# Phylogeny of the family Torymidae (Hymenoptera: Chalcidoidea)

Petr Jašta[1*], Astrid Cruaud[2], Gerard Delvare[2], John Heraty[3], Jean-Yves Rasplus[2]

[1]Charles University in Prague, Department of Zoology, Viničná 7, 128 44 Praha 2, Czech Republic, e-mail: janstapetr@gmail.com; [2]INRA, UMR Centre de Biologie et de Gestion des Populations (CBGP) Campus International de Baillarguet, CS 30016, 34988 Montferriersur Lez, France; [3]Department of Entomology, University of California, Riverside, CA 92521, USA; *coresponding author

INTRODUCTION: Torymidae is one of the middiverse groups of chalcids (together about 982 described species worldwide classified into 68 genera – Jašta et al. 2013). The phylogeny of the family was firstly reconstructed based on morphological characters by Grissell (1995) . He estimated two subfamilies (Megastigminae and Toryminae) and 7 tribes within Toryminae. Phylogenetic position of several genera still remained unresolved and they were classified as incertae sedis within subfamily Toryminae. The majority of the torymids are primarily ectoparasitoids of various gall makers (mainly of Cynipidae and Cecidomyiidae), mantids eggs or larvae of bees, phytophagous species are quite rare within subfamily Toryminae. On the other hand, number of known species of Megastigminae are phytophagous species and they mostly belong to the genus *Megastigmus*. But nearly all of the rest of Megastigminae genera are ectoparasitoids of various gall makers.
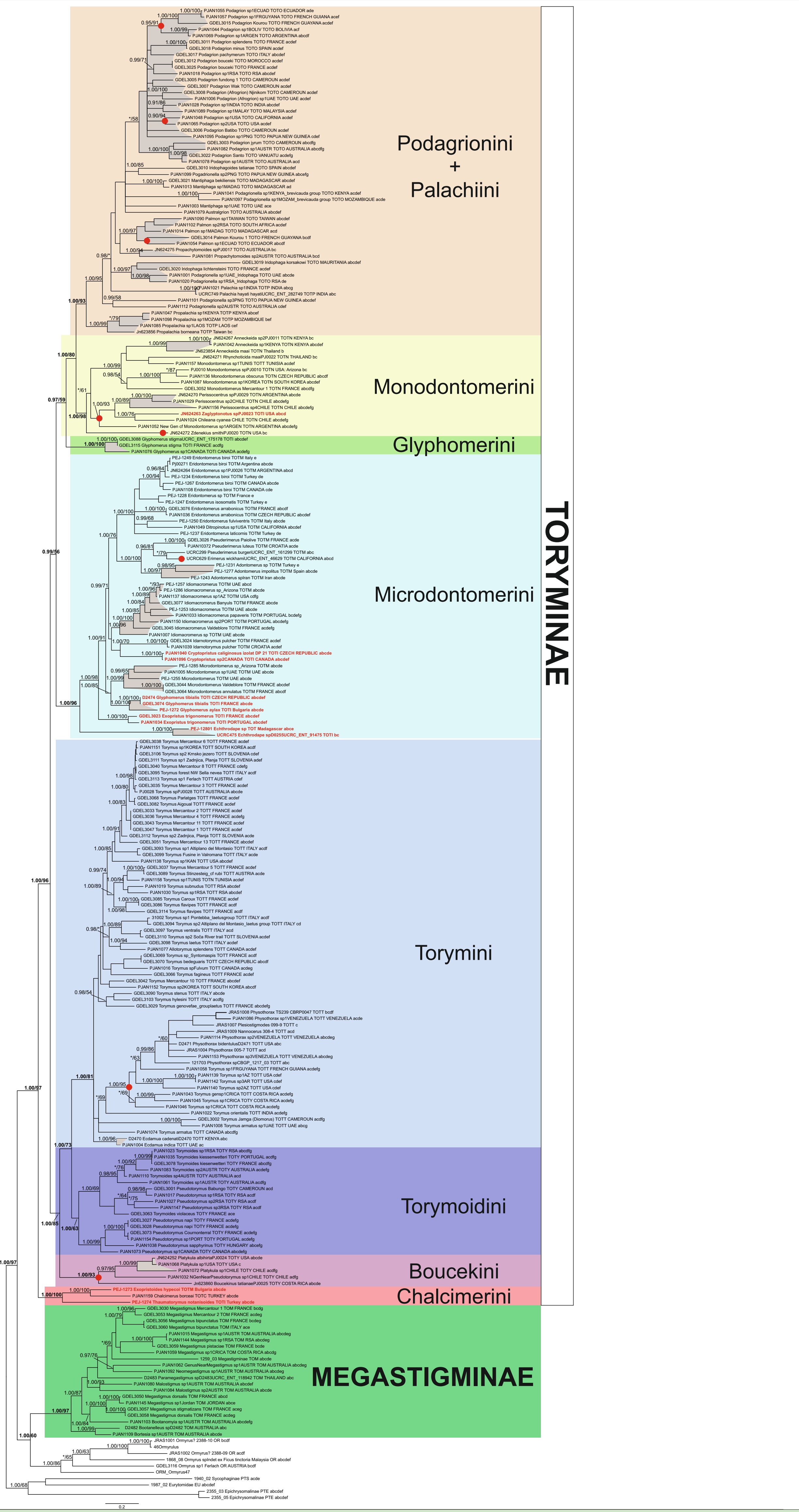
MATERIAL AND METHODS
Altogether, 10 outgroups and 227 ingroups taxa were analysed, representing 46 of the 68 recognized genera from two known subfamilies (Megastigminae and Toryminae) of Torymidae. Five genes regions (18S r DNA, 28S r DNA, EF1α, COI and Wg) representing 4809 nucleotides were sequenced. Nuclear ribosomal genes were aligned based on known secondary structure model (Gillespie et al. 2005, Heraty et al. 2013), protein-coding genes were aligned using MAFFT algorithm. Prior to all analysis, data were divided into 10 partitions. Phylogenetic trees were estimated using maximum likelihood (ML) and Bayesian methods. All analysis (RAxML and MrBayes) were computed on the CIPRES Science Gateway V. 3.1.

RESULTS AND CONCLUSIONS
All analyses produced similar topologies and demonstrated that based only on molecular data Torymidae is probably not monophyletic group and Megastigminae is sister taxa with Ormyridae ((Ormyridae + Megastigminae) + Toryminae). Most of the tribes within subfamily Toryminae recognized by morphological characters (i.e. Chalcimerini, Microdontomerini, Monodontomerini, Torymini, Torymoidini, and Palachiini + Podagrionini) and two tribes are classified for the first time (i.e. Boucekini and Glyphomerini) were supported (see Fig. 1). Within Toryminae, several genera (i.e. *Glyphomerus*, *Torymus*, *Pseudotorymus*, *Mantiphaga*, *Eridontomerus* etc.) were considered as paraphyletic. Seven other genera classified as incertae sedis based on morphology were assigned to specific tribes (i.e. *Cryptopristus*, *Echthrodape*, *Exopristus* and part of *Glyphomerus* to Microdontomerini; *Exopristoides* and *Thaumatorymus* to Chalcimerini; *Zaglyptonotus* to Monodontomerini).
Only tribe Boucekini is exclusively distributed in New World. The rest of tribes have probable Old World origin with some taxa consequently spread into the New World.
Within Megastigminae, genus *Megastigmus* is paraphyletic. Zoophagous species of *Megastigmus* clustered with zoophagous genus *Bootanomyia*, while other species (all of them probable phytophagous) formed one clade with other genera of Megastigminae. We speculate the most probable feeding strategy for ancestor of Megastigminae is zoophagy.

Fig. 1: Phylogram of relationships of Torymidae and ten outgroups taxa based on Bayesian analysis. Letters behind name of each taxa specify gene region sequenced (i.e. 18S, 28SD2, 28SD3-5, Ef1a, COIbarcode, COI2183-3014, Wg). Partitions set for RNA, EF nt1, nt2, nt3, COI nt1, nt2, nt3 and Wg nt1, nt2, nt3. Posterior probablities ≥0.95/bootstrap values ≥ 50 above branches, * indicates posterior probability lower than 0.95/bootstrap value lower than 50. Tribal, subfamilian posterior probabilities/bootstrap values bolded. All tribes/subfamily shaded with specific color. Grey shaded area highlight supported monophyletic genera. Taxa determined by Grissell (1995) as incertae sedis and classified in our analysis are bold red highlighted. Red dots indicate exlusively New World clades.