

## EXTENSIVE POLYMORPHISM OF COMPLEMENT C6 AMONG CRAB-EATING MONKEYS

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### INTRODUCTION

The occurrence of genetic polymorphism of the sixth complement component (C6) in humans was first reported in 1975 (1). The polymorphism is controlled by the alleles at an autosomal locus. Since few studies are known on C6 polymorphism in non-human primates, we attempted to examine C6 variation in crab-eating monkeys, *Macaca fascicularis*.

### MATERIAL AND METHODS

**Material.** Sera were obtained from 150 crab-eating monkeys captured in wild and now bred at Tsukuba Primate Center for Medical Science. Countries of origin are: Indonesia (N=50), Malaysia (N=50) and the Philippines (N=50).

**Determination of polymorphism.** A thin-layer polyacrylamide gel isoelectrofocusing followed by an immuno-blot staining method was used (2).

### RESULTS AND DISCUSSION

A high degree of polymorphism of C6 was confirmed in crab-eating monkeys.

It was first necessary to name the allotypes tentatively. The allotype that is the closest to human type A was named A. Similarly, the type that is the closest to human type B was named B, and the nomenclature followed the one in humans (Fig. 1). On the whole sample, 28 phenotypes were classified, combining the rare allotypes. A-A was the commonest (29%), followed by A-M12 (M1 or M2) and A-M3, the other types being relatively rare. Agreement between observed and expected numbers was good. At least 15 alleles were considered to occur, of which 11 had polymorphic frequencies (i.e. >1%). An overall heterozygosity was estimated at 0.68.

In Table 1, distribution of allele frequencies among three regional sample groups is shown. Type A has the highest frequency in all the groups. The number of alleles was 14 in Indonesian and 12 in Malaysian sample, heterozygosity being 0.7622 and 0.7298, respectively. On the contrary, in the Philippine sample only 5 alleles were found and heterozygosity was reduced to 0.5266, probably due to random genetic drift.

Using the frequency of allele A, heterogeneity test was carried out among three

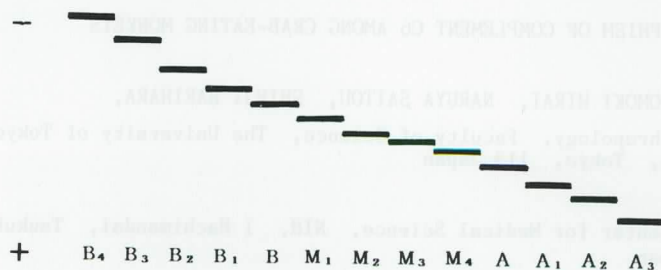


Fig. 1. C6 allotypes of *Macaca fascicularis*. Only the main band is shown.

TABLE I

C6 ALLELE FREQUENCIES IN THREE REGIONAL SAMPLE GROUPS

Allele	Indonesia	Philippines	Malaysia	Combined
A	0.43	0.66	0.48	0.5233
A1	0.05	-	0.03	0.0267
A2	0.01	-	0.06	0.0233
A3	0.01	-	0.03	0.0133
A4	-	-	0.01	0.0033
B	0.08	-	0.06	0.0467
B1	0.02	-	0.06	0.0267
B2	0.01	-	0.01	0.0667
B3	0.03	-	-	0.0100
B4	0.01	-	-	0.0033
B5	0.01	-	-	0.0033
M1	0.03	0.01	0.01	0.0167
M2	0.08	0.10	0.08	0.0867
M3	0.18	0.09	0.14	0.1367
M4	0.05	0.14	0.03	0.0733
Sum	1.00	1.00	1.00	1.0000

regional sample groups. Although no statistically significant difference was observed between Indonesian and Malaysian samples, there were statistically significant differences between these two samples and the Philippine sample ( $0.010 < P < 0.025$ ; d.f.=1).

#### ACKNOWLEDGEMENTS

This study was supported by a grant of Ministry of Education, Science and culture of Japan.

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