Title: Major Histocompatibility Complex (MHC) Genes in the endangered Malayan tapir (*Tapirus indicus*)

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Aim: The main aim of this study is to determine the allelic diversity of the Major Histocompatibility Complex (MHC) gene in the Malayan tapir population in Peninsular Malaysia. It will contribute to the management of both captive and wild populations to have high variable MHC through artificial mate selection and translocation or reintroduction of dissimilar MHC to ensure the sustainability of the population. The prior study stated the MHC gene is lowly diverse in Malayan tapir based on seven individuals. The present study screened more than 50 individuals to assess MHC gene diversity in the population. The study also aims to assess the functionality of the identified MHC gene alleles and evaluate whether the MHC allelic repertoire of the tapir determined the expression level of MHC genes.

Methodology: A total of 86 biological samples of the 84 Malayan tapirs in various forms such as whole blood, dry blood spot (DBS), tissue, and hair were utilized from the Wildlife Genetic Resource Bank (WGRB) of PERHILITAN in Cheras, Selangor to isolate genome DNA (gDNA) using Qiagen QIAamp® DNA Mini Kit. All the 86 gDNA were screened with five sets of MHC loci (exon 2 of class I, DQα, DQβ, DRα, and DRβ) primer pairs to achieve the main objective. Frozen liver, spleen, and lung organs of a Malayan tapir utilized for total RNA extraction using RNeasy Protect Mini Kit to achieve second, and third objectives. Synthesized complementary DNA using Omniscript RT kit.

Results: Based on electrophoresis visualization, 48 samples out of 86 were amplified with class I primer pair, while DQα 20, DQβ 45, DRα 37, and DRβ 18. Based on the Cubit fluorometer, the concentration of amplified products of the five MHC loci was in the range of 0.4-33 ng/µL. The complementary DNA synthesis was unsuccessful due to the low concentration and integrity of total RNA (Omniscript RT kit requires 50ng/µL).

Conclusion and future work: Future work should make use of fresh samples such as blood so that the integrity of samples is high to obtain precise data.

Keywords: Malayan tapir, Major Histocompatibility Complex, gene diversity