Factors shaping genetic variation in the MHC of natural non-human primate populations

Abstract

Across a large distribution range, population-specific factors as well as pathogen-mediated selection may shape species genetic diversity in the major histocompatibility complex (MHC). We have studied genetic diversity and population differentiation in the MHC region of the Southeast Asian cynomolgus macaque (Macaca fascicularis fascicularis), a species with large and discontinuous range, in order to investigate the role of demography vs selection. Genetic variation was assessed at seven MHC microsatellites on 272 individuals from five populations (Indochina, Java, Borneo, Philippines, and Mauritius). A high genetic diversity was observed in all populations and the Philippines but also the Mauritius populations were the most genetically differentiated. The strength and extent of linkage disequilibrium (LD) (up to 4 Mb) varies across populations mainly because of demographic factors. In Indochina, the complete lack of LD could be the signature of ancient hybridization between cynomolgus and rhesus macaques in the Indochinese peninsula. With the additional support of seven autosomal microsatellites, tests for outlier loci based on intrapopulation diversity and interpopulation differentiation (using F-statistic) allowed to dissociate demographic from selective histories: (i) demographic history may itself explain levels of MHC variability in the Mauritius populations and (ii) positive selection could be responsible for the Philippines population differentiation, especially in the MHC class II region. Among various pathogens, Plasmodium knowlesi and Plasmodium coatneyi are two likely candidates to explain the higher frequency of some MHC haplotypes. Indeed, literature describes low parasitemia in the Philippines individuals, contrasting with fatal infections provoked by these parasites in other cynomolgus macaque populations.