Hemoglobin Loci: Mice Classified for Their Hb and Sol Alleles

Abstract. *Two loci which influence the structure of the alpha and beta chains of hemoglobin have been identified and are designated* Sol *and* Hb. *At least four alleles at* Sol *and two at* Hb *have been distinguished among inbred strains.*

The electrophoretic patterns, single and diffuse, of mouse hemoglobin are governed by the alleles Hb^1 and Hb^2 (*1, 2*). Alleles at *Hb* of many strains of mice have been reported (*3, 4*). A second characteristic, solubility in potassium phosphate buffer (*5*), has been used to distinguish hemoglobins with similar electrophoretic properties (*6*). The solubility and the crystalline properties of hemoglobin are governed by alleles at a second locus, *Sol,* which segregates independently from *Hb* (*7*). The alleles at *Sol* of only a few strains have been reported (*7*), but the alleles at *Sol,* and coincidentally at *Hb,* of 20 strains of mice have been identified and are now presented.

Techniques for identifying alleles at *Sol* and *Hb* after salting out of carbonmonoxyhemoglobin in K_2HPO_4—KH_2PO_4 buffer have been reported (*7*). Strain C57BL mice, whose hemoglobin genotype has been defined by the symbols Hb^1/Hb^1, Sol^1/Sol^1, were mated with mice in which the *Sol* type was to be determined. Other strains of mice, for example SEC, BALB/c, and 101, were used for test crosses after their hemoglobin types had been established. The hemoglobin genotypes of F_1, F_2, and BC_1 progeny were classified by comparing the solubility and crystalline properties of the hemoglobin of each mouse with known types of hemoglobin which were analyzed concurrently. Presumably, progeny possessing hemoglobin with solubility and crystalline properties not previously identified had alleles at *Hb* or *Sol* which had not been previously studied. Whether the solubility properties were governed by alleles at *Hb* or *Sol* could be determined when the strains possessed distinguishable hemoglobin and coat-color markers in the first linkage group, since *Hb* and *c* are fairly tightly linked (*3*) and *c* and *Sol* segregate independently (*7*).

The strains and their hemotypes are presented in Table 1. The crossover frequency between *Hb* and *c* is given where the mating permitted it to be determined.

Inbred strains, for example C57BL, C57BL/6, C57BL/6cc and C57L, that were derived from a common line had similar *Sol* types. A similar relationship between the distribution of *Hb* and the history of development of strains was found by Russell and Gerald (*4*). Although strains A, BALB/c, C3H, and DBA/2 were derived from a common non-inbred stock of mice, three *Sol* genotypes were found among these strains which suggests heterogeneity for *Sol* before inbreeding began. Strain SEC mice, which were derived from progeny of an NB × BALB/c mating, carry the Hb^1 and Sol^2 alleles of their NB and BALB/c parents (*8*).

One previously unknown allele at *Sol* (Sol^4) was discovered during this study. A more complete description of the effect of Sol^4 on the physicochemical properties of mouse hemoglobin is in preparation (*9*). This allele was identified on the basis of solubility studies in conjunction with peptide analyses. The *Sol* alleles of some strains listed in Table 1 have not yet been established.

The nomenclature provides a means for designating several types of mouse hemoglobins based on their electrophoretic, solubility, and crystalline properties. Differences in such physicochemical properties correspond to alterations in the primary structure of the α and β chains (*10, 11, 12*). Analyses of tryptic peptides of the α and β chains of hemoglobins of inbred mice

Table 1. Hemotype of 20 strains of mice. The offspring analyzed were F_2 or BC_1, or both. Crossover frequency is based on F_2 data only.

Strain*	Hemotype	Determined from matings with strains	Offspring analyzed (No.)	Crossover frequency ± s.e. of *Hb* and *c*
C57BL/Cum	Hb^1Sol^1	By definition		
C57L/Rl	Hb^1Sol^1	A	71	
C57BL/6Cum	Hb^1Sol^1	DBA/2	28	
C57BL/6ccLs	Hb^1Sol^1	C3H	57	0.0395 ± 0.0264
FUS/Ls	Hb^1Sol^1	BALB/c	43	0.0938 ± 0.0471
SEC/Rl	Hb^1Sol^2	C57BL	703	
HBS	Hb^1Sol^2	(See *7*)		
NB/Rl	Hb^1Sol^3	BALB/c	200	
101/Cum	Hb^2Sol^1	C57BL	397	
		SEC	139	0.0793 ± 0.0242
A/Cum	Hb^2Sol^1	C57L	71	
RFM/Up	Hb^2Sol^1	C57BL	56	
AKR/Up	Hb^2Sol^1	C57BL	40	0.0667 ± 0.0411
HBD	Hb^2Sol^1	(See *7*)		
DBA/2Cum	Hb^2Sol^1	C57BL/6	28	
		SEC	105	0.0936 ± 0.0381
CFCW/Rl	Hb^2Sol^1	C57BL	79	0.0527 ± 0.0259
		SEC	125	
RUS/Rl	Hb^2Sol^1	C57BL	25	
129/Rl	Hb^2Sol^1	C57BL	85	0.0429 ± 0.0225
CFW/Rl	Hb^2Sol^1	C57BL	113	0.0359 ± 0.0179
BALB/cJ	Hb^2Sol^2	C57BL	250	0.0387 ± 0.0141
		SEC	83	
C3H·B/St	Hb^2Sol^4	C57BL	173	
		SEC	45	0.0394 ± 0.0297
SEAB/Rl	Hb^2Sol†	C57BL	124	
		SEC	108	0.0598 ± 0.0289
WC/Re	Hb^2Sol†	C57BL	97	
		SEC	214	0.0612 ± 0.0224
CBA/Cum	Hb^2Sol†	C57BL	82	
		SEC	132	0.0339 ± 0.0227
FU/Rl	Hb^2Sol†	C57BL	92	0.0367 ± 0.0200
C3H/Cum	Hb^2Sol†	C57BL	25	
C3H·K/ccSn	Hb^2Sol†	C57BL	98	0.0788 ± 0.0286
C3H·K/CCSn	Hb^2Sol†	C57BL/6cc	57	0.0395 ± 0.0264
FLEX/1Re	Hb^1Sol†	101	85	
		SEC	144	
FLEX/2Re	Hb^2Sol†	C57BL	79	
		SEC	152	0.0944 ± 0.0374
11G/1Rl	Hb^1Sol†	101	91	
		SEC	116	
11G/2Rl	Hb^2Sol†	C57BL	25	
		SEC	121	0.1096 ± 0.0399

* Source of mice: Cum: Cumberland View Farms, Clinton, Tennessee; Rl: W. Russell, Biology Division, Oak Ridge National Laboratory; Ls: E. Les, Roscoe B. Jackson, Memorial Laboratory, Bar Harbor, Maine; Up: A. Upton, Biology Division, Oak Ridge National Laboratory; J: Jackson, Roscoe B. Jackson Memorial Laboratory; St: L. Strong, Roswell Park Memorial Institute, Springville, New York; Re: E. Russell, Roscoe B. Jackson Memorial Laboratory; Sn: G. Snell, Roscoe B. Jackson Memorial Laboratory. † *Sol* type is not Sol^1 or Sol^2. Present data do not permit further identification.

and F_2 progeny show that the primary structure of the α and β chains of mouse hemoglobins are governed by *Sol* and *Hb* (*10, 11*). The data presented here provide a basis for selecting several different mouse hemoglobins for further studies on: (i) allelomorphism and amino acid sequences, and (ii) molecular structure and biological function.

Additional information on the crossover frequency between *c* and *Hb* and on the position of *Sol* in the mouse genome is also given. Data on the crossover frequency between *c* and *Hb* are presented in Table 1. These values were calculated by the product method (*13*) from F_2 data alone since we obtained comparatively little data on backcrosses in which crossovers between alleles at *c* and *Hb* were phenotypically expressed. Crossover frequencies from different matings varied considerably (Table 1) and ranged from 3.39 to 10.96 percent among relatively small samples. The average recombination value (1459 mice) for the combinations reported here is 0.0647 ± 0.0067, which is slightly higher than the value of 0.0413 ± 0.0061 reported earlier (*3*). Combined analysis of the backcross data (359 mice) gives a crossover value of 0.0947 ± 0.0155, which is somewhat higher. These values were computed from many strains of mice not previously used; for some strains, the recombination frequency between *c* and *Hb* appears to be greater than 5 percent. Since the progeny were classified for coat-color and other visible phenotypic differences, a comparison of such phenotypes with *Sol* types indicates that *Sol* is not sex-linked or closely linked with *p, c, Hb, d, se, W, s, A, Ca, b, Fu, ru, ln, f, Es, fs,* or with the black-eyed white trait of strain C3H.B. Furthermore, no selective survival of mice with any of the *Sol* types was noted.

Inheritance of hemoglobin in mouse and man appears to be similar. Two loci, which segregate independently, control the primary structure of the α- and β-chain polypeptides. In mice with two or more hemoglobins distinguishable by electrophoresis the β-chain locus may be compound, or two loci may be tightly linked as are the β- and δ-chain loci in man. Knowledge of whether the β-chain locus and albinism are linked in man as they are in the mouse would help to determine whether homologous portions of the chromosome have remained intact during evolution. Mating mice of known hemoglobin genotypes makes the mouse useful for investigating some hypotheses concerning the inheritance of hemoglobin.

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Plankton: Optimum Diversity Structure of a Summer Community

Abstract. *The summer plankton community of the York River, Virginia, expends energy to establish and maintain a definite vertical diversity structure in a comparatively unstructured environment. The resultant organization, which involves relationships between diversity, power and efficiency, and stability, is nearly optimal for maximizing profit on the original energy investment.*

How energy balance is achieved in a natural plankton community can be viewed from the standpoint of linear programming (*1*). The community is construed at a given time as having a pool of resources, such as nutrients, growth substances, stocks of organisms with various requirements and properties, and an energy supply. The problem is how to allocate the resources in such a way as to produce an optimum species composition, one which would bring to maximum the community's energy profit under existing conditions in the biotope.

To set this up for linear programming, we might define m as the number of species i in the pool ($i = 1, 2, \ldots, m$); n as the number of resources j ($j = 1, 2, \ldots, n$); a_{ij} as the number of units of resource j required to produce a unit of species i; b_j as the maximum number of units of resource j available; p_i as the energy profit per unit of species i produced; and x_i as the number of units of species i produced. Then, the total amount of the jth resource used is

$$a_{1j}x_1 + a_{2j}x_2 + \ldots + a_{mj}x_m$$

subject to the constraint

$$\sum_{i=1}^{m} a_{ij}x_i \leqq b_j.$$

Since $x_i < 0$ has no meaning, we stipulate $x_i \geqq 0$. The profit derived from producing x_i units of organism i is then p_ix_i, giving for a profit function

$$p_1x_1 + p_2x_2 + \ldots + p_mx_m,$$

which is to be maximized. The solution, readily obtained by established procedures, represents the optimum composition (diversity) of the community corresponding to the prescribed conditions of the problem and the profit-maximizing motive.

Although such a formulation would be difficult to apply empirically (for example, trying to provide data for a_{ij} and p_i), as a model it delineates the enormous problem in logistics and communication associated with evolving and maintaining optimum structure in a community. In this context, let us consider the problem of optimum diversity in a particular summer plankton community.

Energy flow in the community at a station in the lower York River, Virginia, was studied during the summer of 1960 by means of dark and light bottle microcosms (*2*); the primary variables measured were gross production (π) and respiration (ρ) of the enclosed samples. Ten 24-hour experiments were conducted. The depths investigated were 2, 6, and 10 feet. Since the mean 24-hour compensation depth (the depth at which $\pi = \rho$) was 6.5 feet, the samples from 2 feet were naturally in positive energy balance ($\pi - \rho > 0$), those from 6 feet were approximately in steady state ($\pi - \rho \approx 0$), and those from 10 feet were in negative balance ($\pi - \rho < 0$). In the field, water samples were enclosed in paired dark and light BOD bottles and resuspended in the water column. The dark bottles were suspended at the same depths from which the samples they contained had been collected,