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Complete mitochondrial genome and phylogenomics of *Graphium agamemnon* and congeners (Lepidoptera, Papilionidae, Leptocircini)

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ABSTRACT

The complete mitogenome of *Graphium agamemnon* from Peninsular Malaysia (PM) contains 37 genes and a 177bp control region. Phylogenetic analyses based on mitochondrial genes reveal the genus *Graphium* and its subgenera to be monophyletic, forming three clades: Clade A comprising the subgenus *Graphium*; Clade B the subgenus *Pazala*; and Clade C the subgenus *Pathysa*. The subgenera *Graphium* and *Pazala* are closer related compared to subgenus *Pathysa*. The PM *G. agamemnon* and that reported from China (OQ852718), as well as two *Graphium cloanthus* taxa are genetically distinct. In the subgenus *Pazala*, *Graphium timur*, *Graphium eurous*, and *Graphium mullah chungianus* may be closely related members of a species complex. An extensive taxon sampling is needed to resolve the systematic status and phylogeny of the various seemingly similar/disparate taxa.

Introduction

The swallowtail butterflies of the genus *Graphium* Scopoli are members of the family Papilionidae Latreille, subfamily Papilioninae Latreille, tribe Leptocircini Kirby. It is represented by some 105 species (Savela, 2023), classified in four subgenera: subgenus *Graphium* Scopoli (previously subgenus *Idaides* Hübner); subgenus *Arisbe* Hübner; subgenus *Pathysa* Reakirt (now including *Paranticopsis* Wood-Mason & de Nicéville); and subgenus *Pazala* Moore (Hu et al., 2023; Savela, 2023).

The Tailed Jay *Graphium agamemnon* (Linnaeus) is a member of the subgenus *Graphium* (Hu et al., 2023; Savela, 2023). Its type locality is 'Asia' [Guangdong, China] based on *Papilio agamemnon* Linnaeus. It is represented by 20 subspecies (Savela, 2023). Among them, the subspecies *G. agamemnon agamemnon* (Linnaeus) is widely distributed from North India to South China, and throughout Southeast Asia (Hu et al., 2023; Savela, 2023). Its type localities include China (based on *Papilio aegisthus* Linnaeus, *Papilio dorylas* Sulzer, *Papilio agamemnon* var. *rufescens* Oberthür), and 'Bornéo, Dodinga' (*Papilio agamemnon* var. *anoura* Oberthür) (Hu et al., 2023). The larval host plants include members of

the families Annonaceae, Lauraceae, and Magnoliaceae, such as Annona muricata L., Polyathia longifolia L. and Michelia alba L. [M. alba is now recognised as Magnolia \times alba (DC.) Figlar] (Suwarno et al., 2018; Savela, 2023; Yong, 2023).

Although the genus has some 105 species, as of May 2024, only 17 species have the complete mitochondrial genomes (mitogenomes) listed in the GenBank (Table 1), comprising seven species of the subgenus *Graphium*, five species of subgenus *Pathysa*, and five species of subgenus *Pazala*; none from the Afrotropical subgenus *Arisbe*. Out of the 20 subspecies of *G. agamemnon*, only *G. a. agamemnon* from China has been listed (unpublished). A recent study, based on complete mitogenomes, has reported the phylogenetic relationship of 11 species belonging to the genus *Graphium* – five species of subgenus *Graphium*, and three species each of subgenera *Pazala* and *Pathysa* (Wu et al., 2024). The subgenera *Graphium* and *Pazala* are closer related compared to subgenus *Pathysa*. *Graphium agamemnon* was not included in this and an earlier study on four species of the subgenus *Pazala* [with *Graphum timur* (Ney) considered as conspecific with *Graphium mullah* (Alphéraky)] and three species of the subgenus *Graphium* (He et al., 2022).

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