


RESEARCH NOTE

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RNA sequencing of kidney and liver transcriptome obtained from wild cynomolgus macaque (*Macaca fascicularis*) originating from Peninsular Malaysia

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Abstract

Objective: Using high-throughput RNA sequencing technology, this study aimed to sequence the transcriptome of kidney and liver tissues harvested from Peninsular Malaysia cynomolgus macaque (*Macaca fascicularis*). *M. fascicularis* are significant nonhuman primate models in the biomedical field, owing to the macaque's biological similarities with humans. The additional transcriptomic dataset will supplement the previously described Peninsular Malaysia *M. fascicularis* transcriptomes obtained in a past endeavour.

Results: A total of 75,350,240 sequence reads were obtained via Hi-seq 2500 sequencing technology. A total of 5473 significant differentially expressed genes were called. Gene ontology functional categorisation showed that cellular process, catalytic activity, and cell part categories had the highest number of expressed genes, while the metabolic pathways category possessed the highest number of expressed genes in the KEGG pathway analysis. The additional sequence dataset will further enrich existing *M. fascicularis* transcriptome assemblies, and provide a dataset for further downstream studies.

Keywords: *Macaca fascicularis*, Cynomolgus macaque, RNA sequencing, Transcriptome, Biomedical science, Kidney, Liver

Introduction

Cynomolgus macaques (*Macaca fascicularis*) are non-human primate (NHP) models significant to biomedicine due to their close evolutionary relationship with humans. The cynomolgus macaque's recapitulation of human physiology, genetics, and behaviour is advantageous as translational models for various studies in the biomedical field, including drug development and safety testing [1, 2]. Cynomolgus macaque individuals from different geographical locations have been shown to exhibit genetic characteristics that varies between geographical origins [3]. Therefore, it is vital that the genomes

and transcriptomes of cynomolgus macaque NHP models originating from different geographical locations are sequenced as a reference for future biomedical research design and implementation.

This study describes the RNA sequencing (RNA-seq) of two tissues—kidney and liver—harvested from wild Peninsular Malaysian cynomolgus macaques, and is an extension of a previous study [4] whereby the lymph node, spleen, and thymus transcriptomes of wild Peninsular Malaysian *M. fascicularis* were also sequenced with RNA-seq technology. An additional 75,350,240 sequence reads were obtained from this study, supplementing the previous wild Peninsular Malaysian *M. fascicularis* dataset for downstream applications. Furthermore, additional Malaysian cynomolgus macaque RNA-seq datasets will further furnish the cynomolgus macaque genome

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