UNIVERSITI TEKNOLOGI MARA

MOLECULAR PHYLOGENY OF SOCIAL VESPID WASPS INFERRED FROM DNA SEQUENCE OF *28S* AND *COI* GENE

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AUTHOR'S DECLARATION

I declare that the work in this thesis was carried out in accordance with the regulations of Universiti Teknologi Mara. It is original and is the result of my work unless otherwise indicated or acknowledged as referenced work. This thesis has not been submitted to any other academic institution or non-academic institution for any degree or qualification.

I, hereby, acknowledge that I have been supplied with the Academic Rules and Regulations for Post Graduate, Universiti Teknologi Mara, regulating the conduct of my study and research.

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ABSTRACT

Social wasps (Vespidae) display a wide range of diversity in their ecology and social organisation, providing insights into the origins of simple societies and the elaboration and maintenance of complex societies. Cladistic analysis of behavioral data showed that Stenogastrinae have been grouped with social Polistinae and Vespinae in the family of Vespidae. However, it has been reported that Stenogastrinae are more closely related to the solitary wasps Eumeninae than other social subfamilies, based on their morphological characters. The aim of this study was to determine the relationship between the subfamilies in the social vespid wasps (Stenogastrinae, Polistinae, and Vespinae) based on *COI* mitochondrial DNA and *28S* ribosomal nuclear DNA. A total number of 18 species of eight genuses within the three subfamilies of Vespinae, Polistinae and Stenogastrinae, were successfully collected throughout Peninsular Malaysia. Five individuals from each species were selected for genomic DNA extraction, PCR amplification and sequencing. Phylogenetic analyses were conducted using Neighbor-Joining (NJ) and Maximum Parsimony (MP) methods that performed using the computer program MEGA 6. Six topology of the phylogenetic tree were generated. Comparison of both topologies of phylogenetic trees showed that *28S* gave better resolution at higher taxa level while *COI* region resolved better at the lower taxa or species level compared with the higher taxa. The combined locus gave best phylogenetic tree because it carried both properties locus in the topology of the tree. NJ tree of combined locus (*28S* and *COI*) portrayed the best result to understand the relationship between these subfamilies. The topology shows that subfamily Stenogastrinae were the first to diverge from the outgroup. Then this followed by subfamily Vespinae and subfamily Polistinae. Subfamily Vespinae formed a monophyletic clade with the subfamily Polistinae while Stenogastrinae was placed as the sister clade from other two social wasps.

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CHAPTER ONE
INTRODUCTION

1.1 BACKGROUND OF STUDY

Wasps are the members of the order Hymenoptera in the family of Vespidae. Vespidae is a large family consisting abundance of species (Carpenter and Pickett, 2010). According to Hines *et al.* (2007) there are approximately 4200 species presently categorised into six subfamilies according to their morphological evidence. The six subfamilies of the Vespidae family are Eumeninae, Euparagiinae, Masarinae, Polistinae, Stenogastrinae and Vespinae, which can be further subdivided into social and solitary wasps.

Social wasps in the family of Vespidae play an important role in understanding the evolution development of the social habits. Based on the lineage family of the Vespidae, it shows that this family evolves from the solitary behavior to the social behavior (Pickett and Carpenter 2009). Vespidae is also one of the few groups that have retained necessary transitional states to elucidate social evolution, encompassing solitary, pre social, facultatively eusocial and eusocial taxa. Thus, this drawing the attention of the scientific research in evolution as they have the potential for understanding the evolution model.

Stenogastrinae has been grouped together with the social Polistinae and Vespinae based on their behavioral characteristics (Carpenter and Pickett, 2010). However, Schmitz and Moritz (1998) reported that according to the eight morphological characters, Stenogastrinae are similar to the other solitary wasps. Although it is obvious that the Stenogastrinae display a wide range of sociality, it is less clear whether they can perform a potential phylogenetic link between solitary and social wasps. In particular, the usage of behavioral cladistics studies may be difficult as behavioral traits may show great plasticity, rendering them less informative and could not be used for phylogenetic studies (Schmitz and Moritz, 1998). In accordance of a single origin of eusociality, the monophyly of the social subfamilies was supported strongly by Carpenter (1982; 2003). Meanwhile, Schimitz and Moritz (1998) and Hines *et al.* (2007) argued for no close relation of Stenogastrinae to other social wasps, hence a diphyletic