslated sequences. The abbreviations are the same as in Fig. 1; β_1 and β_2 and α_1 and α_3 refer to exons encoding the external domains of the protein.

Antigen triggering of cellular and humoral immune responses requires the recognition by different T-cell populations of antigens presented in the context of class I or class II molecules. The charged nature of the conserved peptide probably ensures its residence on the exterior of the molecule. As a conserved, exposed determinant, this peptide sequence may play a homologous role in T cell recognition of both class I and class II antigens. It is possible then that not only are class I, class II, and β_2-microglobulin related by distant ancestry to immunoglobulin, but that class I and class II antigens are derived from the same ancestral two-chain polypeptide involved in prototypical lymphocyte interactions.

Note added in proof: Comparison of the $A\beta^d$ sequence with that of the b-haplotype allele (*26*) indicates a relative deletion of an Alu-like (β_1) repeat sequence in the second intron of $A\beta^d$. Computer analysis reveals a repeat-like element only vaguely similar to β_1 about 300 bp 5′ of the β_2 domains of both alleles.

Fig. 2. The DNA sequence of 5.8 kb of the cosmid clone 34.2 containing the Aβ gene. The RNA splicing donor and acceptor sites (GT-AG) (G, guanine) are underlined as is the probable 3′ untranslated region. A possible CCAAT box and poly(A) addition signal sequence are boxed. The gap shown between bases 870 and 871 represents less than 200 bases of undetermined sequence. The predicted amino acid sequences encoded by the exons are shown above the DNA. Single-letter amino acid codes are placed above the middle bases of the translated codons. The single-letter amino acid code is abbreviated as follows: A, alanine; C, cysteine; D, aspartic acid; E, glutamic acid; F, phenylalanine; G, glycine; H, histidine; I, isoleucine; K, lysine; L, leucine; M, methionine; N, asparagine; P, proline; Q, glutamine; R, arginine; S, serine; T, threonine; V, valine; and W, tryptophan.

MARIE MALISSEN
TIM HUNKAPILLER
LEROY HOOD

Division of Biology,
California Institute of Technology,
Pasadena 91125

References and Notes

1. J. Klein, A. Juretic, C. Baxevanis, Z. Nagy, *Nature (London)* **291**, 455 (1981).
2. A. Singer, Y. Asano, M. Shigeta, K. S. Hathcock, A. Ahmed, C. G. Fathman, R. J. Hodes, *Immunol. Rev.* **64**, 137 (1982).
3. H. O. McDevitt, *J. Immunogenet.* **8**, 287 (1981).

4. J. M. Cecka, M. McMillan, D. B. Murphy, H. O. McDevitt, L. Hood, *Eur. J. Immunol.* **9**, 955 (1979).
5. E. Sung, M. W. Hunkapiller, L. E. Hood, P. P. Jones, in preparation.
6. H. Kratzin *et al.*, *Hoppe-Seyler's Z. Physiol. Chem.* **362**, 1665 (1981).
7. C. Auffray, A. J. Korman, M. Roux-Dosseto, R. Bono, J. L. Strominger, *Proc. Natl. Acad. Sci. U.S.A.* **79**, 6337 (1982).
8. C. O. Benoist, D. J. Mathis, M. R. Kanter, V. E. Williams II, H. O. McDevitt, *ibid.* **80**, 534 (1983).
9. A. J. Korman, C. Auffray, A. Schamboeck, J. L. Strominger, *ibid.* **79**, 6013 (1982).
10. J. S. Lee *et al.*, *Nature (London)* **299**, 750 (1982).
11. D. Larhammar *et al.*, *Proc. Natl. Acad. Sci. U.S.A.* **79**, 3687 (1982).
12. E. O. Long, C. T. Wake, J. Gorski, B. Mach, *EMBO J.* **2**, 389 (1983).
13. D. J. Mathis, C. O. Benoist, V. G. Williams II, M. R. Kanter, H. O. McDevitt, *Cell* **32**, 745 (1983).
14. J. McNicholas, M. Steinmetz, T. Hunkapiller, P. Jones, L. Hood, *Science* **218**, 1229 (1982).
15. M. Steinmetz *et al.*, *Nature (London)* **300**, 35 (1982).
16. M. Kronenberg, M. M. Davis, P. W. Early, L. E. Hood, J. D. Watson, *J. Exp. Med.* **152**, 1745 (1980).
17. The fifth exon sequence has been demonstrated in the cDNA sequence of the d-haplotype allele of Aβ [E. Choi, K. McIntyre, R. N. Germain, J. G. Seidman, *Science* **221**, 283 (1983)].
18. J. R. Bono and J. L. Strominger, *Nature (London)* **299**, 836 (1982).
19. D. Beale and A. Feinstein, *Quant. Rev. Biophys.* **9**, 135 (1976).
20. F. Sanger, A. R. Coulson, B. G. Barrel, A. J. H. Smith, B. A. Roe, *J. Mol. Biol.* **143**, 161 (1980).
21. J. Messing and J. Vieira, *Gene* **19**, 269 (1982).
22. S. Anderson, *Nucleic Acids Res.* **9**, 3015 (1981).
23. A. M. Maxam and W. Gilbert, *Methods Enzymol.* **65**, 499 (1980).
24. J. R. Parnes and J. G. Seidman, *Cell* **29**, 661 (1982).
25. K. W. Moore, B. T. Sher, Y. H. Sun, K. A. Eakle, L. Hood, *Science* **215**, 679 (1982).
26. D. Larhammar *et al.*, *Cell*, in press.
27. We thank M. Steinmetz for his help during the initiation of this work, K. Minard for preparation of the sequencing gels, and B. Larsh and S. Olive for preparation of the manuscript. Supported in part by NIH grants (L.H.) and by the Fondation pour la Recherche Médicale (M.M.).

16 June 1983

Pancreatic Islet Allograft Prolongation by Donor-Specific Blood Transfusions Treated with Ultraviolet Irradiation

Abstract. *Survival of allografts of islets of Langerhans in nonimmunosuppressed adult rats was prolonged by transfusions of donor blood irradiated with ultraviolet light before transplantation across a major histocompatibility barrier. This treatment is donor blood–specific and has produced greater than 160-day survival of transplanted islets without the administration of immunosuppressive agents.*

The successful transplantation of allogeneic pancreatic islets in mice depleted of cells bearing I region–associated antigens (Ia) by antiserum to Ia and the enhancement of skin allografts with this antiserum (*1*) suggest that allografted tissue depleted of Ia-bearing cells is accepted without being recognized as foreign. The type of Ia-bearing cell eliminated in such experiments is not known, but appears to be the dendritic cell; Ia-bearing dendritic cells are present in frozen tissue sections of islets and in the parenchyma of human kidneys, hearts, thyroid glands, and skin (*2*). Such a wide distribution suggests that the depletion of Ia-bearing cells from organ allografts may have clinical applicability not only to pancreatic islet transplantation but to transplantation of other organs as well.

Table 1. Effect of UV irradiation on the stimulatory activity of Lewis rat peripheral blood lymphocytes (PBL) in MLR's. Values are means ± standard deviations.

Responder	Stimulator	[^{3}H]thymidine incorporation (count/min)
ACI	ACI	465 ± 153
ACI	Lewis PBL	5371 ± 543
ACI	Lewis PBL and UV irradiation for 20 minutes	772 ± 102

Although abolition of the initial recognition of a foreign allograft by the host is critical to successful allografting without further immunosuppression, maintenance of a functioning allograft may depend on the initiation of donor-specific suppressor T lymphocytes in the host (*3*). Such a state of unresponsiveness to allogeneic tissue is seen when Ia-negative platelets and red blood cells are unable to provoke a primary immune response and attenuate the subsequent challenge with Ia-bearing cells (*3*).

This idea was further supported when treatment of diabetic mice with donor blood depleted of Ia-bearing cells allowed successful transplantation of fresh, untreated allogeneic islets of the blood donor strain (*4*). It appears, therefore, that immunization with Ia-negative donor blood cells induces immunological unresponsiveness to the donor strain in recipients by the stimulation of specific suppressor cells.

Our demonstration of a rapid and simple method of inducing donor-specific immunological unresponsiveness in adult animals that allows long-term survival of islet allografts is consistent with recent clinical studies in which donor-specific transfusions led to 1-year survival of kidney allografts in more than 90 percent of mismatched donor-recipient pairs of one haplotype (*5*). Since ultraviolet (UV) irradiation of the stimulating cell population in a primary mixed-lymphocyte reaction (MLR) leads to little or no proliferative response (*6*), we hypothesized that Ia-bearing cells may not need to be eliminated from blood before its use for immunization, but may need to be inactivated with UV light, leading to abrogation of the stimulating allogeneic signal while leaving major histocompatibility complex antigens intact for the induction of donor-specific immunological unresponsiveness.

Rats of strain ACI (RTl^a) were made diabetic with intravenous streptozotocin (60 mg/kg). A rat was used as a recipient of blood and islets only if its blood glucose concentration exceeded 300 mg/dl for more than 3 weeks. Islet allografts were considered to have been rejected when plasma glucose was greater than 200 mg/dl on two successive daily measurements.

Whole blood was obtained from normal Lewis rats (RTl^l) by intracardiac puncture. The blood was diluted 1:50 in phosphate-buffered saline (PBS), placed with a magnetic stirring bar into 250-ml petri dishes, and irradiated for 20 minutes with two Sylvania FS-20 lamps located 10 cm from the dishes. The blood cells were then centrifuged and the resulting pellet was resuspended in PBS to 50 percent packed cell volume. Each diabetic ACI rat received 1 ml of UV-irradiated blood or 1 ml of identically treated nonirradiated blood adjusted to 50 percent packed cell volume through the penile vein 3 weeks, 2 weeks, and 1 week before islet transplantation. One group of diabetic ACI rats received islets without previous transfusions.

Pancreatic islets were harvested from Lewis (RTl^l) and Wistar Furth (WF) (RTl^u) rats by the collagenase technique (*7*) and Ficoll gradient separation (*8*), with subsequent handpicking under a dissecting microscope. Some 1200 to 1500 freshly prepared allogeneic islets

Table 2. Effect of UV light on the serological reactivity of Lewis rat PBL surface antigens. Values are mean counts (± standard deviations) of ^{125}I-labeled staphylococcal protein A bound per assay (background, 200 count/min).

Antigen	PBL	PBL and UV irradiation (20 minutes)
Rabbit antiserum to rat lymphocytes	2996 ± 172	3315 ± 434
Monoclonal antibodies to rat Ia (MRC/OX4)	2050 ± 421	1963 ± 268