

UNIVERSITI TEKNOLOGI MARA

**SCREENING AND
CHARACTERISATION OF
ENDOGENOUS BETARETROVIRUS
IN SMALL MAMMALS**

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ABSTRACT

Betaretrovirus is capable of crossing the barrier between human and other animals through cross-species transmission. Bats and guinea pigs have a great potential as a vector for virus infections as they possess ecological traits that enable them to spread viral diseases geographically. An investigation was carried out using bioinformatic and molecular approaches to search for the presence of endogenous betaretrovirus in bats (PvEB) and guinea pigs (CpEB) genome. A total of 60 genome project databases were screened using BLAST and 46 tissue samples from small mammals were screened for *pro-rt* gene using PCR amplification. Only 2 species were further investigated due to their significant BLAST result, namely flying fox (*Pteropus vampyrus*) and guinea pig (*Cavia porcellus*). Based on *in silico* characterisation work, a full-length genome of PvEB and CpEB was found with the size of 8772bp and 8543bp respectively. Both had a typical genomic organisation of a betaretrovirus. Conserved motifs of *gag*, *pol* and *env* were further supported through Pfam-A analysis and protein structure prediction. Subsequently, phylogenetic tree analysis of *gag*, *pol* and full-length sequence had placed PvEB and CpEB robustly within betaretroviruses clade with strong bootstrap support. Age estimation has revealed that each PvEB and CpEB had diverged from its host 8.8 and 47.1mya respectively. The results of bioinformatic findings were further verified through PCR amplification of *pro-rt* region in PvEB and CpEB. Therefore, based on bioinformatics and molecular approaches, it is evident that PvEB and CpEB have significant characteristics of a type-D betaretrovirus and have involved in cross-species transmission.

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CHAPTER ONE

INTRODUCTION

1.1 BACKGROUND OF STUDY

Guinea pig belongs to the order Rodentia which has the largest number of species in Mammalia. It is a terrestrial small mammal and mostly is domesticated and kept as pet. It serves as animal model in biological field and is widely used in the study of diseases. Guinea pig is more preferable as model rather than mouse as it resembles human in terms of immunologic and hormonal responses. Hence, guinea pig is often used in the study of diseases such as gastrointestinal, sexual transmitted and pulmonary diseases (Padilla-Carlin et al., 2008).

On the other hand, bats, the second diverse order of mammals (Simmons, 2005) are considered as unique small mammals as they are the only mammal that are capable of flying. Due to gregarious roosting behavior, bats are recognized as reservoir of several viruses including SARS-like coronavirus (Li et al., 2005), Nipah virus (Yob et al., 2001) and Ebola virus (Leroy et al., 2005). They are capable of infecting human as well as other mammals that will lead to highly infectious diseases such as SARS, Ebola and rabies (Calisher et al., 2006). Therefore various researches were done in order to rectify the viruses including retroviruses.

Retroviruses can be classified either endogenous or exogenous retrovirus based on its genome features and pattern of transmission into host genome. Exogenous retrovirus is horizontally transmitted from one host to another by infection (Rasmussen, 1997) whereas endogenous retrovirus is vertically transmitted between host genome and exists as normal element in its host. Exogenous retrovirus able to replicate, spread and cause severe diseases unlike most of endogenous retrovirus which are defective and incapable to produce infectious particles. Although they are often intact, they can however be activated and expressed as fully infectious particle (Kurth and Bannert, 2010).

Previous studies showed that endogenous retroviruses were found to occupy diverse host range of vertebrates from all retrovirus genera except for deltaretrovirus. For example, endogenous alpharetrovirus was mostly found in chicken, fowls and birds (Weiss, 2006). On the other hand, endogenous betaretroviruses were detected in