



Title	Molecular Evolutionary Studies on the Major Histocompatibility Complex of Japanese and Russian Raccoon Dogs, <i>Nyctereutes procyonoides</i> [an abstract of dissertation and a summary of dissertation review]
Author(s)	Bartocillo, Aye Mee Forro
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Abstract of Doctoral Dissertation

Degree requested Doctor of Science Applicant's name: Aye Mee F. Bartocillo

Title of Doctoral Dissertation

**Molecular Evolutionary Studies on the Major Histocompatibility Complex
of Japanese and Russian Raccoon Dogs, *Nyctereutes procyonoides***
(日本およびロシアにおけるタヌキ *Nyctereutes procyonoides* の
主要組織適合遺伝子複合体に関する分子進化学的研究)

Raccoon dogs, *Nyctereutes procyonoides*, are native to East Asia, but have been introduced into western Russian and eastern Europe. They have been reported to be affected by various pathogens causing diseases, endoparasites, and viruses. Nevertheless, these pathogens have not prevented the raccoon dog's wide expansion in Far Eastern Asia and Europe. Recently, the major histocompatibility complex (MHC) genes have been widely analyzed to assess the immunological fitness and evolutionary adaptation in different populations, an essential key for conservation biology. Therefore, this study presents the allelic diversity and selection mechanism in the evolution of MHC class I and class II genes of Japanese and Russian raccoon dogs.

A total of 23 class II *DRB* alleles and a total of 48 novel MHC class I alleles were detected from 36 and 31 individuals of Japanese and Russian raccoon dogs, respectively. For both MHC class I and class II *DRB*, some alleles were found across the species' range, while others were geographically restricted. Similarly, the ratio of non-synonymous to synonymous substitution rates for codons at the predicted antigen-binding sites for both classes were greater than 1, indicating that raccoon dog's MHC class I and class II *DRB* genes have evolved under positive selection. Mixed effect model of evolution analysis and an algorithm to detect recombination showed positive selection sites at the amino acid level in both class I and class II molecules. Overall the results suggest that the diversity of MHC class I and class II *DRB* were influenced and maintained by recombination, pathogen-driven positive selection, and geographical barriers.

For MHC class II *DRB*, the Bayesian phylogenetic tree revealed no evidence of trans-species polymorphism (TSP), but instead showed the monophyletic relationships within the Canidae clade. The lack of TSP suggests a possible influence of species-specific pathogens driven by their environments and their long historical divergence from other canids. For MHC class I genes, Bayesian phylogenetic trees showed no evidence of TSP with alleles from carnivore species in other families, but did detect TSP between raccoon dogs and the domestic dog, indicative of long term balancing selection in canids.