

**Supplementary Materials for Interspecific limits within Charipinae (Cynipoidea: Figitidae), insights from molecular data**

Mar Ferrer-Suay <sup>1,\*</sup>, Mariana Bulgarella <sup>2</sup>, George E. Heimpel <sup>3</sup>, Ehsan Rakhshani <sup>4</sup> and Jesús Selfa <sup>1</sup>

**Supplemental Data File S1.** Fasta formatted alignment of 35 individual wasps in the Charipinae plus a cynipid gall wasp as outgroup, concatenating three loci, mitochondrial cytochrome oxidase I gene (COI), 16S ribosomal RNA encoding gene sequences (16S rDNA), and nuclear internal transcribed spacer 2 (ITS2 rDNA). Gaps in this alignment are not coded as separate partitions, the length of the alignment is 1,377 base pairs.

**Supplemental Data File S2.** Fasta formatted alignment of 35 individual wasps in the Charipinae plus a cynipid gall wasp as outgroup, concatenating three loci, mitochondrial cytochrome oxidase I gene (COI), 16S ribosomal RNA encoding gene sequences (16S rDNA), and nuclear internal transcribed spacer 2 (ITS2 rDNA). Gaps are added to the data file as separate partitions, resulting in an alignment of 1,471 base pairs.

**Supplemental Data File S3.** Fasta formatted alignment of 239 individual wasps in the Charipinae and a cynipid gall wasp as outgroup for mitochondrial cytochrome oxidase I gene (COI). Alignment length is 615 base pairs.