

167), 1 ♀ (CZW); Camarines Sur Prov., Lupi, Sooc, dam area, 14.III.2004, leg. H. Zettel & C. Pangantihon (# 380), 1 ♀ (CZW); Camarines Sur Prov., Lupi, Sooc, 13. - 20. IX.1999, leg. H. Zettel (# 206), 1 ♀ (CZW); Leyte Is.: Leyte Prov., Baybay, ViSCA, 50 m, "Forestry", stream, 11.II.2000, leg. H. Zettel (# 235), 1 ♀ (NHMW); Baybay, LSU, 50 m, Lago-Lago River, 19.III.2005, leg. H. Zettel & C. Pangantihon (# 421), 1 ♀ (CZW).

Molecular analyses

The genetic analyses included 30 workers, but because of failure in PCR reactions, probably due to DNA degradation, the final sample comprised 12 workers from 12 colonies: 7 *T. pacificum*, 1 *T. scabrum*, 1 *T. manobo*, 1 *T. cynicum* and 2 *T. insolens*. For DNA extraction from the specimens of *T. pacificum*, *T. scabrum* and *T. manobo*, only the gaster was taken, allowing subsequent morphometric analyses. DNA extractions and PCR reactions using a touchdown program followed the standard procedures of STEINER & al. (2006c), except for annealing temperatures, which were set to 49 - 46 °C. The primers used for amplification of the approximately 950 bp of the *COI* gene segment were the newly developed "COI2f" (5' - AATACCTCATTGATCCATC - 3') with L2-N-3014r alias "Pat" (SIMON & al. 1994). PCR products were purified using the QIAquick PCR purification kit (Qiagen, Hilden, Germany), subsequently sequenced in both directions using the Big Dye termination reaction chemistry (Applied Biosystems, Foster City, CA, USA) and analysed using an ABI 377 automatic sequencer (Applied Biosystems).

Nucleotide sequences were aligned with default settings of Clustal X (THOMPSON & al. 1997). 700 bp of *COI* were used in the phylogenetic analyses under the distance (Neighbour-Joining algorithm, NJ) criterion using PAUP* (test version 4.0b3a; SWOFFORD 1998) and by Bayesian inference using Markov Chain Monte Carlo sampling (MCMC), done in MrBayes 3.1 (RONQUIST & HUELSENBECK 2003). Uncorrected Distances and Tamura-Nei distances were calculated and the latter were used for the NJ tree. Support for the NJ tree was assessed with 1,000 bootstrap replicates. Prior to MCMC analysis the GTR+I+G model (TAVARÉ 1986, YANG 1993) was selected by MrModeltest 2.2. (NYLANDER 2004), using hierarchical likelihood ratio tests (LRT; HUELSENBECK & RANNALA 1997), which determine the concordance of data with competing substitution models. We defined three partitions according to codon positions. In the MCMC analysis 500,000 generations with a sampling frequency of 100 were run twice. After 250,000 generations, stationarity was achieved (average standard deviation of split frequencies constantly staying below 0.01, until the end of the run). The last 2,500 trees of each run were used to compute a majority rule consensus tree, assigning posterior probabilities of tree topology. In all phylogenetic reconstructions we added a homologous sequence of *T. bicarinatum* (AY 909379; sequenced for an earlier study by BCS and FMS; specimen identified using the key and the species descriptions in BOLTON (1977); the correctness of synonymies given by BOLTON (1977) was not questioned). Homologous sequences of the following Myrmicinae were used as outgroup: *T. caespitum* (LINNAEUS, 1758) (AY909170) and *Myrmica rubra* (LINNAEUS, 1758) (DQ074378).

Morphometric analyses

For worker morphometry, 150 workers were analysed: 62 *T. pacificum*, 29 *T. scabrum*, 59 *T. manobo*. Dry-mounted specimens were fixed on a pin-holding goniometer. A Nikon SMZ 1500 high-performance stereomicroscope with a 1.6 × planapochromatic lens and a cross-scaled ocular micrometer was used at magnifications of 50 - 320 ×. The following thirteen morphometric characters were measured:

- CL Maximum cephalic length in median line. The head must be carefully tilted to the position with the true maximum. Excavations of the posterior margin of the head and / or clypeus reduce CL. Surface irregularities due to sculpture, carinae in particular, are considered by averaging between peaks and valleys of sculpture.
- ClyNoD Maximum depth of clypeal notch; measured in same adjustment of ant as for CL, measured as orthogonal distance of caudalmost point of clypeal notch to a transversal reference line between frontal-most points of clypeus, to the left and to the right of the notch.
- CW Maximum cephalic width across eyes.
- FCHL Length of longest hair on frontal carina between deepest point of scape corner pit and posterior margin of the eye; arithmetic mean of both sides.
- MNH Distance of ventral reference line to dorsalmost point of mesonotum, measured in same adjustment and orthogonal to same ventral reference line as for PosSPI. Note that this point is, in the given adjustment, usually behind the median line of the mesonotum and can only be found after focusing movements. With the graduated scale of the ocular micrometer kept perpendicular in the visual field, focusing cannot induce a parallax error.
- MW Maximum mesosoma width.
- PEHL Length of longest hair laterally on petiole; arithmetic mean of both sides.
- PEW Maximum width of petiole.
- PosSPI Orthogonal distance of uppermost point of spine to a ventral reference line of the mesosoma. The ventral reference line is the line from the ventralmost point of the pronotum to the ventralmost point of the metapleuron. With the graduated scale of the ocular micrometer directed perpendicular in the visual field, this reference line is brought to coincidence with the horizontal line of the cross-scale at magnifications of about 100 ×. Then, at a magnification of ≥ 250 ×, the mesosoma is carefully tilted to a position in which the ventralmost point of the metapleuron and the tip of the spine are at the same focal level. Note that this character is not necessarily measured in lateral view, but frequently in a dorsolateral view.
- PPW Maximum width of postpetiole.
- PreOc Preocular distance in lateral view; measured as shortest distance between anterior eye margin and sharp frontal margin of gena; arithmetic mean of both sides.
- SPBA Smallest distance between outer margins of spines at their base, measured in dorsofrontal view. If the lateral margins of spines diverge continuously from the tip to the base, a smallest distance at base is not