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Allelic expression and genetic distance in hybrid macaque monkeys

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THE TIME and place that a given structural gene locus is activated during an organism's development depends in part upon other genes that constitute the genetic regulatory apparatus of a genome[7,8,10]. Regulatory genes of a species have been strongly selected to properly interact with their own structural genes, but there is no reason to suppose that regulatory genes should also properly cope with structural genes belonging to different species that may have evolved independently for thousands or millions of years[30]. At present there are no direct methods of assaying how different are the regulatory genes of species. One indirect approach is to study patterns of structural gene expression in interspecific hybrids combining maternal and paternal genomes with different evolutionary histories.

Attempts to measure regulatory gene divergence have assumed added significance because of recent hypotheses that evolutionary change primarily involves regulatory genes[8,30,34,37,44]. For example, Wilson and his colleagues argue that the rapid evolution of mammals in anatomy and way of life is the result of rapid regulatory evolution relative to that among frogs, which have undergone much slower rates of organismal evolution[45,46]. They propose that structural genes cannot account for different rates of organismal evolution in different groups, because structural genes appear to evolve at roughly constant rates in all lineages[17,24,26,33,43]. Regulatory evolution may have been particularly rapid in certain primates such as man and chimpanzee, who are very different in anatomy and way of life, but are remarkably similar in their structural genes[24]. In order to test whether regulatory evolution has proceeded more rapidly in some types of organisms than in others, regulatory differences must be compared in groups of species of known evolutionary age, or those exhibiting known degrees of structural gene divergence.

As discussed later, allelic repression in interspecific hybrids provides strong evidence for breakdown in genetic regulation. Various degrees of allelic repression have previously been reported[38–42] in hybrids between species of known degrees of structural gene divergence[3]. The objectives of the present study are threefold: 1) to quantify levels of structural genic divergence at 21 loci encoding blood proteins in six species of macaque (*Macaca*) monkeys; 2) to examine patterns of structural gene expression in hybrids of known parentage in order to indirectly estimate the level of regulatory gene divergence between these species; and 3) to compare results in these macaques with previous results from other organisms that may have undergone different rates of organismal evolution.

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Materials and Methods

Macaque species housed at the Yerkes Regional Primate Center Field Station were selected as subjects. The six species examined, and the sample sizes of the parental species used in calculating genetic distances, are listed in Table I. Different groups of monkeys have been maintained in captivity for various periods of time, and occasionally troops of a species have been split or merged. The oldest group (*Macaca nemestrina*) was established in 1964 (generation length approximately 4–10 years) and none of the groups is highly inbred[13].

Adult monkeys were anesthetized (ketamine) and approximately 3 ml of blood drawn from the saphenous vein. A total of 18 serum proteins and red cell enzymes encoded by 21 genetic loci could be reliably scored using the standard laboratory and starch-gel electrophoretic techniques described elsewhere[12]. The proteins examined are: 1) acid phosphatase (locus *ACP*), adenosine deaminase (*AD*), adenylate kinase (*ADK*), alkaline phosphatase (*AKP*), caeruloplasm (*CR*), carbonic anhydrase (*CA-1*, *CA-2*), NADH diaphorase (*DIA*), glucose-6-phosphate dehydrogenase (*G6PD*), glutamate oxalate transaminase (*GOT*), haptoglobin (*HP*), hemoglobin (*Hb*), isocitrate dehydrogenase (*IDH*), lactate dehydrogenase (*LDH-1*, *LDH-2*), malate dehydrogenase (*MDH*), phosphoglucomutase (*PGM-1*, *PGM-2*), 6 phosphogluconate dehydrogenase (*6PGD*), phosphohexose isomerase (*PHI*), and transferrin (*TR*).

These proteins were chosen for study solely on the criteria of available staining procedures and clarity of banding. Proteins from the various individuals and species were run side-by-side on gels in order to accurately compare mobilities. For each protein and each species, allelic frequencies were determined, and genetic similarities and distances were calculated using Nei's coefficients[28]. Nei's similarity (*I*) statistic may assume values

Table I. Genetic similarities* (above diagonal) and distances* (below diagonal) based on blood proteins encoded by 21 genetic loci in 6 species of *Macaca*

Species	Common name	Sample size	1	2	3	4	5	6
1. *Macaca silenus*	lion-tailed macaque	2†	—	0.883	0.851	0.790	0.912	0.793
2. *Macaca nemestrina*	pig-tailed macaque	27	0.124	—	0.923	0.818	0.899	0.817
3. *Macaca fascicularis*	crab-eating macaque	10	0.161	0.080	—	0.904	0.882	0.815
4. *Macaca mulatta*	rhesus monkey	42	0.236	0.201	0.102	—	0.830	0.779
5. *Macaca tonkeanis*	black stumptail macaque	2†	0.084	0.106	0.126	0.186	—	0.852
6. *Macaca nigra (Cynopithecus niger)*	black ape	31	0.232	0.202	0.205	0.250	0.161	—

* Nei's coefficients
† These species are rare in captivity; larger samples could not be obtained, hence genetic distances are tentative

Table II. Hybrid macaques, their parents, and the number of genetic loci in the hybrids for which one-sided and two-sided tests of allelic expression could be conducted (see text). In none of 14 two-sided tests was the product of a maternal or paternal allele not expressed in a hybrid

Hybrid	Sex	Age when tested (in months)	Parental species: mother	Parental species: father	No. 2-sided tests (loci involved)	No. 1-sided tests (loci involved)
F_1 hybrids						
Ahso	♀	140	*nemestrina*	*fascicularis*	0	1 (IDH)
Boris	♂	137	*nemestrina*	*fascicularis*	1 (*CA-1*)	5 (*Hb*, *IDH*, *CA-2*, *PGM-2*, *TR*)
Edie	♀	108	*nemestrina*	*mulatta*	1 (*CA-1*)	3 (*Hb*, *IDH*, *PHI*)
Gumby	♀	83	*nemestrina*	*fascicularis*	1 (*CA-1*)	4 (*Hb*, *IDH*, *TR*, *CA-2*)
Juno	♀	79	*nemestrina*	*silenus*	1 (*AD*)	2 (*Hb*, *CA-1*)
Luke	♂	75	*nigra*	*tonkeanis*	1 (*Hb*)	0
Minerva	♀	74	*nemestrina*	*nigra*	1 (*CA-1*)	0
Okra	♀	65	*nigra*	*nemestrina*	3 (*TR*, *CA-1*, *PGM-2*)	1 (*CA-2*)
Saffron	♀	57	*nigra*	*nemestrina*	3 (*Hb*, *CA-1*, *PGM-2*)	2 (*TR*, *CA-2*)
Trek	♂	48	*mulatta*	*fascicularis*	0	0
Ultra	♂	47	*nemestrina*	*fascicularis*	0	0
Acorn	♀	37	*nigra*	*silenus*	0	0
Filbert	♂	29	*nigra*	*silenus*	0	0
F_2 hybrids						
Bunker	♂	35	*nemestrina* × *mulatta*	*nemestrina* × *fascicularis*	1 (*TR*)	6 (*Hb*, *IDH*, *DIA*, *CA-1*, *CA-2*, *PGM-2*)
Noname	?	0.5	*nemestrina* × *mulatta*	*nemestrina* × *fascicularis*	1 (*TR*)	4 (*Hb*, *CA-1*, *PHI*, *PGM-2*)
Mandy	♀	10	*nigra* × *nemestrina*	*nemestrina* or *nemestrina* × *fascicularis*	0	1 (*Hb*)
Pumpkin	♀	6	*nemestrina* × *nigra*	*nemestrina* or *nemestrina* × *fascicularis*	0	1 (*Hb*)
Backcross						
Homer	♂	23	*nemestrina* × *silenus*	*nemestrina*	0	3 (*Hb*, *DIA*, *CA-1*)
Les	♂	10	*nemestrina* × *mulatta*	*mulatta*	0	4 (*TR*, *Hb*, *IDH*, *CA-1*)

from 0 to 1, with 1 indicating genetic identity. Genetic distance ($D = -\ln I$) can assume values from 0 to ∞, and may be interpreted as the number of electrophoretically detectable codon substitutions per locus that have accumulated since two populations last shared a common ancestor.

Macaque species do not hybridize in nature, with rare exceptions[5]; but two hybrid groups including F_1, F_2, and backcross progeny resulting from matings of several different pairs of these six macaque species have been produced at the Yerkes Primate Field Center. We have sampled blood from 19 hybrids (Table II) of known individual parentage, and compared structural gene expressions at 21 loci in these hybrids with those expected on the basis of the parental genotypes.

Results

Genetic distances among macaque species

Genetic distances based on 21 genetic loci between six species of macaques are summarized in Table I. These are the first estimates of genetic distances between macaques based on a large number of loci, although information on several proteins has previously been published[16,20,21,27,36]. Genetic distances between pairs of macaque species fall within a very narrow range; the most similar are *Macaca fascicularis* and *M. nemestrina*, $D = 0.080$; the most different are *M. nigra* and *M. mulatta*, $D = 0.250$. Between all pairs of macaque species, $\bar{D} = 0.164 \pm 0.015$. The implications of these findings for the systematic and evolutionary relationships among macaques are discussed elsewhere[13].

For our present purposes, we are interested in comparing structural gene distances between macaques with those between other types of organisms. Comparable information based on multi-locus electrophoretic studies are now available for nearly 250 closely related species including members of *Drosophila* and other invertebrate genera, and congeneric members of each of the vertebrate classes (see summaries in Avise[1] and Ayala[4]). Although a number of exceptions exist, the overall results are surprisingly uniform: congeneric species typically exhibit D values in the range 0.20 to >2.0, with overall mean of roughly 0.5–0.6; subspecies and very closely related species often show $D \simeq 0.20$; geographic populations of a species usually show $D \leq 0.10$. Relative to congeneric species of other organisms, macaques are quite similar to one another in structural genic composition (see also Table III). Yet several macaques show conspicuous morphological differences (see front cover).

Allelic expression in macaque hybrids

The protein products of most loci (12 of 21) exhibited indistinguishable mobilities in most and sometimes all of the macaque species. These loci included *ACP*, *ADK*, *AKP*, *CR*, *G6PD*, *GOT*, *HP*, *LDH-1*, *LDH-2*, *MDH*, *PGM-1*, and *6PGD*[13]. Proteins in hybrids of parents with identical alleles should also yield electrophoretic bands of the same mobility, if either or both parental alleles are activated during development. Decreases in staining intensities of some isozymes in hybrids could presumably reflect decreases in enzyme levels due to partial or complete repression of alleles contributed by paternal and/or maternal genomes. Such instances of decreased hybrid enzyme activity were *not* apparent for any of the monomorphic loci examined in this study (see Figure 1). Nonetheless, partial allelic repression would probably be difficult to detect by gross examination of zymogram patterns for these monomorphic loci.

Much stronger tests for allelic repression are provided by the remaining nine polymorphic systems (*TR*, *Hb*, *IDH*, *AD*, *DIA*, *CA-1*, *CA-2*, *PHI*, and *PGM-2*). For each of these, at least one examined hybrid resulted from a mating between parents with different genotypes. Two types of tests for allelic expression are provided by these hybrids. Two-sided tests are the stronger and are possible in hybrids of individual parents sharing no alleles. Absence of either or both products of two alleles in hybrids would constitute prima facie evidence for disruption of proper gene expression in those hybrids. Examples of such matings are as follows: $AA \times BB \rightarrow AB$; $AB \times CD \rightarrow AC, AD, BC$, or BD. One-sided tests are possible in hybrids of parents differing in genotype but sharing at least one allele (examples $AB \times AA \rightarrow AA$ or AB; $AB \times BC \rightarrow AB$, BB, AC, or BC). Presence of products of two alleles in such hybrids evidences a lack of allelic repression, but presence of a single

Table III. Allelic repression and genetic distance among sunfish (family Centrarchidae) and among macaques; evidence for allelic repression is taken from Avise and Smith[2], Whitt et al.[40], and references therein. Genetic distances (Nei's coefficient) of sunfish are taken from Avise and Smith[3]

Hybridizing species or subspecies	No. loci examined for allelic repression	Loci exhibiting allelic repression %	Genetic distance (D)	No. loci
Sunfish				
Lepomis macrochirus macrochirus × *L. m. purpurescens*	15	0.0	0.181	15
Micropterus dolomieui × *M. salmoides*	4	0.0	—	—
Lepomis macrochirus × *L. microlophus*	6	0.0	0.948	11
Lepomis cyanellus × *Micropterus salmoides*	14	21.4	0.769	11
Lepomis microlophus × *"Chaenobryttus" (Lepomis) gulosus*	5	40.0	0.980	14
Macaques				
Various pairs of 6 species	21	0.0	0.164	21

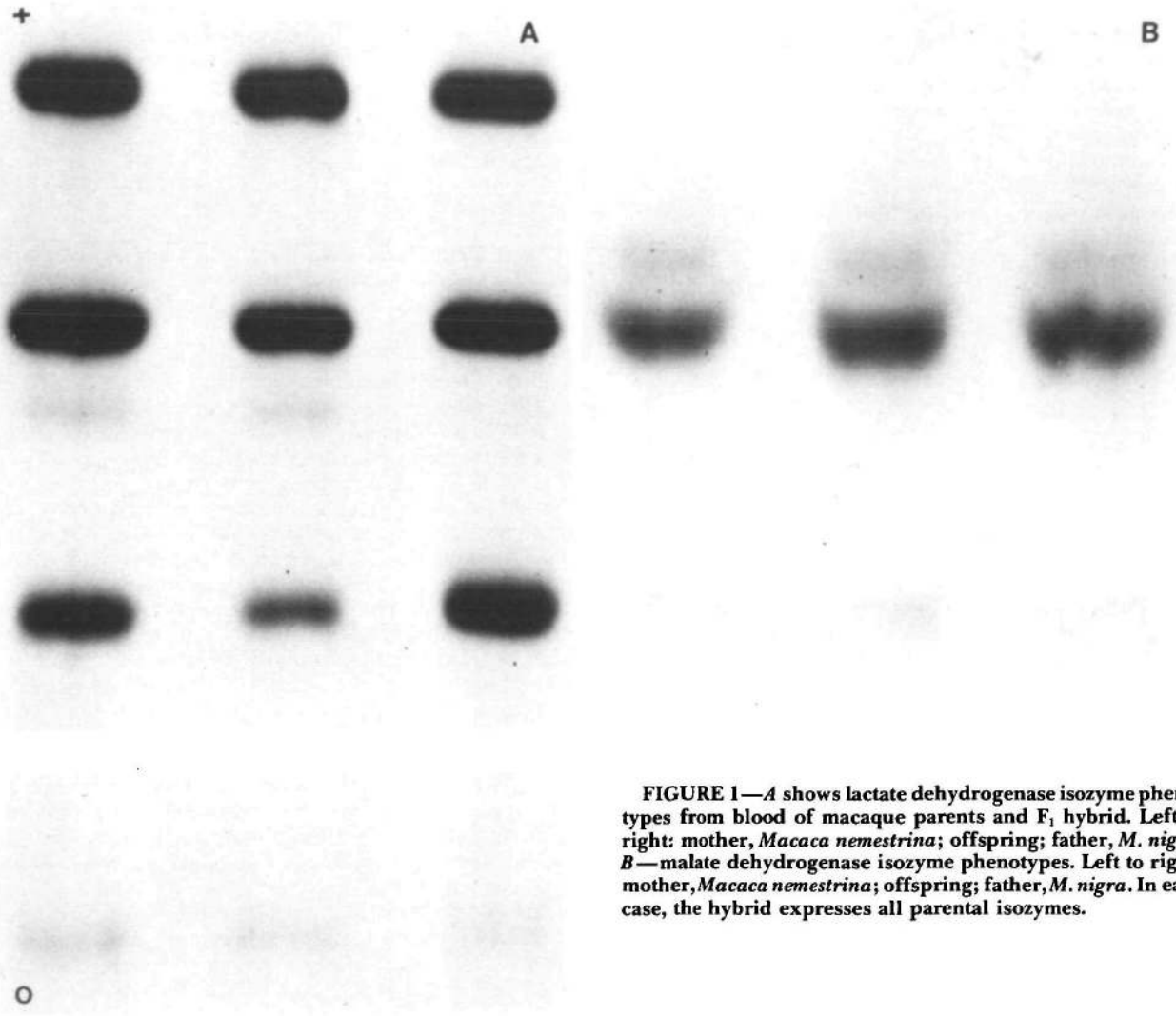

FIGURE 1—*A* **shows lactate dehydrogenase isozyme phenotypes from blood of macaque parents and F_1 hybrid. Left to right: mother, *Macaca nemestrina*; offspring; father, *M. nigra*. *B*—malate dehydrogenase isozyme phenotypes. Left to right: mother, *Macaca nemestrina*; offspring; father, *M. nigra*. In each case, the hybrid expresses all parental isozymes.**

type of allelic product could be due to allelic repression or to structural genotype.

The following is a brief description of zymogram patterns of these eight proteins. 1) *TR*—this locus is extremely polymorphic in most macaques, and a total of nine alleles have been detected in our samples of the six species. Homozygotes show a single band on gels, and heterozygotes show an additive two-banded pattern, indicating monomeric structure. This additive pattern is also present where expected in various F_1 and F_2 hybrids involving genomes from four macaque species (Table II; Figure 2). Both parental alleles in hybrid macaques appear to be expressed equally. 2) *IDH*—this locus is more conservative in macaque species, but five of six F_1, F_2, and backcross hybrids showed equal expression of different parental alleles (all one-sided tests). Since isocitrate dehydrogenase is a dimeric molecule, heterozygotes form 3-banded zymograms (representing one heterodimeric and two homodimeric molecules). Not only are both maternal and paternal alleles active in hybrids, but the proteins also interact to form functional hybrid molecules. 3) *PHI*—Phosphohexose isomerase is also a dimeric molecule. Only two parental crosses were such that one-sided tests of allelic repression could be made in hybrids, and both of these hybrids exhibited the 3 banded phenotypes (plus satellite bands) expected if both parental alleles were present and equally expressed (Figure 3). 4) *AD*—five of six macaque species appear monomorphic for the same adenosine deaminase allele, but one *M. silenus* parent appeared to be homozygous for a distinct allele. In the F_1 hybrid between *silenus* and *nemestrina*, two bands giving an additive zymogram appearance were present. 5) *PGM-2*—the zymogram appearance of phosphoglucomutase is complex because major products of two genetic loci as well as a number of satellite bands are present. Our samples of *M. nigra* and *M. nemestrina* were monomorphic for different alleles at the *PGM-2* locus; however, the allelic products are quite close in mobility. F_1 hybrids between these species exhibit a wide blur of activity encompassing the area on the gel occupied by the parental bands. It seems likely that both alleles

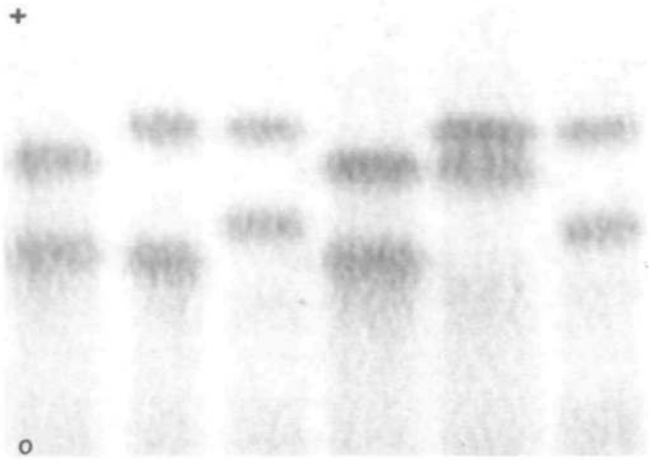

FIGURE 2—Transferrin isozyme phenotypes. Left to right: mother, *Macaca nemestrina* × *M. mulatta* F_1 hybrid; F_2 offspring; father, *M. nemestrina* × *M. fascicularis* F_1 hybrid; mother, *M. nemestrina* × *M. mulatta* F_1 hybrid; F_2 offspring; father, *M. nemestrina* × *M. fascicularis* F_1 hybrid. Both matings provide two-sided tests for allelic repression (see text) and in each case, maternal and paternal alleles are fully expressed in the hybrids.

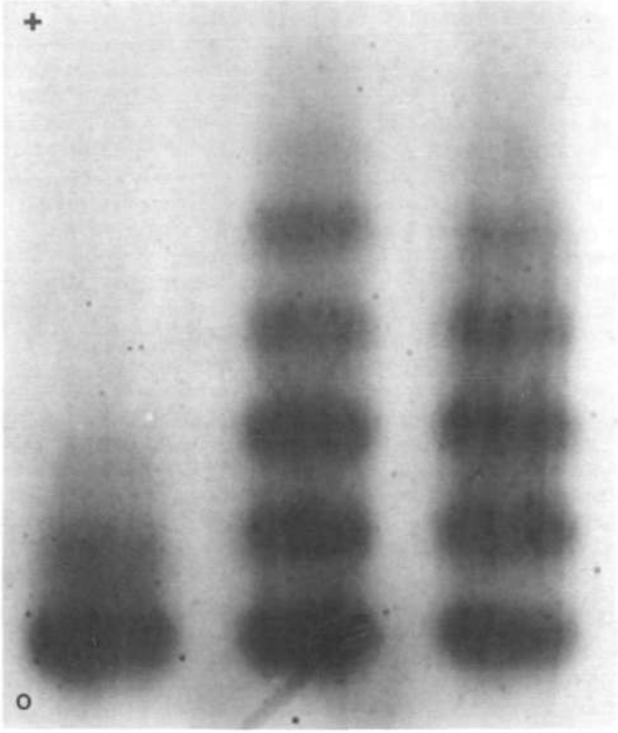

FIGURE 3—Phosphohexose iosmerase isozyme phenotypes. Left to right: mother, *Macaca nemestrina*; offspring; father, *M. mulatta*. This is an example of a one-sided test for allelic repression (see text) in which the hybrid inherited and expressed different parental alleles.

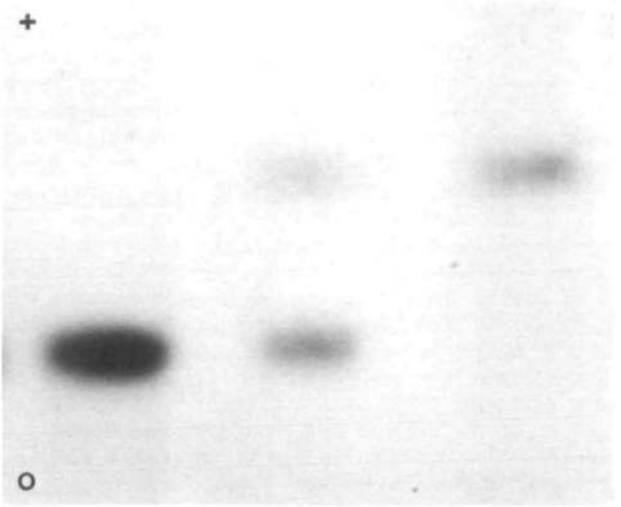

FIGURE 4—Carbonic anhydrase-1 isozyme phenotypes. Left to right: father, *Macaca nemestrina*; offspring; mother, *M. nigra*.

are expressed, although they could not be sharply distinguished in the hybrids. Similar types of zymograms were observed in other F_1 and F_2 hybrids (Table II). 6) *DIA*—a single band appears in homozygotes; in heterozygotes within a species, there are two sharp bands. Unfortunately, only two crosses involved parents with genotypes permitting tests of allelic repression, and both of these were one-sided. An F_2 hybrid from the cross $AC♀ \times CC♂$ had only a single band appear in the *C* position, and a backcross hybrid from an $AA♀ \times AC♂$ had only a single band in position *A*. The combined probability that these hybrids both contain the appropriate homozygous genotype (and hence that no allelic repression is responsible for the zymogram pattern) is 0.25. 7) *CA-1* and *CA-2*—carbonic anhydrases are monomeric proteins encoded by two genetic loci in macaques. The products of *CA-1* usually migrate anodally through our gels (*CA-2* products migrate towards the cathode), and homozygotes and heterozygotes at both loci may be readily scored. Heterozygous parents as well as hybrids typically exhibit both allelic products, as expected in the absence of allelic repression (Figure 4). In addition, a third locus has been described in *M. nemestrina* that primarily affects expression of *CA-1* [11,36]. The suppressor is a dominant allele that when present in homozygous or heterozygous state produces a carbonic anhydrase deficiency represented by the 0 phenotype. We have observed this 0 phenotype also in *M. silenus*, but not in the other macaques. Interestingly, two hybrids (Juno and Homer) each involved one parent with the 0 phenotype and the other parent with a normal phenotype. Both hybrids also exhibited the 0 phenotype, suggesting that the suppressor allele was active in the hybrid and able to "recognize" and suppress the foreign *CA-1* allele. 8) *Hb*—the genetic bases of hemoglobin zymogram patterns in macaques are complex and not well understood (see Nute[29] and references therein). Adult hemoglobin molecules are tetramers composed of two subunits from each of two loci, designated α and β. Homozygous individuals

possessing nonduplicated α and β hemoglobin genes show a single band on gels, representing the protein product $\alpha_2\beta_2$. But all of the macaque populations that we have examined (except *M. mulatta*) have polymorphic electrophoretic patterns on starch gels. Some hemoglobin polymorphism may be attributed to multiple alleles at the α(or β) locus, but several lines of evidence suggest that duplications of the α chain gene are of primary importance[29]. Thus some or all of the macaque species may possess tandemly duplicated α hemoglobin genes that have not yet reached fixation in their respective populations[29].

With our data, we are unable to unambiguously determine whether duplicate genes or multiple alleles are responsible for the polymorphic zymogram patterns, although the great preponderance of the same 2-banded phenotypes in some species (*M. nemestrina* and *M. fascicularis*, 78 and 80 percent of all individuals, respectively), suggests duplicate genes. In either event, gel patterns of hybrids indicate that protein products of both maternal and paternal genomes are produced (Figure 5).

FIGURE 5—Hemoglobin isozyme phenotypes. Left to right: father, *Macaca tonkeanis*; offspring; mother, *M. nigra*; father, *M. nemestrina*; offspring; mother, *M. nigra*. The zymogram of the first hybrid appears faint because the blood sample was dilute.

Discussion

At first thought, one would not expect to observe allelic repression in viable hybrids. The successful development of an organism depends upon proper functional interactions between maternal and paternal genomes. Certainly a limit exists to the degree of regulatory breakdown permitted for zygote development. Nonetheless, evidence has accumulated demonstrating that considerable allelic repression is frequently observed in extreme hybrids. Three patterns of allelic repression have previously been reported in interspecific hybrids: 1) repression of paternal protein synthesis[30,31,40,42]; 2) repression of maternal protein synthesis[32,40,42]; and 3) repression of both paternal and maternal synthesis[40]. Repression or delay of paternal enzyme synthesis is most commonly reported and has been attributed to a failure of proper recognition or interaction of regulatory elements in the egg cytoplasm with those of the paternal genome[30]. Additional regulatory hypotheses are required to explain maternal allelic repression[40].

Whatever the exact mechanisms of genetic regulation, studies of allelic expression in hybrids provide a means of estimating the degree of regulatory breakdown. If, as Wilson[43,44] has suggested, different types of organisms such as mammals and frogs have experienced different rates of regulatory evolution, but comparable rates of structural gene divergence, we might predict different degrees of allelic repression in interspecific hybrids of different types of organisms exhibiting similar degrees of structural gene divergence.

One argument advanced in favor of Wilson's proposal that regulatory evolution has been more rapid in mammals than in lower vertebrates is the observation of the more rapid loss of hybridizing ability in mammals[45]. Mammal species that can successfully produce viable hybrids have not been observed to differ by more than 10 immunological distance units in their albumins, while the mean distance between hybridizing frogs is 36 units and the maximum observed value is 91[45] (immunological distance provides an estimate of structural gene divergence, and is apparently highly correlated ($r \simeq 0.8$) with electrophoretic measures of genetic distance[45]). The small degree of structural gene divergence between most hybridizing mammal species limits the ease with which allelic repression can be examined in their hybrids.

We have examined allelic expression at 21 genetic loci in six macaque species and their hybrids. Genetic distances between all pairs of species are similar ($0.80 \leq D \leq 0.250$) and small relative to congeneric species of most organisms. Twelve of these loci are monomorphic in the parents and hence provide weak information about allelic expression in the hybrids (except that maternal and paternal alleles are not both strongly repressed). Eight of the nine remaining loci provide stronger tests of possible allelic repression, but we have found no evidence of any disruption of maternal or paternal enzyme levels.

Incompatabilities between regulatory elements of genomes in hybrids could also delay gene expression, or cause asynchronous allelic activation[15,19,21,25]. Disruption of structural gene expression might then be observed only during some stages of ontogeny, most likely in embryogenesis and early development. We have been unable to obtain blood from hybrid monkey fetuses, but the ages of the assayed hybrid progeny range from 2 weeks to 140 months. No evidence for strong allelic repression has been observed among any of these hybrids. Abnormalities in enzyme expression have occasionally been reported in F_2 hybrid fishes when F_1 hybrid patterns were normal[23]. We have observed no strong evidence for allelic repression in any of four F_2 and two backcross macaque hybrids.

How much allelic repression has been observed between other species exhibiting amounts of structural gene divergence comparable to that among the macaques? Probably the most extensive multilocus search for allelic repression in hybrids has been conducted among the sunfish (family Centrarchidae—see review in Whitt et al.[40]). Fortunately, estimates of structural gene divergence are also available for these species[3]. Results are summarized in Table III. Macaque species appear about as different in structural genes as do well-marked sunfish subspecies, between which there is no evidence for allelic repression. Genetic distance and degree of allelic

repression appear roughly correlated in sunfish, and the first evidence of allelic inhibition occurs between species exhibiting about five times as much structural gene divergence as do the macaques.

Attempts to hybridize macaques with more distantly related monkeys (such as baboons (*Papio*) and drills (*Mandrillus*)) have generally failed due to fetal abortion or early infant death[9,18]. It seems likely that the genetic distance between *Macaca nigra* and *M. mulatta* ($D = 0.250$) may be near the upper limit of distance between successfully hybridizable macaques. Many sunfish retain the ability to produce viable offspring even when they exhibit levels of structural gene divergence many times greater than that observed among these monkeys.

As discussed earlier, one likely explanation for the more rapid loss of hybridizing propensity in primates is rapid regulatory gene evolution. Yet we have not in the present study observed evidence of regulatory gene differences as reflected in allelic expression of hybrid macaques. Several hypotheses may be advanced: 1) it is certainly possible that great regulatory gene differences exist among the primates but were not detected here. Few data exist, and the reliability of allelic repression as an accurate index of regulatory differences is unclear; 2) regulatory gene evolution may not be proceeding more rapidly in primates, but hybridization propensity is more sensitive to slight regulatory differences. It is conceivable that developmental systems of primates and other mammals are subject to more stringent controls than are those of lower vertebrates, and that fewer regulatory gene differences could result in hybrid death; 3) differences in proteins encoded by structural genes could themselves be responsible for rapid loss of hybridizing propensity in mammals. Nonhistone proteins, for example, may serve important regulatory functions[35]; 4) immunological reactions in primate mothers could lead to antibody formation and subsequent abortion of hybrid fetuses differing only moderately in protein composition[45]. Such reactions would not occur in fishes or frogs with external fertilization and embryonic development. The hypothesis of rapid regulatory evolution in primates and other mammals remains attractive, but further criteria and methodologies to study the phenomenon must be devised.

Summary

Levels of structural genic divergence at 21 loci encoding blood proteins were quantified in six macaque (*Macaca*) species, using standard techniques of starch-gel electrophoresis. Genetic distances between all pairs of species fall within a narrow range ($0.080 \leq D \leq 0.250$; $\bar{D} = 0.164$) which is near the lower limit of genetic distances typically observed between other congeneric organisms. In an effort to measure levels of regulatory gene differences between these species, we have examined the patterns of allelic expression in their F_1, F_2, and backcross hybrids. Nine of the 21 loci examined encode allelic forms of the proteins with different electrophoretic mobilities in at least some of the individual parents of the hybrids. In all cases where expected, hybrids express fully both maternal and paternal allelic products, thus providing no strong evidence for a breakdown in the regulatory mechanisms responsible for proper expression of these genes. Results are compared to degrees of allelic repression previously observed in other hybrids, and are discussed within the context of current ideas about rates of regulatory gene evolution in mammals.

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