**SUPPLEMENTARY METHODS AND RESULTS**

1. **METHODS**
   1. **Startle display and primary defense data**

Studies on mantis displays can be found in publications from several decades (Varley, 1939; Crane, 1952; Maldonado, 1970; Edmunds, 1972, 1976; Pita, 1972; Loxton, 1979; Grandcolas & Desutter-Grandcolas, 1998; O’Hanlon *et al.*, 2018).To generate our dataset, we searched Web of Science and Google Scholar for all published descriptions of praying mantis startle displays. Search terms were: defensive display, deimatic, startle, antipredator, frightening attitude, praying mantis, praying mantid, and Mantodea. Six papers and the observations of scientists therein provided sufficiently detailed accounts of the displays or lack thereof. Nine species were scored based on personal observations of scientists currently working in the field of praying mantis behaviour (G. Holwell, K. Barry and J. O’Hanlon). In total, we gathered behavioural descriptions for 58 praying mantis species, with each species representing a different genus across the Mantodea. Our data therefore represent approximately 13% of mantis diversity at the generic level. We scored the description of the species’ primary defense, i.e. camouflage, as crypsis or masquerade, based on the descriptions of ‘general resemblance’ and ‘special resemblance’ respectively by Edmunds (Edmunds, 1972, 1976) and the overall shape of the mantis (e.g. ‘mantis shaped’, ‘dead leaf shaped’, etc.) in accordance with the conceptual framework outlined by Skelhorn et al (2010b).

We scored the presence of a display as whether the display behaviour had been witnessed first-hand by a scientist and/or a description published. We scored absence of display if the species had been explicitly reported to lack a display despite being exposed to the same stimuli as those reported to have a display (Edmunds, 1972, 1976).

For species with a display (N = 31), we scored the presence and absence of seven components, four behaviours and three colour patterns: (1) wings display – wings raised during the display, (2) arms display – arms raised during the display, (3) mouth display – if the mouth is opened during the display, (4) sound – display includes sound (e.g. rustling wings not related solely to raising the wings), (5) wing colours – wings have contrasting colour markings or ‘eyespots’ that are revealed or highlighted during the display, (6) arm colours – raptorial forelimbs have conspicuous colours or ‘eyespots’ that are revealed or highlighted during the display, (7) abdomen colours – part of the abdomen revealed during the display has a contrasting colour. Display complexity was the unweighted sum of these traits with a maximum possible complexity score of seven.

* 1. **Body size and shape data**

To compile the dataset of mantis body size, we took size data from seven publications and in addition, directly measured 294 specimens from 49 species kept in the collections of the Cleveland Museum of Natural History and the National Museum of Natural History (Smithsonian Institution). We took three measurements of body size in both males and females for each species in the data set where specimens were available: body length, pronotum length, and forewing length (Supplementary Figure 1). We took an average for each measurement from a variety of sample numbers per species. From these measures we created four further variables: ‘flight capacity’ (forewing length divided by body length, larger values indicate larger wings relative to body length and thus greater likelihood of flight), ‘size dimorphism’ (female body length minus male body length, positive values indicate females larger than males), and ‘flight dimorphism’ (male flight capacity minus females flight capacity, positive values indicate male have larger wings per unit body size than females).

* 1. **Mantis phylogeny and timetree estimation**

A total of 94 praying mantis taxa were selected (Supplementary Table 1) from tree topologies recovered in prior studies [1–8]. Four outgroup taxa were selected from Blattodea [3]. The selected taxa provided broad taxonomic and clade specific representation that also allowed collection of attribute data used to test the hypotheses of this study. A total of 10 gene fragments were included, all of which have proven to be phylogenetically informative at multiple levels of the Mantodea phylogeny [1–8]. These genes are 12S rRNA, 16S rRNA, 18S rRNA, 28S rRNA, Cytochrome Oxidase I (COI), Cytochrome Oxidase II (COII), NADH dehydrogenase subunit 4 (ND4), Histone 2A (H2A), Histone 3 (H3), and Wingless (wnt-1) (see Supplementary Table 1 for GenBank accession numbers).

For all included taxa, but one with newly sampled data, sequences were downloaded from GenBank (NCBI) and imported into Geneious v7.1.4 for 10 loci (Supplementary Table 1). The new sequence data (*Negromantis* sp.) was generated in the Cleveland Museum of Natural History DNA Laboratory. Thoracic and coxal muscle tissue was excised from specimens and extracted using the Qiagen DNeasy protocol for animal tissue. Specimen and DNA vouchers and template are deposited in the Department of Invertebrate Zoology at the Cleveland Museum of Natural History (CMNH). New sequence data from four gene loci were generated previously, but not published until this study (GenBank accession numbers in Supplementary Table 1), using well-established protocols for amplification, gel verification, amplicon purification, and sequencing [2,3,7]. Gene regions were sequenced with complements and sufficient overlap with adjacent regions to ensure the accuracy of sequence data.

Gene fragments were aligned in Geneious v7.1.4 using MAFFT v7 [9] and reading frame was determined for coding genes. We used SequenceMatrix v1.7.8 [10] to concatenate the matrix for a dataset including 10207 characters. We used PartitionFinder v2.1.1 [11,12] to determine partitioning strategy and models. A total of 22 partitions were input based on gene and codon position with the BIC and greedy settings for model selection and search strategy, respectively. Four partitions were recovered, each using the GTR+I+G model: 1) 12S, 16S, ND4\_pos1, ND4\_pos3, 2) 18S, 28S, H2A\_pos1, H2A\_pos2, H2A\_pos3, H3\_pos1, H3\_pos2, H3\_pos3, wnt\_pos1, wnt\_pos2, wnt\_pos3, 3) COII\_pos3, COI\_pos3, and 4) COII\_pos1, COII\_pos2, COI\_pos1, COI\_pos2, ND4\_pos2.

We conducted a mixed-model maximum likelihood (ML) analysis using RAxML v8 [13] with partitions corresponding to PartitionFinder results. One thousand non-parametric bootstrap (BS) pseudoreplicates were performed under a GTRGAMMA. We also conducted a mixed-model MrBayes v3.2.3 [14] analysis using PartitionFinder results by implementing four independent runs (four chains each) for 40 million generations. Each Bayesian run was started from a random tree and subsequently monitored for convergence using the program Tracer v1.7.1 [15]. Specifically, the plots for each run for sampled generations (every 1000) were compared using mean likelihoods, standard deviations, and distribution plots to ensure they converged on the same distribution after the burn-in. Bayesian analyses were performed on the Cyberinfrastructure for Phylogenetic Research (**CIPRES) Science Gateway** [16]**.** Sampled trees were used to calculate a 50% majority rule tree to determine posterior probabilities (PP) [17]. FigTree v1.4.4 [18] was used to visualize topologies and produce figures for both ML and Bayesian analyses.

We used the Bayesian output tree as a start tree to estimate divergence times using a lognormal uncorrelated relaxed-clock model of among-lineage rate variation in BEAST v1.8.3 [19]. Like the Bayesian analysis, we utilized the **CIPRES Science Gateway to run BEAST. We** applied an exact root height with the mean set at 197 and the standard deviation set to 20 based on root dates **recovered consistently in prior studies, which used significantly expanded taxon sampling or datasets along with multiple fossil calibrations** [3,20,21]**. We chose this method of calibration because of the lack of an adequate fossil record capable of calibrating later diverging nodes in the phylogeny** [22–24] **and it simply recovered a consistent phylogenetic tree scaled to time (timetree) that can address our evolutionary questions rather than addressing fundamental questions about the temporal origins of lineages [8].** Based on PartitionFinder results, we assigned all four partitions the GTR+I+G model. We executed two independent runs using the Yule process [25] for the tree prior. Trees were sampled every 1,000 generations over 10 million generations. Tracer was used to monitor convergence across runs. We used LogCombiner v1.8.3 to process log and tree files. TreeAnnotator v1.8.3 was used to produce a maximum clade credibility tree (25% burn-in) with median node heights with upper and lower confidence-interval (CI) values.

* 1. **Bias in behavioural trait observation**

Due to the unevenness in our behavioural data sources, we tested for author bias between samples from Edmunds (1972 & 1976) and the rest of the authors (Varley, 1939; Crane, 1952; Maldonado, 1970; Pita, 1972; Loxton, 1979; Grandcolas & Desutter-Grandcolas, 1998; O’Hanlon *et al.*, 2018). We performed Pagel’s binary correlation test, using *fitPagel* [50] in *phytools* [48], between the binary variable ‘author’ (states: ‘Edmunds’ and ‘other’) and (1) presence of display (states: ‘present’, ‘absent’) and (2) primary defense (states: ’masquerade’, ‘crypsis’). We also performed a phylogenetic ANOVA using the R package *phytools* (Revell, 2012), in order to discern whether the different authors differentially reported (or worked on) species that are more evolutionarily distinct. We performed this test for the binary ‘authors’ variable (states: ‘Edmunds’ and ‘other’), and the categorical ‘authors’ variables (with each author as a category). Finally, we ran some of the analyses performed on the whole dataset on a subset that only included the species reported by Edmunds (1972 & 1976), in order to check whether the results were consistent with those from the whole data set.

1. **RESULTS**

**2.1. Startle display and primary defence data**

We found reliable descriptions of the defensive behaviour and morphology of 58 species of mantis in 58 genera, approximately 13% of extant genera. Of the available descriptions, 31 species were reported to perform a startle display when provoked and 27 to not perform such a display despite the same level of provocation.Please see **in Supplementary Methods and Results for further details.** This sample size is likely to have sufficient power to yield meaningful results (Blomberg *et al.*, 2003). The majority of the published descriptions (42/58) were made by two people published in three studies (11 by Jocelyn Crane (1952), 31 by Malcolm Edmunds (1972, 1976) and were largely consistent in format, see section 2.4). Nine species’ behaviour were scored by praying mantis behaviour experts who have worked on their chosen species for more than five years in the field and in the lab (Supplementary Figure 1). The remaining seven species scores were found in three further publications (Roonwal, 1938; Varley, 1939; Maldonado, 1970). Type of primary defence, or camouflage, was scored as crypsis in 39 species and masquerade in 19 based on description in the above publications of ‘general’ and ‘special’ resemblance, and the species morphology (Skelhorn *et al.*, 2010b).

For the 31 species who performed a display, 29 used their wings in the display, 29 used their forelegs (not the same 29), 18 had contrasting colour patterns on their wings (5 with ‘eyespots’), 18 had contrasting colours on the arms (5 with ‘eyespots’) (not the same 18), 1 species had a colour patch on the abdomen, 7 included sound in their display, and 5 opened their mouth. Display complexity ranged from 2 to 5 out of a possible total of 7. The presence of eyespots was not considered a separate character but was scored under ‘wing colour- and ‘foreleg colour’ (Figure 1).

**2.2. Body size data**

We gathered body size data for females for 57 out of 58 species in our tree and 58 species for males from a total of N= 129 females, and N = 165 males (Supplementary Figure 1), and found that female mantis body sizes range from 15 mm to 127 mm in body length, 2 mm to 52 mm in pronotum length, and 4 mm to 68 mm in forewing length. Male mantis body sizes ranges from 14 mm to 118 mm in body length, 2 mm to 47 mm in pronotum length, and 10 mm to 62 mm in forewing length. Our measure of ‘flight capacity’ (ratio of forewing length to body length) ranged from 0 to 1.01 for females and 0 to 1.2 for males. The ratio of ‘flight capacity’ between males and females ranged from 0.8 (females longer wings to body than males) to 5.8 (males longer wings to body than females). Finally, in size dimorphism, values range from 0.7 (males longer body length than females) to 2.0 (female twice the length of the male). Behavioural data were available for both males and females for 30 out of the 58 species in our study of which only 16 perform a startle display and therefore prohibited further quantitative analysis of sex differences, but we present a short descriptive account of the patterns. Of the 16 displays, sexual dimorphism was only present in four species, *Acanthops falcata*, *Acontista multicolour*, *Oxyopsis rubicunda* and *Sphodromantis aurea* with females only displaying (*A. multicolour* and *S. aurea*) and females having the more spectacular display (*A. falcata*, *O. rubicunda*).

**2.3. Tree estimation results**

The partitioned ML analysis recovered a topology (likelihood score: -150062.114978) with high BS values (≧80) across most terminal level nodes and low BS values (<80) across most backbone nodes (Supplementary Figure 2), which is consistent with prior studies [2,3,21]. Bayesian analysis recovered a nearly identical ingroup topology (harmonic mean: -141315.80) with high PPs (≧80) across all but 17 ingroup nodes (Supplementary Figure 2). Only five nodes are in conflict when comparing the Bayesian tree topology with the ML topology. Of these nodes, four are nested within major clades and represent minor generic-level topological incongruities and lack of resolution in the Bayesian tree from PPs less than 0.5. One major difference is the placement of *Ciulfina biseriata* as sister to a large clade that excludes Amorphoscelidae and Iridopterygidae taxa, which is not consistent with prior placement of this taxon [3]. However, the Bayesian tree recovers this taxon as sister to Amorphoscelidae and Iridopterygidae. We represent the final tree topology using the ML results and indicate nodal support values for both BS and PP to indicate areas of congruence and conflict (Supplementary Figure 2). For time tree estimation, the Yule process model analysis recovered a mean likelihood of -152629.1362 and a root height of 197.93589231785 (median) and range of 50.8572 to 272.9793. Because this estimate was based on a prior estimated split between Blattodea and Mantodea, both the root date and the crown dates are consistent with the studies [3,20] **from which the calibration dates were sourced (Supplementary Figure 2).**

**2.4. Bias in behavioural trait observation**

Pagel’s binary correlation test between the binary variable ‘author’ and presence of display and primary defense were negative (log-lik = 3.709, p = 0.447 and log-lik = 2.301, p = 0.681, respectively). There wasn’t a significant difference in the evolutionary distinctiveness of the species reported by different authors (F12,57 = 1.015, p = 0.516), and even though Edmunds (1972 & 1976) described 31 of the behaviours (accounting for 53.5% of all species behaviourally described), the results found in the whole dataset were consistent with those found in Edmunds (1972 & 1976) for evolutionary distinctiveness and (1) presence of display (F1, 31 = 9.765, p = 0.024), and (2) display complexity (F4, 31 = 4.743, p = 0.010). All these results support the conclusion that there wasn’t a significant bias between behavioural observations from Edmunds (1972 & 1976) and the other authors.

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