Abstract

Species delimitation is fundamental for many biological studies; its importance extends from regional faunistics over behavioral research to the reconstruction of evolutionary history. However, species delimitation in the Palearctic Tetramorium caespitum species complex (formerly Tetramorium caespitum / impurum complex) has stayed ambiguous over a century. A 2006 study argued for the presence of eight Western Palearctic cryptic species but did not draw formal taxonomic conclusions due to multiple unresolved issues. Using 1428 nest samples in an in-depth integrative-taxonomy approach, we here revise the European species of the complex. Unsupervised analyses provide independent species hypotheses based on molecular and morphological disciplines. Following the unified species concept, we show the presence of ten clearly distinguishable European species differing in mitochondrial DNA, nuclear DNA, morphology of workers and males, and ecology. We explain the evolution of the observed mitochondrial-nuclear discordances by peripatric speciation, historical introgression, and recent hybridization, and that of morphological-nuclear discordances by interspecific similarity and intraspecific variability, that is, morphological crypsis. Based on the final species hypotheses, we confirm T. caespitum (LINNAEUS, 1758), T. impurum (FOERSTER, 1850), T. indolice SANTSCHI, 1927, T. hungaricum RÖSSLER, 1935, and T. alpestre STEINER, SCHLICK-STEINER & SEIFERT, 2010 as good species. We raise T. fasciculata CONSANI & ZANGHERI, 1952 stat.n., T. staerckei KRATOCHVIL, 1944 sp.rev., and T. immigrans SANTSCHI, 1927 stat.n. (as an introduced species also in the Americas) to species rank and synonymize T. semilaevae var. kutteri SANTSCHI, 1927 under T. indolice and T. staerckei var. gregori KRATOCHVIL, 1941 under T. impurum. Finally, we newly describe T. breviscapus sp.n. and T. caucasicum sp.n. We present dichotomous determination keys to workers and males and make freely available an online identification key to workers at https://webapp.uibk.ac.at/ecology/tetramorium/. Of relevance to resolving other highly complicated taxonomic problems, we highlight that no single data type was sufficient to disentangle the final species boundaries, which underlines the importance of integrating multiple data sources in taxonomy.

Key words: CO1 gene polyphyly, amplified fragment-length polymorphism, morphometrics, nest centroid clustering, interspecific hybridization, European pavement ants.

Introduction

The species level is the basis of many biological studies – most research in, for example, conservation, phenology, morphology, behavior, and physiology, makes sense only if the study organism is correctly determined at the species level. Some species are, from a human point of view, cryptic, which means they are not morphologically distinguishable using conventional methods (BICKFORD & al. 2007, SMITH & al. 2008, SEIFERT 2009). Their delimitation challenges taxonomists and increasingly leads to inter-disciplinary approaches (SCHLICK-STEINER & al. 2010). Species delimitation is also the basis of investigating the evolution of crypsis itself. Processes such as stasis, convergence, interspecific gene flow, and postglacial migration can only be understood using correctly delimited species units.

Ants have been considered as difficult to determine at the species level (SEIFERT 2007). Within ants, the genus Tetramorium seems to stand out in this quality, as its taxo-
nomical situation has remained unclear even in the relatively well studied Central European area (Steiner et al. 2002, Csösz & Markó 2004, Schlick-Steiner & al. 2005, 2006, Seifert 2007). Species of the Tetramorium caespitum complex (formerly T. caespitum / impurum complex sensu Schlick-Steiner & al. 2006) inhabit areas up to 2500 meters above sea level (m a.s.l.) and 63° N and include the most widespread and abundant Tetramorium ants of Central and Northern Europe. Representatives of the complex are found in open, xerothermous habitats such as dry grasslands, block fields, and urban areas. Dense forests are avoided, but light pine and oak woodlands in southern Europe are frequently inhabited.

Before the 20th century, two still valid species of the complex were described from Europe, Tetramorium caespitum (Linnaeus, 1758) and T. impurum (Foerster, 1850). In the first half of the 20th century, multiple new Tetramorium species and subspecies names were assigned (e.g., Emery 1925, Santschi 1927, Rössler 1936, Kratochvil 1941, 1944), but strong delimitation arguments were missing in most cases. Hence, in the following decades, myrmecologists ignored those nomenclatural changes. Csösz & Markó (2004) found distinct differences between T. caespitum s.l. and T. hungaricum Rössler, 1935 and redescribed the latter based on morphological arguments. After that, the detection of cryptic species by Schlick-Steiner & al. (2006) was based on sequences of the mitochondrial cytochrome C oxidase subunit I (CO1) gene, traditional morphometrics (TM), male genital morphology, and cuticular hydrocarbons. These authors proposed the presence of five further species additionally to T. caespitum, T. impurum, and T. hungaricum and handled them as operational taxonomic units labeled A - E. Additionally, they labeled six smaller CO1-haplotype (HT) clades (henceforth, CO1 clades) without data of other disciplines as U1 - U6. Since then, operational taxonomic unit A has been newly described as T. alpestre Steiner, Schlick-Steiner & Seifert, 2010 (Steiner & al. 2010) and C redescribed as T. indocile Santschi, 1927 (Csösz & al. 2014b). Besides T. tsushimae (see Steiner & al. 2006b), species E has been shown to be the only species of the complex introduced to the Americas (Steiner & al. 2008).

In this study, we aimed to delimit the European species of the Tetramorium caespitum complex based on integrative taxonomy. Additionally, we showed the linkage between operational taxonomic units and type material, drew taxonomical consequences, and presented identification keys. Thereby, we provide the basis for reconstructing the evolutionary history of the cryptic species complex. Due to the obvious difficulties in delimiting species of the T. caespitum complex (Schlick-Steiner & al. 2006, Steiner & al. 2006a, Seifert 2007, Steiner & al. 2010), we used an in-depth integrative-taxonomy approach and applied genetic and morphological data on a high-density sample from most European regions. We chose mitochondrial DNA (CO1 gene), a whole-genome scan (amplified fragment-length polymorphism; AFLP), male genital morphology, TM of workers, geometric morphometrics (GM) of workers and gyne wings, and thermal niche as data sources for integrative species delimitation. We followed an established protocol to handle cryptic species by integrative taxonomy (Schlick-Steiner & al. 2010). To link operational taxonomic units with valid species names, we investigated Palearctic type material from the west of the Johansen line in Siberia (see Johansen 1955) as well as the type of a species introduced to the Americas (T. immigrans Santschi, 1927).

Material and methods

Diagnosis of the Tetramorium caespitum complex: At least 28 Tetramorium species are native to Europe (Borowiec 2014); most of these do not belong to the Tetramorium caespitum complex. The differentiation of complexes is not always simple since the traits of morphological characters often overlap. Therefore, the morphological criteria for inclusion into the T. caespitum complex are characterized in detail here (see Taxonomy, Diagnosis of the T. caespitum complex).

Integrative-taxonomy workflow: The study follows a coherent protocol for integrative taxonomy (Schlick-Steiner & al. 2010). As far as possible, data were generated by using the same individuals in all disciplines. In doing so, gasters of workers were cut off for DNA extraction, degastered workers mounted for morphometrics, and males from the same nests dissected for genital investigation. Data of CO1, AFLP, male genital morphology, TM, and GM were analyzed without prior hypotheses, that is, in an unsupervised fashion. The results of disciplines were compared and discordance rates between genetic and morphometric methods determined. The unified species concept (De Queiroz 2007) was used; it defines species as independently evolving metapopulations and considers the ability of different disciplines to delimit species at different stages of speciation. Following ideas of Wiens & Servedio (2000) and Seifert (2014), species delimitation criteria were decisions considering thresholds of evolutionary divergence. For the CO1 phylogeny, the multi-rate Poisson Tree Processes method (Kapli & al. 2017) was used to delimit CO1 clades; after comparison with other results, these clades were treated either as intra-specific entities or species. For AFLP data, BAPS (Corander & al. 2008) clusters (Mallet 1995) with the highest marginal likelihood were considered either as intra-specific entities or as species, depending on morphological findings. Male genital morphology was qualitatively scanned for distinct trait differences; delimitable morphometric entities were considered to confirm or reject DNA-based species hypotheses. For morphometric species delimitation, Nest-Centroid clustering (Seifert & al. 2014b) was used; discordance rates between Nest-Centroid-clustering-based and DNA-based species hypotheses were calculated by pairwise comparisons of species; discordance rates < 5% of nests were accepted and considered to confirm DNA-based species hypotheses. Discordances between results of different data types required evolutionary explanations. Finally, operational taxonomic units were linked to type material and nomenclatural consequences drawn.

Sample: Material of the Tetramorium caespitum complex was collected from 31 nations in Europe and – to a lesser extent – from Asia and the Americas mainly between 1992 and 2015, resulting in more than 2400 nest samples. The material was stored at -20 °C in 96% ethanol at the Institute of Ecology, University of Innsbruck, Austria (Tab. S1, as digital supplementary material to this article, at the journal’s web pages). Material outside the T. caespitum complex was used to delimit the species com-
plex within the *T. caespitum* group sensu BOLTON (1995) (see Taxonomy, Diagnosis of the *T. caespitum* complex). Only species of the *T. caespitum* complex occurring in Europe were considered for detailed analyses. First, a 1113-bp stretch of the CO1 gene of a worker of 1391 nests originating from all relevant biogeographical regions was sequenced (partly published in SCHLICK-STEINER & al. 2006, STEINER & al. 2010, CSŐSZ & al. 2014b, and KINZNER & al. 2015). Incomplete CO1 sequences were not used for phylogenetic reconstruction but for distribution maps whenever assignment to a CO1 clade was possible. The rationale for investigating samples under further, ideally all, disciplines was to representatively sample HT diversity and geographic distribution of CO1 clades. Material of 476, 96, 468, 245, and 81 nests was used for AFLP, male genital morphology, worker TM, worker GM, and gyne GM, respectively. Additionally to this material, for distribution maps and calculation of thermal niches, also data published by SCHLICK-STEINER & al. (2006), NEUMAYER (2008), WAGNER (2009, 2011a, b, 2012), STEINER & al. (2010), WAGNER & al. (2010, 2016), BRAČKO & al. (2014), and CSŐSZ & al. (2014b) were used, providing that the species determinations were plausible.

**PCR amplification and sequencing of the CO1 gene:**
Total genomic DNA of the gasters of one to two workers per nest was extracted with the GenElute Mammalian DNA Extraction Kit (Sigma, St. Louis, USA) following the instructions of the manufacturer. A 1280 bp fragment of the CO1 gene was amplified using the primers CO1H (5'-CCC CCC TCT ATT AGA TTA TT-3'; STEINER & al. 2005) and UEA10 (5'-TCC AAT GCA ATA ATC TGC CAT ATT A-3'; LUNT & al. 1996). Standard PCR was performed using 1 × MyTaq buffer (Bioline, UK), 200 nM of each primer, 0.25 U MyTaq DNA polymerase (Bioline), 0.3% Bovine Serum Albumin (Roche, Switzerland), and ca. 50 ng template DNA in a total volume of 10 µl. When the standard PCR failed, reactions were repeated using 1 × RotorGene Probe PCR Master Mix (Qiagen, Germany), 100 nM of each primer, and ca. 50 ng template DNA in a total volume of 10 µl. Reactions were carried out on a UnoCycler (VWR, USA) with an initial denaturation at 95 °C for 3 min, followed by 35 cycles of 95 °C for 30 s, 48 °C for 45 s, and 72 °C for 2 min, and 10 min of final extension at 72 °C. PCR products were purified by incubation with 2 U Exonuclease I and 0.1 U FastAP (both Thermo Scientific, USA) at 37 °C for 15 min, followed by an inactivation step at 80 °C for 15 min. Purified PCR products were Sanger sequenced by a commercial sequencing facility (Eurofins MWG Operon, Germany) using both amplification primers. To eliminate PCR errors, sequences revealing singleton HTs were verified with an independent PCR.

**CO1 alignment and nuclear mitochondrial sequences (NUMT) detection:** Sequences were aligned with the ClustalW algorithm implemented in MEGA5.05 (TAMURA & al. 2011) using default settings. A four-step workflow to detect nuclear copies of mtDNA (NUMTs; see SONG & al. 2008) was applied: (I) Electropherograms were checked for double peaks, translated, and controlled for correct amino acid sequence and premature stop codons. (II) A mitochondrial DNA enrichment protocol (TAMURA & AOTSUKA 1988) was used to check samples of 14 CO1 clades of which nests with > 15 workers were available. (III) RNA of the nests 18538 (HT225) and 18535 (HT439), both stored in RNA-later (Qiagen) and belonging to CO1 clade U2 sensu SCHLICK-STEINER & al. (2006), was isolated using the Nucleospin RNA Kit (Macherey Nagel, Düren, Germany). Complementary DNA was synthesized with the RevertAid First Strand cDNA Synthesis Kit (Thermo Scientific) following the manufacturer’s instructions and using the primer CO1H. The complementary DNA was amplified with the primers CO1H and negOR. 5'-CCT CTT TCA TTA ATA ATA TG-3'. (IV) Based on the CO1 polyphyly within *Tetramorium caespitum* (see results), we hypothesized that the Iberian nests of clade D sensu SCHLICK-STEINER & al. (2006), henceforth D-w, might have amplified NUMTs. As CO1 clade U2 (belonging to *T. caespitum* according to our final species hypotheses) occurs in the geographic area neighboring the samples of D-w and likewise belongs to *T. caespitum*, a forward-primer specific for the CO1 clade U2, u2_spec_f, 5'-TCA CTC GGA ATA ATT TAC GCC-3', was developed. Since some nests of CO1 clade D-w were morphologically similar to and geographically overlapped with *T. impurum*, we developed also a CO1 forward-primer specific for *T. impurum*, imp2_spec_f, 5'-TAC AGC AAC TCT CCT TCT CC-3'. Extracts of all 23 D-w-nests were amplified using these forward primers and UEA10 using Rotor-Gene Probe PCR Master Mix as described in Section PCR amplification and sequencing of the CO1 gene. Only CO1 HTs without suspicious results in any of these four steps were used for the phylogenetic reconstruction; other sequences were considered as potential NUMTs and thus excluded. Sequences of new CO1 HTs and NUMTs were deposited in GenBank (Tab. S1).

**Phylogenetic reconstruction and species delimitation using CO1:** For phylogenetic reconstruction, every HT was used only once. *Tetramorium capitale* (MCAREEVEY, 1949) (GenBank accession AY641664) was chosen as outgroup. For model selection, PartitionFinder v1.1.1 (LANFEAR & al. 2012) was used. TrN + G + I, F81, and GTR + G were suggested for codon positions 1, 2, and 3, respectively. These best-fit partitioning schemes were used for the Maximum-Likelihood (ML) tree reconstruction in Garli v2.0 (Zwickl 2006). Phylogenetic trees were also reconstructed using a Bayesian approach (MrBayes v3.2.0; RONQUIST & al. 2012). Here, the alignment was partitioned into three codon positions as suggested by PartitionFinder. Two parallel runs, each consisting of four chains, were iterated for 8 × 10⁶ generations using the algorithm "mixed". The first 25% were discarded as burn-in. The final average standard deviation of split frequencies was still above 0.01 (0.0144). Additional runs using 15 × 10⁶ and 30 × 10⁶ generations did not improve the standard deviation of split frequencies values (data not shown). Convergence of model parameters was checked using Tracer v1.6 (RAMBAUT & al. 2014). After resolving polytomies, the resulting tree was used for species delimitation based on the multi-rate Poisson Tree Processes method (KAPLI & al. 2017) excluding the outgroup.

**Amplified fragment-length polymorphism (AFLP):** DNA of 508 *Tetramorium* workers (476 of the *T. caespitum* complex) was used for AFLP genotyping following a modified protocol of VOS & al. (1995), described in detail in WACHTER & al. (2012). Briefly, digestion was performed with the enzymes EcoRI and MseI; AFLP ad-
Tab. 1: Acronyms and definitions of the worker traditional morphometrics characters. For illustrations, see Figures 1 - 6.

<table>
<thead>
<tr>
<th>Acronym</th>
<th>Definition</th>
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<tbody>
<tr>
<td>CL</td>
<td>Maximum cephalic length in median line (Fig. 1); head is carefully tilted to position with true maximum; excavations of occiput and/or clypeus reduce CL. Peaks due to sculpture are ignored and only valleys are considered.</td>
</tr>
<tr>
<td>CW</td>
<td>Maximum cephalic width across eyes (Fig. 1).</td>
</tr>
<tr>
<td>dAN</td>
<td>Minimum distance between antennal fossae (Fig. 1); measured in dorsofrontal view.</td>
</tr>
<tr>
<td>EL</td>
<td>Maximum diameter of one eye. All structurally defined ommatidia, pigmented or not, are included (Fig. 2).</td>
</tr>
<tr>
<td>EW</td>
<td>Minimum diameter of one eye. All structurally defined ommatidia, pigmented or not, are included (Fig. 2).</td>
</tr>
<tr>
<td>EYE</td>
<td>Arithmetic mean of EL and EW.</td>
</tr>
<tr>
<td>FL</td>
<td>Maximum distance between external margins of frontal lobes (Fig. 1). If this distance is not defined because frontal carinae constantly converge frontad, FL is measured at FRS level (definition of FRS see SEIFERT 2003) as distance between the outer margins of frontal carinae.</td>
</tr>
<tr>
<td>HFL</td>
<td>Length of hind femur in dorsal view (Fig. 3). Second trochanter, which could appear to be portion of femur, must not be mistakenly included.</td>
</tr>
<tr>
<td>MC1TG</td>
<td>Quantification of stickman-like or reticulate microsculpture units on base of 1st gastral tergite (use &gt; 150 x magnification; Fig. 4); Number of connected lines building units and being separated by line intersections and by reflections angled &gt; 10° is counted. Also very short lines are full counts. Arithmetic means of at least three units per worker are taken.</td>
</tr>
<tr>
<td>ML</td>
<td>Mesosoma length measured in dorsal view from caudalmost portion of propodeum to dorsofrontal corner of pronotal slope (i.e., where coarsely structured dorsal shield meets finely structured pronotal neck; Fig. 5); equivalent measuring also possible in lateral view.</td>
</tr>
<tr>
<td>MPPL</td>
<td>Distance between most anteroventral point of metapleuron and most dorsocaudal point of propodeal lobe in lateral view (Fig. 6). If there are two points coming into question to be dorsocaudalmost point on propodeal lobe, the one which is provided with a carina is taken.</td>
</tr>
<tr>
<td>MPST</td>
<td>Distance between most anteroventral point of lateral metapleuron and distalmost point of propodeal spine (it does not need to be uppermost point of spine; Fig. 6).</td>
</tr>
<tr>
<td>MtpW</td>
<td>Maximum metapleural width measured in dorsal view (Fig. 5). (In most cases, maximum is at caudal and in few cases at central or frontal region of metapleuron.)</td>
</tr>
<tr>
<td>MW</td>
<td>Maximum mesosoma width (Fig. 5).</td>
</tr>
<tr>
<td>PEH</td>
<td>Petiole height. Measured from uppermost point of concave ventral margin to node top (Fig. 6).</td>
</tr>
<tr>
<td>PEL</td>
<td>Petiole length. Measured in lateral view from center of petiolar stigma to caudal margin of petiole (both measuring points on same focal level; Fig. 6).</td>
</tr>
<tr>
<td>PEW</td>
<td>Maximum petiole width (Fig. 5).</td>
</tr>
<tr>
<td>PLSp</td>
<td>Distance between most dorsocaudal point of propodeal lobe (if there are two points coming into question to be dorsocaudalmost point of propodeal lobe, the one which is provided with a carina is taken) and distalmost point of propodeal spine (it does not need to be uppermost point of spine; Fig. 6).</td>
</tr>
<tr>
<td>PLST</td>
<td>Distance between most dorsocaudal point of propodeal lobe and center of propodeal stigma (Fig. 6).</td>
</tr>
<tr>
<td>PnHL</td>
<td>Length of hair at frontolateral corner of pronotum (Fig. 6). Take longest hair of both sides.</td>
</tr>
<tr>
<td>PoOc</td>
<td>Postocular distance. Using cross-scaled ocular micrometer, head is adjusted to measuring position of CL; causal measuring point: median posterior margin of head, microsculpture peaks are ignored and valleys are considered; frontal measuring point: median head crossing line between posterior eye margins (Fig. 1).</td>
</tr>
<tr>
<td>POTCos</td>
<td>Number of postoculo-temporal costae and costulae (Fig. 2). With head in lateral view and longitudinal axis of head adjusted horizontally, counted by focussing along perpendicular line from caudalmost point of eye down to underside of head. Costae / costulae just touching measuring line are counted as 0.5, those positioned just at ventral margin of head silhouette are not counted. Arithmetic mean of both sides.</td>
</tr>
<tr>
<td>PPH</td>
<td>Maximum postpetiole height (Fig. 6).</td>
</tr>
<tr>
<td>PPL</td>
<td>Postpetiole length; distance from center of postpetiolar stigma to caudalmost intersection point of tergite and sternite (both measuring points at same focal level; Fig. 6).</td>
</tr>
<tr>
<td>Ppss</td>
<td>Maximum height of smooth and shiny area on lateral side of propodeum (Fig. 6). This area is brought into visual plane; a line is positioned perpendicular to main costae on propodeum and maximum height of smooth and shiny area without any costules and costae is measured. Take arithmetic means of both sides.</td>
</tr>
<tr>
<td>PPW</td>
<td>Maximum postpetiole width (Fig. 5).</td>
</tr>
<tr>
<td>PreOc</td>
<td>Preocular distance in lateral view. Measured as minimum distance between anterior eye margin and sharp frontal margin of gena (Fig. 2).</td>
</tr>
<tr>
<td>RTI</td>
<td>Distance between tops of ridges between antennal fossae and clypeus (Fig. 1). Tops are defined as dorsofrontalmost points of ridges, provided with a costa on clypeus. Measured in dorsoanterior view.</td>
</tr>
<tr>
<td>SLD</td>
<td>Maximum scape length, including scape lobe, excluding articular condyle (Fig. 1).</td>
</tr>
<tr>
<td>SPST</td>
<td>Distance between distalmost point of propodeal spine (it does not need to be uppermost point of spine) and center of propodeal stigma (Fig. 6).</td>
</tr>
<tr>
<td>SPWI</td>
<td>Maximum distance between outer margins of propodeal spines (Fig. 5). Measured in dorsoanterior view.</td>
</tr>
</tbody>
</table>
Figs. 1 - 6: Measurement lines for the morphometric characters: (1) CL, CW, dAN, FL, PoOc, RTI, and SLd; (2) EL, EW, and PreOc; including an artificial line for the meristic character POTCos, as well as a hind for the position of c-shaped, crinkly, or sinuous hairs (arrow); (3) HFL; (4) Meristic character MC1TG. In this example, MC1TG = 18; (5): ML, MtpW, MW, PEW, PPW, and SPWI; (6) MPPL, MPSP, MPST, PEH, PEL, PLSP, PLST, PhHL, PPH, PPL, Ppss, and SPST.
aptors were ligated simultaneously. Preselective amplification was carried out with the primers Eco-N and Mse-C. Selective amplification was performed using the five primer combinations Eco-AA / Mse-CAA, tEco-AA / Mse-CTA, tEco-AA / Mse-CTT, tEco-AC / Mse-CTA, and tEco-TG / Mse-CTA incorporating FAM / NED / PET labels by an M13-tail method. Plate position of samples was chosen randomly. As quality control, two kinds of replicates were used: (I) Preselective amplicon of four workers was included on each 96-well plate used in the selective PCR ("fixed replicates"). (II) DNA of eight randomly chosen workers per plate was replicated on another position of the same plate already in the digestion-ligation-step ("pairwise replicates"). Capillary electrophoresis was performed by a commercial sequencing facility (Comprehensive Cancer Center DNA Sequencing & Genotyping Facility, University of Chicago, USA) on an ABI 3730 sequencer (Applied Biosystems). Trace files were converted to comma separated tables using PeakScanner v1.0 (Applied Biosystems) and scored automatically using optiFLP v1.54 (ARTHOFER et al. 2013; tab. 1). The quality of individual AFLP profiles was assessed in tinyFLP v1.40 (ARTHOFER 2010). Profiles falling into the 10th percentile of peak count in more than one primer set were considered of low quality and excluded from further analysis. For each primer set, a Neighbor Joining (NJ) tree was constructed with MEGA6. Plate position of samples was chosen randomly. As quality control, two kinds of replicates per plate were replicated on another position of the same plate already in the digestion-ligation-step ("pairwise replicates"). Capillary electrophoresis was performed by a commercial sequencing facility (Comprehensive Cancer Center DNA Sequencing & Genotyping Facility, University of Chicago, USA) on an ABI 3730 sequencer (Applied Biosystems). Trace files were converted to comma separated tables using PeakScanner v1.0 (Applied Biosystems) and scored automatically using optiFLP v1.54 (ARTHOFER et al. 2011) with the same parameter space as in ARTHOFER et al. (2013: tab. 1). The quality of individual AFLP profiles was assessed in tinyFLP v1.40 (ARTHOFER 2010). Profiles falling into the 10th percentile of peak count in more than one primer set were considered of low quality and excluded from further analysis. For each primer set, a Neighbor Joining (NJ) tree was constructed with optiFLP, and tree topologies were compared as done by DEJACO et al. (2016); samples grouping into more than three NJ clades were excluded.

Bayesian clustering was performed using BAPS v5.3 (CORANDER et al. 2008). First, the "clustering of individuals" option was executed with K = 1; 30 and all other parameters in default. The results were pipelined into the clustering-based admixture analysis using minimum population size = 3, 500 iterations, 50 reference individuals, and 50 iterations for reference individuals.

**Male genital morphology:** We qualitatively investigated male genital morphology of 96 males (Tab. S1). Mounted genitalia were used for z-stack imaging with a Z6 APO macroscope (Leica, Wetzlar, Germany) providing a magnification of 72 x, a Leica DFC 420 camera, and Leica Application Suite v3.6. Final images were composed with Helicon Focus v5.1 (Helicon Soft Ltd., Charkow, Ukraine). Representative images were used to draw anatomical figures (Fig. S1, as digital supplementary material to this article, at the journal's web pages). Terminology of the considered structure, the parameters, follows COLLINGWOOD (1979). Interspecific differences of male genital morphology allowed a qualitative assessment in most cases.

**Traditional morphometrics (TM) of workers:** Dissected gasters of workers were used for DNA extraction; the degastered bodies were mounted for morphometric analyses. Measurements were made using a Leica M165 C high-performance stereomicroscope with magnifications of 120 - 360 x. Workers were positioned on a pin-holding stage permitting spatial adjustment in all directions. Measurements always referred to cuticular surface and not pustulence surface. A cross-scaled ocular micrometer with 120 graduation marks ranging over 52% of the visual field was used. Its measuring line was continuously kept in vertical position to avoid parallax error (SEIFERT 2002). A Schott KL 1500 LCD cold-light source equipped with two flexible light ducts combined with a Leica coaxial polarized-light illuminator was used.

Morphometric data of 968 workers from 468 nests were collected (on average, 2.1 workers per nest). For 459 and 237 of these individuals also CO1 and AFLP data, respectively, were available (min. one worker per nest). We defined 33 characters (Tab. 1; Figs. 1 - 6); 26 of them followed STEINER & al. (2006), SEIFERT (2007), and CSÓSZ & al. (2014b), and seven (dAN, HFL, MCT1G, MtpW, PPL, Pps) were new. Twenty-nine characters were collected morphometrically, MCT1G and POTCos meristically; CS and EYE were arithmetic means of other characters.

Nest-Centroid clustering (SEIFERT et al. 2014b) was used as unsupervised approach to establish morphological species hypotheses independent from genetic data using R v3.0.1 and the packages MASS, ecodist, cluster, plyr, stringr, and scatterplot3d (R DEVELOPMENT CORE TEAM 2012). The hierarchical Nest-Centroid-Ward clustering was run first to build a species hypothesis. Afterwards, non-hierarchical Nest-Centroid-K-means clustering was performed with the number of classes suggested by Nest-Centroid-Ward. For a final evaluation, to minimize the number of mismatches, only pairwise species comparisons were used (Fig. 7). To assign samples to species pairs, the DNA-based species hypotheses were followed, that is in most cases, the AFLP results. Since AFLP data of ten small CO1 clades containing one or two HTs were missing, we usually assigned them to neighboring clades if no conflict with other disciplines was obvious. In doing so, we aimed to avoid oversplitting. In CO1 clade 1 (= Tetramorium brevicapsus, see Results and discussion) only, the clade itself represented the DNA-based species hypotheses due to obvious morphologic differences of neighboring clades. Nests concordantly classified by Nest-Centroid-Ward and Nest-Centroid-K-means were fixed as either hypothesis "1" or "2", while discordantly classified nests were used as wild cards ("0"). The species hypotheses formed by this procedure were used in confirmatory linear discriminant analyses (LDA) on the level of workers using the method "stepwise selection" in selecting characters, performed with the software package SPSS Statistics v21 (IBM, USA) as follows: In a first step, following SEIFERT & al. (2014b), consistently classified nests and wild cards of Nest-Centroid-Ward and Nest-Centroid-K-means with P > 0.66 belonging to either hypothesis "1" or "2" were fixed as new calibration set, while all cases with P < 0.66 were set as wild cards. In a second LDA, cases with P > 0.58 were hypothesis-fixed, in a third LDA also cases > 0.5, so that finally no unassigned case remained. Then, species-pair-wise discordance rates between the Nest-Centroid-clustering-based hypotheses and the DNA-based species hypotheses were calculated.
ages of head in frontal view (Fig. 8), mesosoma in dorsal view (Fig. 9), and mesosoma in lateral view (Fig. 10). Pinned dried specimens were put in identical positions using a goniometer. Approximately 15 - 20 images were taken in different focal planes (distance 10 - 20 µm) with a Leica DFC420 camera attached to a Leica Z6 APO macroscope. Images were stacked using the software Helicon Focus v5.1. In frontal view of the head, the focus was on the frontal ridge of the antennal fossa. Then the head was tilted until the posterior margin was maximum focused (at ergotubus magnification of 2.0). Lateral orientation was achieved by adjusting the frontal ridge of the eyes in one focal plane (at ergotubus magnification of 3.6; Fig. 8). Mesosoma was adjusted in dorsal view with two anterior and two posterior reference points in focal plane (i.e., at same horizontal level). The anterior reference points were the bases of setae on the frontolateral corners of pronotum. The posterior reference was the horizontal portion of the upper margin of propodeal lobes just before they ascend to subspinal excavation (rough adjustment at ergotubus magnification of 2.0, fine adjustment at ergotubus magnification of 3.6) (Fig. 9). Mesosoma was adjusted in lateral view with the tips of the propodeal spines exactly super-imposed (Fig. 10).

Shape variation of the forewings was analyzed in 148 gynes (Fig. 11). To allow analyses of directional and fluctuating asymmetry, both forewings were detached from the specimen and placed between slides. One of the wings (when available, the right one) was photographed from the dorsal and ventral side, the other only from the dorsal side. To reduce measurement error, Procrustes coordinates across replicates were averaged. Otherwise, the technical procedure and equipment were the same as for workers.

We used tpsDig2 v2.22 (ROHLF 2015) to digitize landmarks: 10 landmarks in head frontal (Fig. 8), 13 in mesosoma dorsal (Fig. 9), 9 in mesosoma lateral (Fig. 10), and 12 in gynae wings (Fig. 11). The nomenclature of veins follows PERFILIEVA (2015). If not indicated otherwise, Procrustes superimposition and all subsequent analyses were performed with MorphoJ v1.06d (KLINGENBERG 2011). Head frontal and mesosoma dorsal were symmetric structures; corresponding landmarks were set at both sides of the symmetry axis and analyzed with the methods of object symmetry (KLINGENBERG & al. 2002). Only the symmetric component of variation was used in the downstream analyses.

For error assessment of the worker dataset, we took two images of mesosoma lateral per specimen in a sample...
of 32 workers (16 from each of two putative species, *Tetramorium alpestre* and *T. immigrans*) and digitized the landmarks twice. Procrustes ANOVA (Klingenberg & al. 2002) was used to quantify the measurement error in relation to biological factors as follows: As the imaging error was 1.54 times greater than the digitizing error, and variation among individuals was 11.37 times greater than imaging error (Tab. S2), measurement error was considered negligible. Similarly, Procrustes ANOVA of the gyne forewing dataset showed that the most subtle biological aspect, that is, fluctuating asymmetry, was > 5 times greater than the error from imaging the wings from dorsal and ventral side (Tab. S3).

The datasets of the workers were significantly affected by allometry. Centroid size accounted for 5.8%, 4.4%, and 3.4% of the shape variation in head frontal, mesosoma lateral and mesosoma dorsal, respectively (multivariate regression of shape on size, all p < 0.001). To correct for allometric effects, regression residuals were used subsequently. Since allometries may differ across species, pooled within-group regression for specific size corrections was used. Allometry was not significant in gyne forewings (1.1% predicted, p = 0.11).

A combination of relative warp analysis and LDA was used (following Bagherian Yazdi & al. 2012) to compare the performance of GM with TM in cryptic species delineation. Relative warps (with no weighting with respect to bending energy) were calculated as principal components of Procrustes coordinates (gyne wings) or regression residuals of Procrustes coordinates (head frontal, mesosoma dorsal, mesosoma lateral). The relative warps of the three datasets of the workers were combined in a single matrix (cf. Bagherian Yazdi & al. 2012). This matrix was the input for unsupervised Nest-Centroid clustering (Seifert & al. 2014), as described for TM. The dataset of the gyne wings was analyzed separately.

Reanalyzed linear discriminant analysis (LDA) of morphometric data: After development of final species hypotheses by the integrative-taxonomy approach, all nests were reanalyzed in a supervised approach using the same data as for Nest-Centroid clustering of worker TM, worker GM, and gyne GM. SPSS Statistics v21 was used to perform the LDAs. To avoid overfitting, the number of individuals of each group had to be at least three times larger than the number of characters (Moder & al. 2007 and references therein).

**Thermal niches**: Standard air temperature (TAS) in °C of sampling sites two meters above ground were used as a rough approximation of ecological niche (Steiner & al. 2010, Seifert & al. 2014a). Following Seifert & Pannier (2007), TAS was calculated as mean air temperature from 1 May to 31 August of the nearest three meteorological stations of the years 1961 to 1990 provided by Klimaabteilung der Zentralanstalt für Meteorologie und Geodynamik (1996). Values were corrected for an altitudinal temperature decrease of 0.661 °C per 100 m: TAS = 0.694 * LAT + 0.078 * LON - 0.00661 * ALT + 52.20, where LAT = latitude, LON = longitude, and ALT = altitude. TAS was not used in an unsupervised approach for species delimitation but to explore ecological differences in reanalyses. TAS values were tested for species-specific differences using SPSS Statistics v21.

**Type material**: Since type material of the following six taxa could not be excluded from conspecificity with European species of the *Tetramorium caespitum* complex based on qualitative morphological and geographical arguments (details in Taxonomy), it was investigated morphometrically: *T. caespitum* var. *immigrans* Santschl. 1927; *T. semilaeve* var. *kutteri* Santschl. 1927; *T. staerckei* Kratochvil. 1944; *T. caespitum* var. *fusciclavum* Consani & Zangheri 1952; *T. gonioniommae* Poldi, 1979; *Pe- lagium* Mel. 1995. After species delimitation, worker types belonging to the *T. caespitum* complex were set as wild cards in an LDA including all morphometric data of the complex.

**Results and discussion**

**Cytochrome C oxidase subunit I (CO1) gene**: Sequences of 1257 nests yielded complete data, that is, 1113 bp. Furthermore, sequences of 134 nests contained missing data but allowed assignment to CO1 clades. All 189 singletons HTs were confirmed by sequencing an independent PCR reaction. Our four-step NUMT check led to the interpretation that three of 386 HTs, that is, HT36, HT330, and HT388, were NUMTs. In detail, (I) reviewing electropherograms, we found distinct double peaks in three cases: Firstly, in HT36, belonging to CO1 clade D _ w and already published by Schlick-Steiner & al. (2006). In this study, HT36 contained overlaid peaks with HTs of CO1 clade *impurum* _ w _ six times (for species affiliation of CO1 clades, see Figs. 12 - 14). Secondly, HT330 contained overlaid peaks identical with HT52 of clade B sensu Schlick-Steiner & al. (2006). Thirdly, HT388 contained overlaid peaks of *impurum* _ e (Tab. S1). (II) After mitochondrial-DNA enrichment, electropherograms showed a relative decrease of peaks belonging to HT36, HT330, and HT388 as well as a relative prominence of those belonging to *impurum* _ w, B, and *impurum* _ e sequences. In contrast, there was no change in electropherograms of CO1 clades *alpestre*, *caespitum*, *indocile*, B, D _ e, E, H, I, J, U5, and two remaining nests of D _ w. (III) The complementary-DNA PCR of workers from nests 18535 and 18538 (Tab. S1), belonging to CO1 clade U2 (= *T. caespitum* in final species hypotheses), showed identical HTs as the standard PCR, that is, HT439 and HT225, respectively. (IV) The use of U2 and *impurum*_ w specific primers on all extracts of D _ w samples yielded neither U2 nor *impurum*_ w sequences. Summarizing these results, we found evidence in the first and second step of our assessment that HT36 (D _ w), HT330, and HT388 are NUMTs, and no indication for further NUMTs in the other steps. Hence, the alignment comprised 383 HTs. While two NUMTs represent only HTs of their clades, HT36 is a NUMT clustering basal in the CO1 clade D _ w. Sequences retrieved from the same nests resembled HT36 when whole DNA was extracted but five other HTs when extracts enriched for mitochondrial DNA were used. This finding is in line with the higher mutation rate of mitochondrial DNA compared with NUMTs, and HT36 can be seen as an ancestral state from which the current diversity of mitochondrial DNA in D _ w evolved (Lopez & al. 1997, Haag-Liautard & al. 2008, HAZKANI-Covo & al. 2010).

Multi-rate Poisson Tree Processes yielded 30 CO1 clades (Figs. 12, 14; for details, see Tabs. S1, S4); compared with other established tree-based delimitation methods, multi-rate Poisson Tree Processes seems to be less

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Fig. 12: Cytochrome C oxidase subunit I gene (CO1) phylogeny and species estimation using multi-rate Poisson Tree Processes (30 white and grey bars), amplified fragment-length polymorphism BAPS clusters, and male genital morphology of species. Labels refer to former entity names (SCHLICK-STEINER & al. 2006, STEINER & al. 2010, CSÓSZ & al. 2014b) and entities first delimited here (I, J, H, impurum_e, impurum_w) as well as final species hypotheses newly established here following equal signs. The final species hypotheses drawn here match in color those of Figures 7, 13, and 14. AFLP data for I = breviscapus sp.n. as well as male genital data for I = T. breviscapus sp.n. and J = T. fusciclava stat.n. are not available.

prone to oversplitting (also in the present case; data not shown) but, in such cases of clades consisting of very few HTs, still seems to tend towards it. Most of these clades were already recovered by SCHLICK-STEINER & al. (2006). However, four CO1 clades are new (H, I, J, and impurum_w), and twelve small clades consisting of one or two HTs (caespitum2, B2, D_w1, D_w2, indocile2, hungaricum2, impurum_e2 - e7) were split off other clades. Since the latter represent no taxonomic units based on the integrative taxonomic approach (see Integrative-taxonomy approach), we mostly treat these twelve clades under their earlier, more inclusive clade names.
Fig. 13: Geographic distribution of *Tetramorium alpestre*, *T. caespitum*, *T. hungaricum*, *T. breviscapus* sp.n., *T. indocile*, *T. caucasicum* sp.n., *T. fusciclava* stat.n., *T. staerckei* sp.rev., *T. impurum*, and *T. immigrans* stat.n.
Amplified fragment-length polymorphism (AFLP): After quality checks, 269 workers profiles remained. These belonged to 20 of the 30 CO1 clades; for ten clades, each consisting of one or two HTs (Tab. S4), no AFLP data were available. After concatenation of the five primer sets, the final binary matrix contained 890 loci. BAPS identified ten well-separated AFLP clusters (Fig. 12; Tab. S5). Several instances of mitochondrial-nuclear discordance were found, which are discussed under Integrative-taxonomy approach.

Male genital morphology: We found two different basic forms of paramere structure (for specific details of male genital morphology, see Taxonomy, Treatment of species and Key to males of the Tetramorium caespitum complex), the impurum-like form (incl. AFLP clusters alpestre, U5, D_e, impurum_e, and impurum_w; for species affiliation of CO1 clades, see Figs. 12 - 14) and the caespitum-like form (incl. AFLP clusters caespitum (incl. U1, U2, B, and D_w), hungaricum, indocile, and E). Within the impurum-like form, AFLP clusters U5 (n = 2 nests), alpestre (n = 18), D_e (n = 3), and impurum_w / impurum_e (n = 20) exhibited distinct differences. However, AFLP clusters impurum_w and impurum_e differed in only 83% of males (n = 18): Visible in lateral view, ventral paramere lobe in impurum_w was typically more rounded, while impurum_e had a slightly pronounced corner on dorsal end of ventral paramere lobe (Fig. S1). In the caespitum-like form, AFLP clusters caespitum / hungaricum (n = 20), indocile (n = 4), and E (n = 8) exhibited distinct differences. AFLP cluster hungaricum typically had a truncated end of ventral lobe in ventral view (n = 3); because the latter morphology was also found in 11% of caespitum (n = 17), we were not able to delimit these two based on male genital morphology.

Traditional and geometric morphometrics (TM, GM): Nest-Centroid clustering had discordance rates < 5% in 78%, 71%, and 60% of hypothesized pairwise species comparisons of worker TM (n = 55, mean discordance rate 2.7%), worker GM (n = 28, mean discordance rate 4.7%), and gyne GM (n = 10, mean discordance rate 7.7%; Tab. 2; raw data in Tabs. S6 - 8), respectively. The worker TM data yielded the strongest support of the DNA-based species hypotheses. The discordance rates of worker GM data were mostly equal to or higher than in TM (Tab. 2). Compared with worker TM and GM, gyne GM data yielded higher discordance rates; however, delimitation of alpestre / caespitum, alpestre / impurum_e, and alpestre / impurum_w was morphometrically supported by gyne GM only (Tab. 2; for species affiliation of CO1 clades, see Figs. 12, 14). Discordance rates varied across hypothesized species: While data of the morphologically hypothesized species hungaricum, I, J, D_e, and E conformed largely with DNA-based species hypotheses, alpestre, caespitum, indocile, U5, impurum_w, and impurum_e provided several times discordance rates > 5% (Tab. 2). Our discordance rates were distinctly higher than TM error rates of other studies on myrmicine ants (CsÖSZ & al. 2014a, 2015, SEIFERT & al. 2014a, SEIFERT & CSÖSZ 2015, CSÖSZ & FISHER 2016). High level of crypsis, that is, interspecific similarity, and intraspecific variability, might cause high discordance rates. However, additionally to morphometric data, here we have a DNA-based background
to justify species delimitations (see Integrative-taxonomy approach). The species of the *Tetramorium caespitum* complex could represent more pronounced morphological crypsis than most other ants analyzed.

**Integrative-taxonomy approach:** Based on the integrative-taxonomy approach combining CO1, AFLP, male genital morphology, and Nest-Centroid-clustering data (Figs. 12 - 14), we present arguments for delimiting ten species, that is, *Tetramorium alpestre*, *T. caespitum*, *T. hungaricum*, *T. breviscapus* (= I), *T. indocile*, *T. caucasicum* (= U5), *T. fusciclava* (= D_e) *T. staerckei* (= D_e), *T. impurum* (= J), *T. impurum* (= E), *T. impurum* (= E), and *T. impurum* (= E), respectively. Missing data are indicated by “-”. Values < 5% in bold.

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Tab. 2: Discordance rates between Nest-centroid clustering and DNA-based species hypotheses for pairwise comparisons [%]. n = number of nests, f = number of individuals. Values in the first row of each species show results of worker traditional morphometric data, in the second row of worker geometric morphometric (GM) data, in the third row of gyne GM data. Missing data are indicated by “-”. Values < 5% in bold.
and T. sp. U5 in all applied morphometric methods; this weakness does not challenge species status and we interpret it as extreme morphological crypsis. *Tetramorium caespitum* is polyphyletic in CO1 (Fig. 12): CO1 clades *caespitum*1, *caespitum*2, and U1 were closer related to *alpestr* than to U2 and B. CO1 clades D_w1 and D_w2 were not close to all other CO1 clades of *T. caespitum*, but to those of T. sp. J and T. sp. D_e. We identified evolutionary explanations for this CO1 polyphyly (see Reasons for mitochondrial-nuclear discordances).

(3) *Tetramorium hungaricum*: AFLP clusters and discordance rates between Nest-Centroid clustering and DNA-based species hypotheses suggested conspecificity of CO1 clades *hungaricum*1 and U4 (Fig. 12, Tab. 2, Tab. S5). CO1 clade *hungaricum*2 consisting of only one HT yielded no AFLP and male genital results; however, based on Nest-Centroid clustering, it belongs to *T. hungaricum*. Distinct male genital morphology differences from *T. caespitum* were not found (Fig. S1: 9 - 12).

(4) *Tetramorium* sp. I: The CO1 clade was a supported monophony (Fig. 12). AFLP and male genital data were lacking. Nest-Centroid clustering allowed a safe delimitation from all other taxa (Tab. 2).

(5) *Tetramorium indocile*: All workers of CO1 clade *indocile*1 coincided in one AFLP cluster (Fig. 12); male genital morphology showed the same pattern (Fig. 12, Fig. S1: 13 - 16). CO1 clade *indocile*2 consisting of only two HTs (Tab. S1) yielded no AFLP and male genital results; Nest-Centroid clustering results are doubtful and we tentatively consider it as isolated population of *T. indocile*. Nest-Centroid clustering resulted in discordance rates with DNA-based species hypotheses > 5% with *T. alpestr*, *T. caespitum*, and T. sp. U5 (Tab. 2), based on high crypsis and geographic variability. *Tetramorium indocile* is a representative example of a cryptic species showing congruent results in CO1, AFLP, and male genital morphology through its large distribution area from Iberia to Central Asia, despite sympatric occurrence with nearly all species of the complex.

(6) *Tetramorium* sp. U5: We found complete mitochondrial-nuclear concordance (Fig. 12). Additionally, male genital morphology allowed distinguishing this from all other species of the complex (Fig. 12, Fig. S1: 17 - 20). Based on high morphological crypsis and low number of samples, Nest-Centroid clustering led to discordance rates > 5% with DNA-based species hypotheses with *T. alpestr*, *T. caespitum*, *T. indocile*, *T. impurum*, and T. sp. E (Tab. 2). However, based on CO1, AFLP, and male genital morphology results, morphological crypsis of workers does not challenge species status.

(7) *Tetramorium* sp. J: All workers of CO1 clade J grouped in one AFLP cluster (Fig. 12). Male genital morphology data are missing, but Nest-Centroid clustering results always matched with DNA-based species hypothesis (Tab. 2).

(8) *Tetramorium* sp. D_e: CO1 clade and AFLP cluster coincided perfectly (Fig. 12). Differentiation from all other species based on male genital morphology was possible (Fig. 12, Fig. S1: 21 - 24); discordance rates between Nest-Centroid clustering and DNA-based species hypotheses supported delimitation from all other species (Tab. 2).

(9) *Tetramorium impurum*: AFLP clusters suggested conspecificity of CO1 clades *impurum*_w and H as well as *impurum*_el - e4, respectively (Fig. 12, Tabs. S4, S5); also Nest-Centroid clustering supported affiliation of these CO1 clades to *T. impurum*. Four CO1 clades consisting of only one or two HTs (*impurum*_e5 - 7, U6) yielded no AFLP and male genital results; based on Nest-Centroid clustering, they belong most likely to *T. impurum*. However, the affiliation of some Greek and Anatolian nests is difficult. Here, we consider them as southern relict populations of *T. impurum*. Male genital morphology of *T. impurum* was different from all other species of the complex (Fig. 12, Fig. S1: 25 - 31), discordance rates between Nest-Centroid clustering and DNA-based species hypotheses separated *T. impurum* from all species except T. sp. U5. The two main CO1 clades of *T. impurum*, that is, *impurum*_w (incl. H) and *impurum*_el - 4, had separate AFLP clusters (Fig. 12, Tab. S5). However, no distinct difference in male genital morphology (error rate 17%) and high discordance rates between DNA-based and Nest-Centroid clustering-based species-hypotheses were found (Tab. 2). To avoid oversplitting (CARTENS et al. 2013), we set aside describing *impurum*_w as new species. Henceforth, we term intraspecific units of *T. impurum* eastern and western clade.

(10) *Tetramorium* sp. E: All nests except one (i246) of CO1 clade E grouped in a single AFLP cluster (Fig. 12, Tab. S5). Male genital morphology was different from all other species of the complex (Fig. 12, Fig. S1: 32 - 35). Nest-Centroid clustering separated species E well from all other taxa except T. sp. U5 (Tab. 2). One nest (18375) with a lack of AFLP data mismatched as *T. caespitum* in Nest-Centroid clustering. The outliers, i246 and 18375, showed mitochondrial-nuclear discordance that we explained biologically (see Reasons for mitochondrial-nuclear discordances).

Reasons for mitochondrial-nuclear discordances: In five of ten species, that is, *Tetramorium alpestr*, *T. caespitum*, *T. hungaricum*, *T. impurum*, and *T. sp. E (= T. immigrans* according to our final species hypotheses), at least one nest showed mitochondrial-nuclear discordance. In identifying reasons for the discordances, the geographic distribution of clades is relevant. Thus, in *T. caespitum*, the five CO1 clades constituted distinct geographic patterns (Fig. S2). Similarly, in *T. alpestr*, *T. hungaricum*, and *T. impurum*, we found rare CO1 clades only close to distribution edges (Tab. S1). Following the argumentation of TOEWS & BRELSFORD (2012), distinct geographic patterns of CO1 clades exclude incomplete lineage sorting as explanation. We hypothesize (I) peripatric speciation or (II) ancient hybridization with subsequent backcrossing of hybrids into parental populations, that is, introgression, as sources of most cases of mitochondrial-nuclear discordance (cf. FUNK & OMLAND 2003, cf. SLOAN & al. 2017). In the latter, introgression might be followed by divergence of mitochondrial DNA from that of the maternal species. As we outline in the following, distinguishing between these explanations is difficult, but all of the possible explanations result in the need to prioritize the nuclear over the mitochondrial DNA results. In more detail: (I) *T. alpestr* could have speciated in peripatry, that is, as a smaller and local population in spatial isolation and under different ecological conditions along the periphery of the
Tab. 3: Error rates of linear discriminant analyses (LDA) / cross-validation LDA results for pairwise species comparisons [%]. \( n \) = number of nests, \( i \) = number of individuals. Values in the first row of each species are results of worker traditional morphometric data, in the second row of worker geometric morphometric (GM) data, in the third row of gyne GM data. Missing data indicated by ".". Values < 5% in bold.

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<th>breviscapus (= I)</th>
<th>indoeile</th>
<th>caucasicum (= U)</th>
<th>fusciclava (= J)</th>
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larger range of the parental species. Under such conditions, the budding population would lose HTs by drift faster than the parental species. As a result, the monophyletic T. alpestre (excl. CO1 clade U3) would be embedded in the more widely distributed paraphyletic T. caespitum. (II) If U2 and B were the ancient CO1 clades of T. caespitum (Fig. 12), the CO1 clade caespitum (incl. U1) could have descended from T. alpestre. Here, a single introgression event suffices to explain the paraphyly between T. caespitum. Especially the CO1 polyphyly of T. caespitum, combined with a distinct geographic pattern of CO1-clade distributions (Fig. S2), but no geographic difference in AFLP data, could be interpreted as resulting from male-biased dispersal and female philopatry (cf. RUPPELL & al. 2003).

To a lesser extent, recent hybridization is presumably the source for mitochondrial-nuclear discordance: Two nests of CO1 clade E represented mitochondrial-nuclear discordance: Nest i246 belonged to clade E (HT79), and AFLP cluster as well as Nest-Centroid cluster of Tetramorium caespitum (Tab. S1). Similarly, nest 18375 (HT70) Nest-Centroid clustered with T. caespitum, and its ecology (TAS = 15.8 °C) differed from that of T. sp. E (Tabs. 4, 5). AFLP data are missing here, but as phenotypes are mainly determined by nuclear genes (cf. SMITH 1992), we assume mitochondrial-nuclear discordance. Hybrids of these two species were also found based on microsatellite data (B. Kaufmann & J. Gippet, pers. comm. 2015). Hybridization of these two species might be facilitated by similar male genital morphology (see Taxonomy, Redescriptions of species), and frequent syntopic occurrence (Tab. S1), especially in anthropogenically influenced habitats (cf. SEIFERT 1999).

Across all species, our data suggest that hybridization on the individual level is rare (cf. SEIFERT 1999). However, on evolutionary time scales, it may have played a central role in forming these Tetramorium species’ genomes (cf. ABBOTT & al. 2013).

Reanalyzed linear discriminant analysis (LDA) of morphometric data: The LDA had error rates < 5% in 98%, 71%, and 70% of pairwise species comparisons of worker TM (n = 45, mean error 0.9%), worker GM (n = 21, mean error 3.3%), and gyne GM (n = 10, mean error
Tab. 4: Standard air temperature (TAS) comparison as an overview of ecological niches. Given are arithmetic means of localities ± standard deviation [lower extreme, upper extreme]; n = number of localities, TAS in °C.

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<td>16.1 ± 2.0 [7.9, 21.1]</td>
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<td>20.6 ± 2.7 [16.2, 26.2]</td>
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<tr>
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<td>22.1 ± 1.4 [20.6, 23.2]</td>
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<td>indicule</td>
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<td>15.6 ± 3.2 [11.5, 25.4]</td>
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<tr>
<td>causicism (= US)</td>
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<td>13.5 ± 2.8 [10.2, 18.2]</td>
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<td>fusclava (= I)</td>
<td>13</td>
<td>21.3 ± 1.6 [16.1, 21.8]</td>
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<td>staercke (= D_e)</td>
<td>79</td>
<td>18.1 ± 3.1 [11.0, 26.4]</td>
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<td>impurum</td>
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<tr>
<td>immigrans (= E)</td>
<td>201</td>
<td>19.9 ± 2.5 [13.0, 26.7]</td>
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</table>

3.7%; Tab. 3; raw data in Tabs. S6 - 8). We got LDA error rates < 5% at least in one morphometric method in all cases except _Tetramorium alpestre_ / US. Due to the small sample size in the smallest class, with only 32 workers in _T. causicism_, an LDA reduced to 10 characters had to be performed (MODER & al. 2007).

**Thermal niches:** Species-specific ecological differences were significant in 34 of 45 pairwise species comparisons (76%) (Tabs. 4 - 5). _Tetramorium alpestre_ had by far the lowest TAS values, followed by the four moderately thermophilous species _T. sp. U5_ (for final species names, see Figs. 12 - 14), _T. impurum_, _T. indicule_, and _T. caespitum_. Five species were distinctly thermophilous: _T. sp. D_e_, _T. sp. E_, _T. hungaricum_, _T. sp. I_, and _T. sp. I_.

**Type material assignment:** Type material belonging to the _Tetramorium caespitum_ complex was assigned to species based on qualitative morphology, morphometrics, thermal niche, and biogeography (for details, see Taxonomy, Treatment of species): _T. semilaeve_ var. _kutteri_ and _T. staercke_ var. _gregori_ are synonyms of _T. indicule_ and _T. impurum_, respectively. Further, types of _T. staercke_ belong to _T. sp. D_e_, those of _T. caesiptum_ var. _fusciclava_ to _T. sp. J_, and those of _T. caesiptum_ var. _immigrans_ to _T. sp. E_; we redescribe these three species (see Taxonomy, Treatment of species; Figs. 17 - 19). Since no type material proved to be conspecific with _Tetramorium_ sp. I and _T. sp. U5_, we newly describe these species as _T. breviscapus_ sp.n. and _T. causicism_ sp.n., respectively (see Taxonomy, Treatment of species; Figs. 15, 16).

**Were all data types used necessary for the final species delimitation?** We applied six methods using mostly the same ant material (in sexuals, material from the same nests): mitochondrial DNA (CO1 gene), nuclear DNA (AFLP), male genital morphology, traditional worker morphometrics, geometric worker morphometrics, and geometric gyne wing morphometrics. Obviously, (ant) biologists will not perform such comprehensive analyses on all taxonomic problems. Choosing an efficient but still reliable array of methods for future studies will depend on the particular taxonomic problem. In many cases of ant taxonomy, morphometric analysis alone suffices (see SEIFERT 2003, SEIFERT & al. 2014a, b, SEIFERT & CSOSZ 2015). However, single methods can lead to simplified assumptions (e.g., CARSTENS & al. 2013, CLOSE & al. 2016, SANTOS & al. 2016). Thus, to solve highly intricate problems, we strongly recommend the use of integrative taxonomy combining molecular studies with morphology (see also PUBLANDRE & al. 2012). The use of three disciplines seems worthwhile since hereby the error rate should fall below the level of 5% (SCHLICK-STEINER & al. 2010).

In doing so, mitochondrial DNA data are helpful to get a first impression of diversity and to select material for further analyses. Furthermore, when combined with nuclear DNA, mitochondrial DNA allows the insight into evolutionary processes such as introgression and thus interspecific gene flow. However, even well-separated mitochondrial DNA clades must not automatically be treated as species. In contrast, nuclear DNA data repeatedly proved reliable in generating species-delimitation hypotheses (recent ant examples: WARD 2011, WARD & SUMNICH 2011). In the case of the _Tetramorium caesiptum_ complex, AFLP results appear authoritative and frequently concur with morphological data and the final species hypotheses. The disadvantage of AFLP is that all samples have to be processed simultaneously due to poor reproducibility; hence, technical and human resources limit the sample size. Next-Generation-Sequencing-based approaches will likely become important in taxonomy, such as restriction site-associated DNA sequencing (animal example: BERNARDI & al. 2017). De novo whole-genome sequencing, as it is becoming more and more affordable (NYGAARD & WURM 2015), might at some point in the future even replace CO1 sequencing and AFLP in taxonomy.

Among the morphological approaches chosen here, qualitative male genital investigations were very successful and relevant. However, in other ant genera, this approach may be less successful either due to a lack of sampled males or of species-specific differences. Carefully collected morphometric data are precious because of the possibilities of multivariate statistics. Traditional morphometrics is time- but not money-intensive if a microscope is available; once data have been published, they can also be taken for future studies of taxonomic or evolutionary research. In the study by BAGHERIAN YAZDI & al. (2012), GM data performed better than TM data in discriminant analyses of cryptic species, but the opposite was true in our study (Tab. 2). Especially in gyne GM, we explain the lower success by the smaller sample size. GM data are useful for species delimitation but have the disadvantage to be available only as principal components (Tabs. S7, S8) and thus are not usable for all kinds of interest (e.g., discriminant functions for keys, individual integration of characters with data from other studies). Nonetheless, distance matrices derived from GM analyses can easily be compared with genetic distances, and subtle shape variation among species can be made visible using GM tools. Anyway, we recommend at least one large-scale morphometric discipline for future taxonomic studies. Morphometric analyses usually are cheaper and easier than molecular-genetic ones, and they were found to have lower failure rates in a literature analysis (SCHLICK-STEINER & al. 2010). Moreover, the linkage between type material or other historical material of interest and operational taxonomic units frequently can only be made with morphometric

Conclusion and outlook

Using integrative taxonomy, we solved a major problem in ant taxonomy and (re)described ten cryptic species of the Tetramorium caespitum complex. Data of two molecular and four morphological data types were analyzed in an unsupervised fashion to build species hypotheses independently. The results revealed a surprisingly high number of large-scale discordances, especially between mitochondrial and nuclear DNA. Whether such pattern is an exception, will crystallize when more in-depth studies of cryptic species have become available. Mitochondrial and nuclear discordances allowed insights into evolutionary processes of species. We interpreted them mostly as due to either peripatric speciation or ancient interspecific hybridization but to a lesser extent also as due to recent hybridization. Additionally, based on the investigation of type material, we linked the operational taxonomic units with their valid scientific names. Since only this step enables the stable use of correct species names, we encourage other biologists to publish nomenclatural consequences of species delimitations whenever feasible. Our findings constitute the basis of future research on the evolution of cryptis itself, for example into the role of stasis and / or convergence. However, we cannot exclude the presence of further, rare cryptic species in southernmost Europe and expect further species outside Europe, for example, in Anatolia. We expect that the increasing trend to discover cryptic species (BICKFORD & al. 2007) will continue. Biologists will have to get increasingly used to them and to handle them in their daily research routine. We hope that integrative taxonomy will disentangle further intricate species complexes to bring us closer to understanding the global species richness and the evolution of species.

Taxonomy

Diagnosis of the Tetramorium caespitum complex

BOROWIEC (2014) listed 28 species of the genus Tetramorium MAYR, 1855 as native to Europe (Canary Islands and Cyprus excluded), all belonging to the T. caespitum group sensu BOLTON (1979). Four species complexes of this group have been outlined so far: The T. semilaeve ANDRÉ, 1883 complex (CSÓSZ & SCHULZ 2010), the T. ferox RÜSZKY, 1903 complex (CSÓSZ & SCHULZ 2010; 5 taxa), the T. chefketi FOREL, 111 complex (GUSTEN & al. 2006, CSÓSZ & al. 2007; 11 taxa), and the T. caespitum complex (SCHLICK-STEINER & al. 2006). Additionally, there are further species not allocated to any of these complexes, for example, T. meridionale EMERY, 1870, T. brevicorne BONDROIT, 1918, T. hippocratis AGOSTI & COLLINGWOOD, 1987, and T. pelagium.

Characters of species of the Tetramorium caespitum complex are as follows:

(1) At least some workers of a nest with c-shaped, crinkly, or sinuous hairs arising just behind buccal cavity (Fig. 2, arrow). Most typical character for Tetramorium caespitum complex; absent from T. semilaeve complex, T. ferox complex, T. chefketi complex, T. meridionale, T. brevicorne, T. hippocratis, and T. lucidulum MENÖSSL 1933, but also present in T. pelagium and T. goniommoide POLDL 1979.

(2) Workers with microsculpture on basal part of 1° gastric tergite varying from few, scattered stickman-like to complex reticulate structures (Fig. 4), MC1TG < 30 (error 0.0% in 993 workers). Very complex polygonal structure in Tetramorium chefketi complex, MC1TG > 40 (error 0.0% for 34 workers).

(3) Propodeal spines small to medium, PEW / SPST < 2.055 (error 0.0% for 471 nest means), 33.959 * POTCos - 8.569 * PPH + 7.487 * SPST + 649 < 0 (error 0.4% for 471 nest means). In European species of Tetramorium ferox complex and T. interme MAYR, 1877, propodeal spines reduced to slightly developed corners, PEW / SPST > 2.055 (> 2.08 in 11 workers). In T. brevicorne, propodeal spines rather long and number of postoculo-temporal costae and costulae high in relation to postpetiole height: 33.959 * POTCos - 8.569 * PPH + 7.487 * SPST + 649 > 0 (error 0.0% for 9 workers).

(4) Worker head, mesosoma, petiole, and postpetiole surface partly smooth (as in Tetramorium hungaricum) to coarsely sculptured (as in T. staerckei), but not largely

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</tbody>
</table>
| immigrans| 0.000*    | 0.000*          | 0.084          | 0.132   | 0.000*          | 0.000*         | 0.010          | 0.000*  | 0.000*        

Tab. 5: Species-specific Standard air temperature. Significances at α = 0.05 Student’s t-test after Bonferroni-Holm-correction are labeled with *.
smooth (as in *T. inerme*) or very coarsely sculptured as in *T. cheffeti* complex and *T. goniommaide*.

(5) Worker head, dorsum, and occiput with longitudinal costae and costulae, but occiput never with transversal costae and costulae as in *Tetramorium meridionale*.

(6) Often dark brown to black. In Benelux, Central Europe, and Balkan mountain areas sometimes light brown (*Tetramorium impurum*); rarely reddish (*T. immigrans*); most species not yellowish (as in *T. diomedea*, *T. lucidulum*, *T. flavidulum* EMERY, 1924) or reddish (as typical in *T. ferox*, *T. punicum* (F. SMITH, 1861)).

(7) Worker eye moderately sized, in nest mean EYE / CS = 0.155 - 0.196 (n = 471), but not > 0.197 as in *Tetramorium pelagium* and *T. biskrense* FOREL, 1904 (n = 8 workers).

(8) Male with ten antennal segments, and not nine as in *Tetramorium pelagium* and *T. biskrense*.

(9) Male paramere length > 843 µm and thus larger than in *Tetramorium semilaeve* complex, *T. brevicorne*, *T. punctatum* SANTSCHI, 1927, and *T. pelagium*.

(10) Large sexuals. Gyne MW > 1198 µm and thus larger than in *Tetramorium semilaeve* complex, *T. brevicorne*, *T. punctatum* SANTSCHI, 1927, and *T. pelagium*.

**Treatment of species**

We evaluated all Palearctic *Tetramorium caespitum* group names listed by BOLTON (2014) concerning their possible affiliation to the *T. caespitum* complex (Tab. S9). Based on information given in the original descriptions and in recent taxonomic revisions (*SANETRA* & al. 1999, CSÓSZ & MARKÓ 2004, GUSTEN & al. 2006, SCHLICK-STEINER & al. 2006, CSÓSZ & al. 2007, CSÓSZ & SCHULZ 2010, CSÓSZ & al. 2014b, STEINER & al. 2010, RADCHENKO & SCUPOLA 2015, BOROWIEC & al. 2016), we excluded taxon names using the following criteria: (I) Unavailable names. (II) Names of material outside the *T. caespitum* complex based on original descriptions because of, alone or in combination, (a) workers with yellowish, brownish-yellowish or reddish color, (b) pronounced reticulate structures or longitudinally striato-punctated 1° gastral tergite, (c) general surface smooth, (d) frontal carinae reaching (almost) until the occiput, (e) transversal carinae on head, (f) or head, petiole, postpetiole, or proportions of eye, mesosoma, petiole, and postpetiole in figures different from the *T. caespitum* complex, (g) too small sexuals, or (h) gynes with a deep median insertion of petiolar node. (III) Names of material belonging to other species complexes based on (a) SANETRA & al. (1999), (b) GUSTEN & al. (2006), (c) CSÓSZ & SCHULZ (2010), (d) CSÓSZ & al. (2007), (e) CSÓSZ & al. (2014b), (f) RADCHENKO & SCUPOLA (2015), (g) and BOROWIEC & al. (2016). (IV) Names of material already linked to the operational taxonomic units of the *T. caespitum* complex (*T. hungaricum*: CSÓSZ & MARKÓ 2004; *T. caespitum* and *T. impurum*; SCHLICK-STEINER & al. 2006; *T. alpestre*; STEINER & al. 2010; *T. indoelici*; CSÓSZ & al. 2014b). (V) Names of material originating from Great Britain or Fennoscandia (where only in *T. caespitum* occurs). (VI) Names of material originating from outside the Palearctic and east of the Johansen line. This line in the Yenisei area at around 85° E represents the most important zoogeographical boundary in the northern Palearctic (JOHANSEN 1955). Since only species with very wide ecological valence cross this zoogeographical boundary (MÜLLER 1974), we did not expect that type material collected east of it was relevant for this study. Especially the two new species we describe, *T. sp. U5* (= *T. caucasicum*) and *T. sp. I* (= *T. brevicapillus*), have restricted distribution areas limited to the Caucasus above 1000 m a.s.l. and to the Western Balkans, respectively. In contrast, *T. sp. E* has been introduced to non-native regions (STEINER & al. 2008), and one could argue its origin might be, for example, east of the Johansen line. However, we found a distinctly higher HT diversity (Tab. S1) in Anatolia and the Caucasus region compared with Europe and North America. High haplotype-diversity in mitochondrial DNA has been frequently used to detect a species’ geographical origin (ant examples include SCHLICK-STEINER & al. 2007b, GOTZER & al. 2015). Following this idea, Anatolia and the Caucasus region are the most likely geographical origin of *T. immigrans*.

After this selection, 16 taxon names remained as possible candidates for valid names of operational taxonomic units: *Tetramorium banyulense* BERNARD, 1983; *T. caespitum* var. *typicum* RUSZYK, 1902; *T. caespitum oxyomma* KARAVAIEV, 1912; *T. caespitum tenuicornis* EMERY, 1925; *T. caespitum* var. *immigrans* SANTSCHI, 1927; *T. semilaeve* var. *kutteri* SANTSCHI, 1927; *T. semilaeve* var. *transbaicalense* RUSZYK, 1936; *T. moravicum* var. *caespito-moravicum* KRATOCHVIL, 1941; *T. staerckeii* KRATOCHVIL, 1944; *T. staerckeii* var. *gregori* KRATOCHVIL, NOVÁK & SNØFLAK, 1944; *T. caespitum* var. *fusciclavum* CONSANI & ZANGHERI, 1952; *T. goniommaide* POLDI, 1979; *T. hippocratis* AGUSTI & COLLINGWOOD, 1987; *T. pelagium* MEI, 1995; *T. persignatum* BOLTON, 1995, and *T. tauerei* BOLTON, 1995. Type material of *T. semilaeve* var. *transbaicalense* is lost (RADCHENKO 1992). We did also not receive type material of *T. caespitum* var. *typicum*, *T. moravicum* var. *caespito-moravicum*, and *T. staerckeii* var. *gregori*, which is not housed in St. Petersburg (Dmitry A. Dubovikoff in litt. 2012), Moscow (Elena Fedoseeева in litt. 2013), or in the private collection of Klára Bezděčková and Pavel Bezděčka (Klára Bezděčková & Pavel Bezděčka in litt. 2013). Probably, type material of *T. caespitum* var. *typicum* was never defined as that author’s intention was not to describe a new taxon but simply the “typical” form of *T. caespitum*. In *T. moravicum* var. *caespito-moravicum*, no type material has been defined (KRATOCHVIL 1941, 1944); because of this and because the description cannot be interpreted, we consider it as nomen dubium. In *T. staerckeii* var. *gregori*, we tried to interpret a possible synonymy based on information of the original description. *Tetramorium persignatum* BOLTON, 1995 is housed in the Menozzi Collection of DISTA of the University of Bologna. Department policy did not allow to loan types (Mario Marini in litt. 2012). However, transmitted images of type workers allowed the exclusion of this species from the *T. caespitum* complex (see below). We also found distinct morphological characters by qualitative analysis to exclude *T. banyulense*, *T. hippocratis*, *T. oxyomma*, *T. caespitum tenuicornis*, and *T. tauerei* from the *T. caespitum* complex. Type material of the six remaining taxa was not excluded from the complex based on qualitative analysis and was investigated in detail:

*Tetramorium caespitum* var. *fusciclavum* [sic!] CONSANI & ZANGHERI, 1952 (2 workers) [Italy]; 2 workers labeled as: “Riccione” [-] SYNTYPY *Tetramorium caes-*
pitum c. var. fusciclava C. Emery, 1925 [-] "var fusciclava Emery" [-] MUSEO GENOVA coll. C. Emery (dono 1925) [-] ANTWENT CASENT 904802.

Tetramorium caespitum var. immigrans SANTSCHI, 1927 (8 workers) [Chile]: 5 workers labeled as: TYPE [-] "Chili Valparaiso, Miss Edwards," [-] "Tetramorium caespitum L. immigrants Sant". SANTSCHI det. 19.26 [-] Samm- lung Dr. F. Santschi Kairouan; [thereof we have chosen the lectotype worker]. 2 workers labeled as: "Chili M. Edwards [sic!]" [-] "Were found in road could not find next any where" [-] Sammlung Dr. F. Santschi Kairouan.

Tetramorium goniommoide POLDI, 1979 (3 workers) [Turkey]: 2 workers on 2 separate pins in each case labeled as: Sarayköy 4.15.X.215m [-] Türkiye 1977 C. Baroni Urbani [-] Collezione Bruno Poldi (Mus. St. Nat. Milano) [-] "T. goniommoide[s] [sic!] synTypus". 1 worker labeled as: Sarayköy 4.15.X.215m [-] Türkiye 1977 C. Baroni Urbani [-] "3" [-] "coTypus". [-] Collezione Bruno Poldi (Mus. St. Nat. Milano).


Tetramorium semilaeve var. kutteri SANTSCHI, 1927 (2 workers) [Switzerland]; 2 workers labeled as: Cytotus [-] "Brig Pfingsten 3. VI 1922" [-] "T. semilaeve v. kuppeti" [-] GBIFCO 00190422.


Since type material of Tetramorium persignatum was not loanable, we investigated images of type workers and excluded this material from our complex by measurements of head and mesosoma (CW / ML = 1.01; in T. caespitum complex CW / ML = 0.85 ± 0.05). Tetramorium goniommoide was described from Anatolia and seems to be mis- sing in Europe. Like the T. caespitum complex, it shows c-shaped, crinkly, or sinuous hairs on the ventral head. However, a strongly developed sculpture, giving the surface a dull impression (like chefket complex; GÜSTEN & al. 2006, CSÖZS & al. 2007), distinguishes T. goniommoide from the species of the T. caespitum complex. Sculpture on lateral side of propodeum builds clear and straight lines. Propodeal spines are shorter than in typical work- ers of the T. caespitum complex. With all measurements in µm, a distinct separation for workers is given by the discriminant D (goni): 2.695 * MW + 17.189 * POTCos + 5.738 * EYE - 7.209 * PPW - 270. Workers of T. caespitum complex have D (goni) < 0 (error 0.0% in 975 workers) and those of T. goniommoide D (goni) > 0 (> 120 in 3 type workers). Tetramorium pelagium, described from the island Linosa, also has c-shaped, crinkly, or sinuous hairs on ventral head. However, its gynes differ by small size and a depressed mesosoma (as in T. semilaeve) clearly from the T. caespitum complex. Additionally, males have only nine and not ten antennal segments. With all measurements in µm, a clear separation for workers is given by the discriminant D (pela): 2.813 * HFL + 16.891 * MCITGT - 17.610 * POTCos - 13.020 * EL + 490. Workers of the T. caespitum complex have D (pela) > 0 (error 0.0% in 975 workers) and those of T. pelagium D (pela) < 0 (< -60 in 6 type workers). Type material of T. caespitum var. fusciclavla, T. caespitum var. immigrans, T. semilaeve var. kutteri, and T. staerckei belongs to the T. caespitum complex. A wild-card run of morphometric data in a 10-class LDA including all workers investigated by integrative taxonomy in this study clearly assigned T. staerckei = D e (p = 1), T. caespitum var. fusciclavla = J (p = 1), and T. caespitum var. immigrans = E (p = 1). We redesign these species (see Redescriptions below). However, material of T. semilaeve var. kutteri, consisting of two dwarf work- ers, is ambiguous, and the results permit conspecificity with either T. indicole (p = 0.81) or T. hangaricum (p = 0.19). Based on three arguments, we propose synonymy with T. indicole: (I) Biogeography: T. hangaricum is limited to Eastern Europe, the Balkans, and the Pannonian zone (see redescription below). There is no record west of 16° E, while the type material of T. semilaevae var. kutteri originates from 8° E. Contrariwise, we found T. indicole on the type locality of T. semilaeve var. kutteri. (II) Ecol- ogy: T. hangaricum is thermophilic with TAS 20.6 ± 2.7 °C [16.2, 26.2], while TAS on the type locality is 15.5 °C only. Contrariwise, T. indicole shows TAS 15.6 ± 3.2 °C [11.5, 25.4]. (III) Qualitative morphology: Head and mesoso- ma of T. hangaricum are typically without sculpture and largely smooth and shining. The type material of T. semilaeve var. kutteri has moderately pronounced, but distinct lines on head and mesosoma, especially similar to T. in- dicole originating from the type locality of T. semilaeve var. kutteri. Since type material of T. staerckei var. gregori was not traceable, we aimed at linking the material based on the original description to a species. The male genital morphology drawing 7e in KARATZIAV (1944: 65) shows typical impurum-like parameres without a corner like T. staerckei on the ventral paramere lobe (Fig. 12, Figs. S1: 21 - 31). Hence, we consider T. staerckei var. gregori as a synonym of Tetramorium impurum.

Tetramorium alpestre STEINER, SCHLICK-STEINER & SEIFERT, 2010 (including U3 sensu SCHLICK-STEINER & al. 2006)

Tetramorium alpestre STEINER, SCHLICK-STEINER & SEIFERT, 2010: 249-250. CO1 gene from material of the type nest inves- tigated.

Type locality, Vent (Austria), 46.8548° N, 10.9097° E, 2000 m a.s.l., leg. H. Müller, 15.VIII.2007.

CO1 gene. Here and in the following, we use two different abbreviations for HTs, "HT" (HTs published by SCHLICK-STEINER & al. 2006, STEINER & al. 2010, KINZ- NER & al. 2015, and in this study) and "H" (HTs pub-
lished by Csösz & al. 2014b), 65 HTs from 210 nests: HT101 (15.2%), HT102 (12.9%), HT114 (8.1%), HT116 (6.7%), HT169 (4.3%), HT113 (3.3%), HT172, HT258 (each with 2.9%), HT271 (2.4%), HT115, HT170 (each with 1.9%), HT93, HT111, HT173, HT242, HT257, HT263, HT430 (each with 1.4%), HT91, HT96, HT100, HT103, HT231, HT292, HT294, HT367, HT424, HT426, HT429 (each with 1%).

**Description of worker.** Medium size, CS = 741 ± 51 [605, 850] µm. Dark brown to blackish.

Head moderately elongate, CL / CW = 1.016 ± 0.014 [0.981, 1.049] µm. Eye rather small, EYE / CS = 0.171 ± 0.005 [0.160, 0.182]. Scape length moderate, SLD / CS = 0.775 ± 0.014 [0.738, 0.802]. Mesosoma long and wide, ML / CS = 1.174 ± 0.025 [1.092, 1.225], MW / CS = 0.644 ± 0.012 [0.615, 0.674].

Promesonotal dorsum convex, metanotal groove shallow. – Head dorsum and occiput with longitudinal costae and costulae. Postcortal-temporal area of head with moderate number of longitudinal costae and costulae, POTCos = 8.11 ± 1.45 [4.50, 11.00]. Mesosoma dorsum longitudinally or partly circularly rugose, lateral side of propodeum with moderately pronounced smooth and shiny area, Pps = 37.4 ± 14.5 [14.1, 92.3]. Dorso of petiolar node ML / CS = 1.174 ± 0.025 [1.092, 1.225], MW / CS = 0.644 ± 0.012 [0.615, 0.674].

**Social parasites.** Here and in the following, the species names of social parasites follow traditional nomenclature, which reflects morphological and biological traits but is questionable from a cladistic point of view (WARD & al. 2015). Extensive nomenclatural changes among social parasites are currently on the way, but not yet broadly implemented in the literature. Strongylognathus testaceus (SCHENCK, 1852) (n = 3; host sub "Tetramorium caespitum" in SANETRA & al. 1999 and Tab. S1), Strongylognathus alpinus Wheeler, 1909 (n = 1; host sub "T. caespitum" in SANETRA & al. 1999), and Teleutomyrmex schneideri Kutter, 1950 (n = 1; Tab. S1) were found associated with T. alpestre.

**Tetramorium caespitum (LINNAEUS, 1758)** (including B. U1, U2, and D partim sensu SCHLICK-STEINER & al. 2006)

**Formica caespitum LINNAEUS, 1758:** neotype designation: SCHLICK-STEINER & al. 2006: 270. CO1 gene and morphology of material from the neotype investigated here.

**Tetramorium caespitum var. hammi DONISTHORPE, 1915:** junior synonym of Tetramorium caespitum: Smith 1851: 118; junior synonym confirmed hereby based on biogeography (type locality: New Forest, England).

**Type locality.** Floghult Bohuslan (Sweden), 58.97° N, 11.42° E, 100 m a.s.l., leg. C.A. Collingwood, 21. VI. 2000.

**CO1 gene.** 129 HTs from 495 nests: HT1 (27.1%), HT15 (10.7%), HT52 (9.9%), HT58 (8.7%), HT225 (4.6%), HT57 (2.2%), HT43 (2.0%), HT184, HT229 (each with 1.2%), HT5, HT181 (each with 1.0%), HT48, HT53, HT191 (each with 0.8%), HT32, HT220, HT222, HT224, HT295, HT396 (each with 0.6%), HT6, HT8, HT17, HT35, HT50, HT56, HT126, HT180, HT183, HT223, HT280, HT296 (each with 0.4%), HT2 - HT4, HT7, HT9 - HT14, HT16, HT18, HT22, HT24, HT26, HT33, HT34, HT42, HT46, HT47, HT49, HT51, HT55, HT70, HT79, HT117, HT124, HT125, HT127 - HT129, HT182, HT190, HT192, HT218, HT219, HT226 - HT228, HT230, HT247, HT255, HT296, HT269, HT273, HT275, HT279, HT281, HT283, HT286, HT292, HT300, HT302, HT304, HT309 - HT311, HT313, HT319, HT324, HT325, HT335 - HT342, HT356 - HT358, HT369, HT372, HT373, HT377, HT389 - HT392, HT395, HT398, HT401, HT405, HT410, HT414, HT416, HT417, HT434, HT438, HT439 (each with 0.2%).

**Tetramorium caespitum var. hammi DONISTHORPE, 1915:** junior synonym of Tetramorium caespitum: BOLTON 1995: 408; junior synonym confirmed hereby based on biogeography (type locality: New Forest, England).

**Type locality.** Floghult Bohuslan (Sweden), 58.97° N, 11.42° E, 100 m a.s.l., leg. C.A. Collingwood, 21. VI. 2000.

**CO1 gene.** 129 HTs from 495 nests: HT1 (27.1%), HT15 (10.7%), HT52 (9.9%), HT58 (8.7%), HT225 (4.6%), HT57 (2.2%), HT43 (2.0%), HT184, HT229 (each with 1.2%), HT5, HT181 (each with 1.0%), HT48, HT53, HT191 (each with 0.8%), HT32, HT220, HT222, HT224, HT295, HT396 (each with 0.6%), HT6, HT8, HT17, HT35, HT50, HT56, HT126, HT180, HT183, HT223, HT280, HT296 (each with 0.4%), HT2 - HT4, HT7, HT9 - HT14, HT16, HT18, HT22, HT24, HT26, HT33, HT34, HT42, HT46, HT47, HT49, HT51, HT55, HT70, HT79, HT117, HT124, HT125, HT127 - HT129, HT182, HT190, HT192, HT218, HT219, HT226 - HT228, HT230, HT247, HT255, HT296, HT269, HT273, HT275, HT279, HT281, HT283, HT286, HT292, HT300, HT302, HT304, HT309 - HT311, HT313, HT319, HT324, HT325, HT335 - HT342, HT356 - HT358, HT369, HT372, HT373, HT377, HT389 - HT392, HT395, HT398, HT401, HT405, HT410, HT414, HT416, HT417, HT434, HT438, HT439 (each with 0.2%).

**Distribution.** Iberian mountains, Pyrenees, Massif Central, Mont Ventoux, Corsica, Alps, Appenines, Calabrian Appenines, Monti Nebrodi, Dinaric Alps (Fig. 13).

**Ecology.** Less thermophilous than all other species of complex (Tab. 5), TAS of 182 sites 8.6 ± 2.1 °C [5.2, 17.6]. In Alps and Pyrenees often above timberline; never below 900 m a.s.l. Southern Italian population more thermophilous, TAS of three sites 14.8 ± 2.9 °C (t-test, p = 0.000). In Alps, typical habitats are south-facing, non-forested alpine meadows, subalpine dwarf-shrub heathland, dry pastures, stony embankments, or block fields. In Pyrenees, known from stony pine forests. Nests often under stones, but also in moss, rootage, and dead wood.


**Phenology.** Adult sexuals in nests on 30 July ± 17d [18 June, 10 September] (n = 34).
Tetramorium hungaricum found in nests of building soil mounds higher than 10 cm. in soil, under stones, rarely in dead wood; only species sides. Nest construction more flexible than other species:

Ecology. Moderately thermophilic, TAS of 465 sites 16.1 ± 2.0 °C [7.9, 21.1], different from all species except Tetramorium indocile. Most common species in most of Europe and more euryoecious than other species of complex. Most records from non-forested habitats like meadows, pastures, heaths, arid or semi-arid grasslands, vineyards, fallow grounds, ruderal areas, road embankments, rock heaps, gravel pits, river banks, but also light pine and oak forests. Urban areas like parks, pavements, and road-rock heaps, gravel pits, river banks.

Biological. Monogynous (SCHENCK 1915). Description of male, Paramere structure belongs to caespitum-like form: ventral paramere lobe with one or two sharp corners; without distinct emargination between paramere lobes in posterior view, both paramere lobes reduced in size; in ventro-posterior view, second corner on ventral paramere lobe missing or < 87 μm apart from first. In posterior view, typically only one sharp corner on ventral lobe.

Distribution. Whole Europe (after SEIFERT 2007 up to 63° N), Caucasus (Fig. 13).

Ecology. Modernly thermophilic, TAS of 465 sites 16.1 ± 2.0 °C [7.9, 21.1], different from all species except Tetramorium indocile. Most common species in most of Europe and more euryoecious than other species of complex. Most records from non-forested habitats like meadows, pastures, heaths, arid or semi-arid grasslands, vineyards, fallow grounds, ruderal areas, road embankments, rock heaps, gravel pits, river banks, but also light pine and oak forests. Urban areas like parks, pavements, and road-sides. Nest construction more flexible than in other species: in soil, under stones, rarely in dead wood; only species building soil mounds higher than 10 cm.

Biological. Monogynous (SEIFERT 2007). Hybridizes with Tetramorium immigrans (results of this study, samples i246 and 18375).

Phenology. Adult sexuals in nests on 20 June ± 6 [8 June, 24 June] (n = 7).

Tetramorium breviscapus sp. n. (= as defined in this study)

Etymology. Named after its proportionally short scope, one of the best morphological characters for discrimination from related species. Because "breviscapus" is a noun in apposition, "as" is the correct ending.

Type locality. Dubrovnik (Croatia), 42.650° N, 18.038° E, 3 m a.s.l., leg. D. Dender, 29.X.2005.

Type material. All type material from one nest, labeled "CRO: 42.650° N, 18.038° E Dubrovnik coast, 3 m D.Dender 2005.10.29-18071". Holotype worker (Fig. 15) and eleven paratype workers in Senckenberg Naturkundemuseum Görlitz (Germany). Five paratype workers in Museum of Comparative Zoology, Cambridge, Massachusetts (USA), five in Natural History Museum in London (UK), five in Natural History Museum Basel (Switzerland), five in Museum of Nature South Tyrol (Bozen, Italy), five in Tiroler Landesmuseum (Hall, Austria), five in Natural History Museum in Vienna (Austria), five in Budapest Hungarian Natural History Museum (Hungary), and five in Schmalhausen Institute of Zoology Kiev (Ukraine). CO1 gene of type nest: HT329. Morphometric data of holotype in mm: CL = 724, CW = 724, dAN = 197, EL = 130, EW = 99, FL = 276, HFL = 551, MCI1TG = 15.7, ML = 789, MPPL = 234, MPSP = 309, MPST = 189, MtpW = 361, MW = 449, PHE = 245, PEL = 149, PFW = 245, PLPS = 168, PLST = 176, PoOc = 292, POTCos = 7.8, PPH = 269, PPL = 106, Pps = 79, PPW = 306, PreOc = 180, RTI = 295, SLd = 512, SPST = 133, SWp = 200.

Tetramorium immigrans

Type locality. Dubrovnik (Croatia), 42.650° N, 18.038° E, 3 m a.s.l., leg. D. Dender, 29.X.2005.

Type material. All type material from one nest, labeled "CRO: 42.650° N, 18.038° E Dubrovnik coast, 3 m D.Dender 2005.10.29-18071". Holotype worker (Fig. 15) and eleven paratype workers in Senckenberg Naturkundemuseum Görlitz (Germany). Five paratype workers in Museum of Comparative Zoology, Cambridge, Massachusetts (USA), five in Natural History Museum in London (UK), five in Natural History Museum Basel (Switzerland), five in Museum of Nature South Tyrol (Bozen, Italy), five in Tiroler Landesmuseum (Hall, Austria), five in Natural History Museum in Vienna (Austria), five in Budapest Hungarian Natural History Museum (Hungary), and five in Schmalhausen Institute of Zoology Kiev (Ukraine). CO1 gene of type nest: HT329. Morphometric data of holotype in mm: CL = 724, CW = 724, dAN = 197, EL = 130, EW = 99, FL = 276, HFL = 551, MCI1TG = 15.7, ML = 789, MPPL = 234, MPSP = 309, MPST = 189, MtpW = 361, MW = 449, PHE = 245, PEL = 149, PFW = 245, PLPS = 168, PLST = 176, PoOc = 292, POTCos = 7.8, PPH = 269, PPL = 106, Pps = 79, PPW = 306, PreOc = 180, RTI = 295, SLd = 512, SPST = 133, SWp = 200.
**CO1 gene.** 2 HTs from 3 nests: HT329 (66.7%), HT290 (33.3%).

**Description of worker.** Smaller than most species of complex, CS = 714 ± 26 [689, 740] µm. Dark brown to blackish, mesosoma frequently lighter than head and gaster.

Head rather truncated compared with other species of complex, CL / CW = 1.002 ± 0.012 [0.989, 1.010]. Eye rather small, EYE / CS = 0.169 ± 0.010 [0.163, 0.180]. Scape shortest of complex, SLd / CS = 0.728 ± 0.010 [0.722, 0.739]. Mesosoma short and moderately wide, ML / CS = 1.119 ± 0.013 [1.107, 1.133], MW / CS = 0.631 ± 0.002 [0.629, 0.634].

Promesonotal dorsum convex, metanotal groove shallow. – Head dorsum and occiput with longitudinal costae and costulae. Postoculo-temporal area of head with rather few longitudinal costae and costulae, POTCos = 5.95 ± 0.53 [5.45, 6.50]. Mesosoma dorsum longitudinally rugulose, lateral side of propodeum with large smooth and shiny area, Pps = 73.6 ± 16.6 [57.9, 91.0]. Dorsum of petiolar node usually smooth, exceptionally microreticulated. General surface appearance rather smooth and shiny compared with other species of complex. – Connected stickman-like or reticulate microsculpture: moderate-sized units scattered over 1st gastric tergite, MC1TG = 15.77 ± 1.20 [14.58, 16.97]. – Some workers with long c-shaped, crinkly, or sinuous hairs on ventral head just posterior to buccal cavity.

**Distribution.** Croatia, Bosnia-Herzegovina, and Greece (Fig. 13).

**Ecology.** More thermophilic than *Tetramorium alpestre*, *T. caespitum*, *T. indocile*, *T. caucasicum*, and *T. impurum*; TAS of three sites 22.1 ± 1.4 °C [20.6, 23.2]. Open habitats.

*Tetramorium indocile* SANTSCHI, 1927


*Tetramorium semilaevae* var. *kutteri* SANTSCHI, 1927: 57; junior synonymy fixed hereby based on type investigation and biogeography (type locality: Brig, Switzerland). **Syn.n.**

**Type locality.** Ssemiretschie, Kisil-Kijapass (Kyrgyzstan), 40.27° N, 72.13° E, 2100 m a.s.l., leg. N. Kusnezow, 15. VIII.1924.

**CO1 gene.** 21 HTs from 47 nests: HT87 (25.5%), HT83 (17.0%), HT85 (10.6%), H28, HT82 (each with 6.4%), H27, H29, H30, HT80, HT81, HT86, HT90, HT154, HT155, HT243, HT301, HT354, HT360, HT380, HT412, HT443 (each with 2.1%).

**Description of worker.** Smaller than most other species of complex, CS = 717 ± 52 [575, 822] µm. Dark brown to blackish.

Head moderately elongate, CL / CW = 1.011 ± 0.014 [0.982, 1.051]. Eye medium-sized, EYE / CS = 0.174 ± 0.005 [0.162, 0.181]. Scape moderately long, SLd / CS = 0.764 ± 0.013 [0.734, 0.790]. Mesosoma moderately long and moderately wide, ML / CS = 1.155 ± 0.020 [1.107, 1.205], MW / CS = 0.637 ± 0.011 [0.609, 0.667].

Promesonotal dorsum convex, metanotal groove shallow. – Head dorsum and occiput with longitudinal costae and costulae. Postoculo-temporal area of head with rather few longitudinal costae and costulae, POTCos = 6.08 ± 1.69 [2.63, 9.75]. Mesosoma dorsum longitudinally rugulose, lateral side of propodeum with rather pronounced smooth and shiny area, Pps = 50.0 ± 23.8 [17.6, 110.5]. – Dorsum of petiolar node often smooth, rarely feebly microreticulated. General surface appearance on average rather smooth and shiny compared with other species. – Connected stickman-like or reticulate microsculpture: small units scattered over 1st gastric tergite, MC1TG = 14.01 ± 2.44 [6.41, 19.96]. – Some workers with long c-shaped, crinkly, or sinuous hairs on ventral head posterior to buccal cavity.
Description of male. Paramere structure belongs to caespitum-like form: ventral paramere lobe with one or two sharp corners; without distinct emargination between paramere lobes in posterior view, paramere lobes reduced in size; in ventro-posterior view, second corner on ventral paramere lobe missing or < 87 µm apart from first. In posterior view, two sharp corners on ventral lobe.

Distribution. Disjunct: Iberia, France, Central Europe, Italy, Balkans, Eastern Europe, Caucasus, Central Asia (Fig. 13).


Phenology. Adult sexuals in nests on 17 July ± 24 [20 June, 16 August] (n = 7).

Tetramorium caucasicum sp.n. (= U5)

Etymology. Named after its distribution area, the Caucasus.

Type locality. River Bashil valley (Russia), 43.211° N, 42.987° E, 2206 m a.s.l., leg. Z.M. Yusupov, 18.VI.2009.

Type material. All type material from one nest, labeled "RUS: 43.211° N, 42.987° E River Bashil valley, 2206 m S slope, timberline, under stone Z.M. Yusupov 2009.06.18-17372". Holotype worker (Fig. 16) and two paratype workers in Senckenberg Naturkundemuseum Göt- litz (Germany). Two paratype workers in Museum of Comparative Zoology, Cambridge, Massachusetts (USA), two in Natural History Museum in London (UK), two in Natural History Museum Basel (Switzerland), one in museum of Nature South Tyrol (Bozen, Italy), one in Tiroler Landesmuseum (Hall, Austria), two in Natural History Museum in Vienna (Austria), two in Budapest Hungarian Natural History Museum (Hungary), and two in Schmalhausen Institute of Zoology Kiev (Ukraine). CO1 gene of type nest: HT234. Morphometric data of holotype in µm: CL = 714, CW = 691, dAN = 205, EL = 131, EW = 97, FL = 270, HFL = 563, MC1TG = 13.5, ML = 798, MPPL = 240, MPSP = 300, MPST = 183, MtpW = 338, MW = 433, PEH = 243, PEL = 157, PEW = 216, PLSP = 151, PLST = 171, PnHL = 183, PoOc = 286, POTCos = 8.5, PPH = 259, PPL = 111, Ppss = 57, PPW = 274, PreOc = 177, RTI = 289, SLd = 546, SPST = 134, SPWI = 185.

CO1 gene. 5 HTs from 7 nests: HT343 (42.9%), HT234-HT236, HT378 (each with 14.3%).

Description of worker. Larger than most other species of complex, CS = 757 ± 44 [706, 839] µm. Dark brown to blackish.

Head strongly elongate, CL / CW = 1.027 ± 0.021 [0.987, 1.052]. Eye medium-sized, EYE / CS = 0.172 ± 0.005 [0.162, 0.178]. Scape moderately long, SLd / CS = 0.779 ± 0.015 [0.749, 0.798]. Mesosoma moderately long and moderately wide, ML / CS = 1.160 ± 0.022 [1.131, 1.211], MW / CS = 0.637 ± 0.015 [0.612, 0.670].

Promesonotal dorsum convex, metanotal groove shallow. – Head dorsum and occiput with longitudinal costae and costulae. Postoccipital-temporal area of head with rather many costae and costulae, POTCos = 8.71 ± 1.44 [6.17, 10.63]. Mesosoma dorsum longitudinally rugulose, lateral side of propodeum with moderately pronounced smooth and shiny area. Ppss = 45.0 ± 20.2 [16.4, 80.4]. Dorsum of petiolar node smooth or with sculpture. General surface appearance on average moderate smooth and shiny compared with other species. – Connected stickman-like or reticulate microsculpture: small units scattered over 1st gastric tergite, MC1TG = 14.47 ± 1.81 [11.64, 17.33]. – Some workers with long c-shaped, crinkly, or sinuous hairs on ventral head posterior to buccal cavity.
Description of male. Paramere structure belongs to *impurum*-like form: rounded ventral paramere lobe without any sharp corner in dorsal or ventral view but with clear division of ventral and dorsal paramere lobes, visible by deep emargination between lobes in posterior view. Sharp corner at end of ventral lobe in posterior view.

Distribution. Caucasus: Southern Russia, Georgia, and Armenia (Fig. 13).

Ecology. Less thermophilic than most other species of complex, TAS of seven sites 13.5 ± 2.8 °C [10.2, 18.2] and different from all species except *Tetramorium indocile* and *T. impurum*. Often above timberline; typical habitats are pastures and steppic meadows.

Phenology. Adult sexuals in nests on 2 August (n = 1).

*Tetramorium fusciclava* CONSANI & ZANGHERI, 1952

* (= J as defined in this study)

*Tetramorium caespitum caespitum* var. *fusciclava* EMERY, 1925: 187 (unavailable name); first available use: *Tetramorium caespitum* var. *fusciclavum* [sic!] CONSANI & ZANGHERI 1952: 42; junior synonym of *Tetramorium caespitum*: SANETRA & al. 1999: 320; revived from synonymy, raised to species rank and lectotype designation hereby.

Type locality. Riccione (Italy), 43.999° N, 12.656° E, 11 m a.s.l., leg. C. Emery, 1925.

Lectotype designation. Top worker of two syntype workers (of two cards on one needle), labeled "Riccione" [--] SYNTYP Tetramorium caespitum c. var. fusciclavum C. Emery, 1925 [--] "var fusciclavum Emery" [--] MUSEO GENOVA coll. C. Emery (dono 1925) [--] ANTWEB CASENT 904802, designated as lectotype (Fig. 17). Lectotype worker and one paralectotype worker in Museo Civico di Storia Naturale, Genova (Italy). Morphometric data of lectotype in µm: CL = 701, CW = 697, dAN = 199, EL = 150, EW = 109, FL = 273, HFL = 584, MC1TG = 19.9, ML = 777, MPPL = 228, MPSP = 298, MPST = 190, MtpW = 336, MW = 422, PEH = 244, PEL = 148, PEW = 217, PLSP = 168, PLST = 186, PnH = 186, PoOc = 275, POTCos = 9, PPH = 252, PPL = 98, PpsS = 23, PPW = 279, PreOc = 167, RT1 = 309, SLd = 564, SPST = 133, SPWI = 170.

CO1 gene. 4 HTs from 16 nests: HT189 (56.3%), HT305 (31.3%), HT272, HT404 (each with 6.3%).

Description of worker. Rather small, CS = 724 ± 42 [667, 829] µm. Dark brown to blackish.

Shortest head of complex, CL / CW = 0.996 ± 0.012 [0.976, 1.029]. Largest eye of complex, EYE / CS = 0.188 ± 0.004 [0.183, 0.196]. Scape moderately long, SLd / CS = 0.774 ± 0.006 [0.763, 0.784]. Mesosoma short and narrowest in complex, ML / CS = 1.136 ± 0.021 [1.101, 1.175], MW / CS = 0.615 ± 0.012 [0.596, 0.646].

Promesonotal dorsum convex, metanotal groove shallow. – Head dorsum and occiput with longitudinal costae and costulae. Postoculo-temporal area of head with a moderate number of longitudinal costae and costulae, POTCos = 6.76 ± 2.12 [4.63, 13.50]. Mesosoma short and narrowest in complex, ML / CS = 1.136 ± 0.021 [1.101, 1.175], MW / CS = 0.615 ± 0.012 [0.596, 0.646].

Dorsum of petiolar node typically with few strong costae, sometimes smooth or microreticulated. General surface appearance moderately smooth and shiny compared with other species. – Connected stickman-like or reticulate microsculpture: large units scattered over 1st gastral tergite, MCI1TG = 20.57 ± 1.85 [16.34, 23.74]. – Some workers with long c-shaped, crinkly, or sinuous hairs on ventral head posterior to buccal cavity.

Distribution. Italy (Fig. 13).

Ecology. More thermophilic than all species except *Tetramorium hungaricum*, *T. breviscapus*, and *T. immigrans*; TAS of 13 sites 21.3 ± 1.6 °C [16.1, 21.8]. Preference for...
coastal areas: Twelve of 13 localities closer than 10 km to sea. Nests in grasslands, cornfield reins, beaches, pine forests; especially on sandy soil.

**Phenology.** No adult sexuals found, records of sexual larvae and pupae from 13 and 14 May.

**Tetramorium staerckei** KRATOCHVIL, 1944 *sp.rev.*

=Tetramorium caespitum* var. staerckei* RÖSSLER, 1936 (unavailable name); first available use: KRATOCHVIL 1944: 65; junior synonym of *Tetramorium impurum* KUTTER 1977: 159; revived from synonymy based on type investigation and lectotype designation hereby.

**Type locality.** Nagytétény (Hungary), 47.391° N, 18.987° E, leg. P. Rössler, 17.VI.1935.

**Lectotype designation.** Worker closer to needle (of two syntype workers of one card), labeled "Hongrie Nagytétény Coll: Rössler [\(N\] 17. VI. 1935 [\(N\] Typus [\(N\] "Tetramorium caespitum var. hungaricum v. Staerckei worker Rößl. Typus! No. 500" [\(N\] "PAUL RÖSSLER BASS GABOR-TELEP HONGRIE – EUROPE", designated as lectotype (Fig. 18). Lectotype worker, one paralectotype worker, one paralectotype gyne, and one paralectotype male in Museum of Natural History, Sibiu / Hermannstadt (Romania). Morphometric data of lectotype worker in µm:

- CL = 871, CW = 849, dAN = 266, EL = 181, EW = 133, FL = 350, HFL = 739, ML = 1072, MPPL = 322, MPSP = 396, MPST = 238, MW = 581, PEH = 321, PEL = 203, PEW = 303, PLSP = 201, PLST = 239, PnHl = 241, PoOc = 329, POTCos = 10, PPH = 359, PPL = 126, PW = 378, PreOc = 212, RTI = 347, SLd = 692, SPST = 186, SPW1 = 277.

**CO1 gene.** 31 HTs from 74 nests: HT38 (18.9%), HT28, HT245, HT347 (each with 9.5%), HT29, HT37, HT39 (each with 4.1%), H20, H21, HT25, HT31, HT38 (each with 2.7%), H15, H16, HT27, HT30, HT40, HT41, HT144, HT185, HT186, HT244, HT253, HT254, HT268, HT276, HT307, HT371, HT376, HT383 (each with 1.4%).

**Description of worker.** Rather large compared with other species of complex, CS = 746 ± 57 [655, 878] µm. Dark brown to blackish.

Most elongate head of complex, CL / CW = 1.032 ± 0.014 [1.003, 1.062]. Eye rather large, EYE / CS = 0.178 ± 0.005 [0.168, 0.189]. Longest scape of complex, SLd / CS = 0.787 ± 0.016 [0.750, 0.817]. Mesosoma longest within complex and wide, ML / CS = 1.188 ± 0.025 [1.141, 1.247], MW / CS = 0.645 ± 0.014 [0.614, 0.681].

Promesonotal dorsum convex, metanotal groove shallow. – Head dorsum and occiput with longitudinal costae and costulae. Postoculo-temporal area of head with many costae and costulae, POTCos = 10.53 ± 1.75 [7.38, 13.75]. Mesosoma dorsum longitudinally rugulose, lateral side of propodeum with strongest sculpture of complex, Ppss = 16.9 ± 5.3 [11.3, 33.1]. – Dorsum of petiolar with sculpture or smooth. General surface appearance on average dull compared with other species. – Connected stickman-like or reticulate microsculpture: moderate-sized units scattered over 1st gastral tergite, MC1TG = 15.93 ± 2.35 [11.00, 22.00]. – Some workers with long c-shaped, crinkly, or sinuous hairs on ventral head posterior to buccal cavity.

**Description of male.** Paramere structure belongs to impurum-like form: rounded ventral paramere lobe without any sharp corner in dorsal or ventral view but with clear division of ventral and dorsal paramere lobes, visible by deep emargination between lobes in posterior view. No sharp corner at end of ventral lobe visible in posterior view. Relatively short dorsal paramere lobe, visible in posterior and dorsal view. Paramere structure length in lateral view > 1014 μm. In dorsal and posterior view, distinct corner on ventral paramere lobe between lobe top and emargination with dorsal lobe.

**Distribution.** Pannonian zone, Balkans, southern Russia, Central Asia (Fig. 13).

**Ecology.** Thermophilic, TAS of 79 sites 18.1 ± 3.1 °C [11.0, 26.4], different from all species except *Tetramorium breviscapus*. Avoids Mediterranean areas, but occurs on Black Sea coast. Typical European habitats are semi-dry and dry grasslands, semi-arid pastures, road embankments, fallow vineyard, rock heaps, sand dunes; exceptionally urban areas. Might be more salt-tolerant than other species, as it was mentioned under "Tetramorium cf. caespi-
tetra-“ as most frequent ant species in saline field in Ocnă Sibiului (Romania) (TAȘAN & MARKÓ 2011; material determined by us). In Kyrgyzstan in meadows, steppes, semi-deserts, groves. Soil nests often under stones, sometimes covered with grass; small soil mounds exist.

**Phenology.** Adult sexuals in nests on 13 June ± 10 d [1 June, 27 June] (n = 6).

**Tetramorium impurum** (FÖRSTER, 1850) (including U6 sensu SCHLICK-STEINER & al. 2006)

*Myrmica impura* FÖRSTER, 1850: 48; junior synonym of *Tetramorium caespitum*; CURTIS 1854: 215; revived from synonymy: KUTTER 1977: 159; neotype designation: SCHLICK-STEINER & al. 2006; 267. CO1 gene, AFLP data, and morphology of material from the neotype nest investigated in the present study.

**Tetramorium caespitum penninum** SANTSCHI, 1927: 54; junior synonym of *Tetramorium caespitum*; SANETRA & al. 1999: 321. Morphology of type material investigated.

**Tetramorium staerckei** var. grigori KRAOTCHVIL, 1941: 65; junior or synonymy fixed hereby based on description (type locality: Czech Republic). **Synn.**

**Type locality.** Mirwart vic. Saint-Hubert (Belgium), (50.03° N 05.27° E), 360 m a.s.l., leg. Y. Roisin, 4.VIII.2000.

**CO1 gene.** 61 HTs from 161 nests: HT22 (19.9%), HT21 (19.3%), HT122 (9.9%), HT148 (4.3%), HT147 (2.5%), HT20, HT149, HT152, HT285 (each with 1.9%), HT118, HT143, HT246, HT326, HT353, HT355, HT420 (1.2%), HT19, HT23, HT119 - HT121, HT139, HT140, HT118, HT143, HT246, HT326, HT353, HT355, HT420 (1.2%), HT19, HT23, HT119 - HT121, HT139, HT140, HT142, HT145, HT146, HT150, HT151, HT153, HT237, HT238, HT248, HT249, HT256, HT266, HT267, HT270, HT277, HT278, HT284, HT289, HT291, HT308, HT315, HT320, HT321, HT323, HT327, HT334, HT351, HT352, HT368, HT374, HT375, HT379, HT385, HT397, HT399, HT402, HT403, HT441 (each with 0.6%). Smallest eye of complex, EYE / CS = 0.168 ± 0.005 [0.155, 0.181]. Scape moderately long, SLd determined by us). In Kyrgyzstan in meadows, steppes, semi-covered with grass; small soil mounds exist.

**Phenology.** Adult sexuals in nests on 23 August ± 27 [29 June, 14 October] (n = 36).

**Social parasites.** *Anergates atratulus* (n = 1; Tab. S1), *Strongylognathus testaceus* (n = 1; Tab. S1), and *Strongylognathus alpinus* (n = 1; host sub "Tetramorium caespitum penninum" in SANTSCHI 1927) were found in nests of *T. impurum.*

**Tetramorium immigrans** SANTSCHI, 1927 stat.n. (= E sensu SCHLICK-STEINER & al. 2006)

**Tetramorium caespitum var. immigrans** SANTSCHI 1927: 54; junior synonym of *T. caespitum*; BOLTON 1979: 171; revived from synonymy, raised to species rank, and lectotype designation hereby.

**Type locality.** Valparaíso (Chile), 33.05° S, 71.61° W, 18 m, leg. Edwards, 1926.

**Lectotype designation.** Worker of middle card closer to needle than second worker, labeled "TYPE [-] "Chili Valparaíso, Miss Edwards" [-] "Tetramorium caespitum L immigrans Sant"." SANTSCHI det. 19 "26" [-] Samm-lung Dr. F. Santschi Kairouan", designated as lectotype (Fig. 19). Lectotype worker and seven paralectotype workers in Naturhistorisches Museum Basel (Switzerland). Morphometric data of lectotype in µm: CL = 914, CW = 912, dAN = 246, EL = 183, EW = 142, FL = 355, HFL = 783, MC1TG = 25.1, ML = 1100, MPPL = 318, MPS = 427, MPST = 236, MtpW = 461, MW = 592, PEH = 313, PEL = 218, PEW = 310, PLSP = 223, PLST = 243, PnHL = 238, PoOc = 363, POTCoS = 12, PPH = 343, PPL = 144, Pps = 68, PPW = 379, PreOc = 223, RTI = 359, SLD = 727, SPST = 213, SPW1 = 289.

**CO1 gene.** 44 HTs from 213 nests: HT75 (34.3%), HT79 (18.8%), HT70 (12.2%), HT72 (3.8%), HT60 (2.8%), HT76, HT78 (each with 2.3%), HT61, HT74, HT194 (each with 1.9%), HT64, HT77, HT381, HT382 (each with visible by deep emargination between lobes in posterior view. No sharp corner at end of ventral lobe visible in posterior view. Relatively short dorsal paramere lobe, visible in posterior and dorsal view. Paramere structure length in lateral view > 1014 µm. No corner on ventral paramere lobe between lobe top and emargination with dorsal lobe in dorsal and posterior view.

**Distribution.** Eastern clade: Anatolia, Balkans, Italy, Central Europe, Benelux northward to 52° N. Western clade: Iberia, western France (Fig. 13).

**Ecology.** Less thermophilic than most other species of complex. TAS of 155 sites 14.1 ± 2.7 °C [7.7, 21.4] (n = 155), different from all species except *Tetramorium cau-

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Fig. 19: Lectotype of *Tetramorium immigrans* stat.n. in (A) full face, (B) dorsal, and (C) lateral view (specimen CAS-ENT0913997 from www.AntWeb.org, photographer Zach Lieberman).

0.9%), HT62, HT63, HT65 - HT69, HT71, HT73, HT193, HT195 - HT199, HT202, HT203, HT293, HT312, HT314, HT317, HT318, HT331, HT332, HT345, HT348, HT349, HT384, HT394, HT413 (each with 0.5%).

**Description of worker.** Largest species of complex, CS = 834 ± 56 [713, 943] µm. Dark brown to blackish, rarely reddish.

Head moderately elongate, CL / CW = 1.012 ± 0.013 [0.985, 1.035]. Eye medium-sized, EYE / CS = 0.176 ± 0.004 [0.167, 0.189]. Scape long, SLd / CS = 0.784 ± 0.014 [0.755, 0.817]. Mesosoma moderately long and narrow, ML / CS = 1.158 ± 0.020 [1.109, 1.201], MW / CS = 0.629 ± 0.012 [0.605, 0.649].

Promesonot al dorsum convex, metanotal groove shallow. – Head dorsum and occiput with longitudinal costae and costulae. Postoculo-temporal area of head with highest number of costae and costulae in complex, POTCos = 12.33 ± 1.67 [8.25, 16.13]. Mesosoma dorsum longitudinally rugulose, lateral side of propodeum with pronounced sculpture, Ppss = 30.5 ± 14.5 [13.6, 63.3]. Dorsum of petiolar with sculpture, reticulate microsculpture, or smooth. General surface appearance rather dull. – Connected stickman-like or reticulate microsculpture: large units scattered over 1st gastric tergite, MC1TG = 21.67 ± 2.68 [16.07, 27.00]. – Some workers with long c-shaped, crinkly, or sinuous hairs on ventral head posterior to buccal cavity.

**Description of male.** Paramere structure belongs to caespitum-like form: ventral paramere lobe with one or two sharp corners; without distinct emargination between paramere lobes in posterior view, both paramere lobes reduced in size. In ventro-posterior view, second corner on ventral paramere lobe > 87 µm apart from first. In posterior view, two corners on ventral lobe.

**Distribution.** Mediterranean, Western Europe, Central Europe, Balkans, Eastern Europe, Anatolia, Caucasus (Fig. 13), introduced to North (STEINER & al. 2008) and South America (SANTSCHI 1927).

Ecology. More thermophilic than all species except *Tetramorium hungaricum*, *T. breviscapus*, and *T. fasciata*. TAS of 201 sites 19.9 ± 2.5 °C [13.0, 26.7]. In France and partially Central Europe synanthropic: roadsides, ruderal areas, parks, gardens, pavements, railway constructions, stone pits, balconies, inside of buildings. In Pannonian zone, Mediterranean, and Caucasus most common species in anthropogenic areas, but also primary habitats like semi-arid and arid grasslands, rocky and sandy grasslands, beaches, river banks, rock walls. Bulgarian records from forests. Nests often between cracks of concrete, asphalt, rocks, as well as under stones; small soil mounds exist.

**Biology.** Hybrids with *Tetramorium caespitum* (results of this study).

**Phenology.** Adult sexuals on 27 June ± 39d [17 March, 29 September] (n = 16).

**Social parasites.** Anergates atratulus (n = 1; Tab. S1) was found in a nest of *Tetramorium immigrans*.

**Key to workers of the *Tetramorium caespitum* complex**

We present a dichotomous key for Europe (incl. Caucasus and Ural) and Kyrgyzstan here and an online identification key at https://webapp.ubik.ac.at/ecology/tetramorium. The application of this key requires magnifications of at least 100 × and good lighting conditions. Morphometric characters are always in µm. Arithmetic means and standard deviations of indices always refer to means of nest means. Species-specific means for further characters are available in Table S10. The online identification key necessitates morphometric and geographic data of workers and provides correct classifications in 88.0% of individual workers and 97.4% of nest means of two workers.

1 British Isles (excl. Channel Islands), Fennoscandia, Baltic. ................................................. *T. caespitum*

- Central Europe north of 53° N. .............. *T. caespitum*
- Alps or Pyrenees > 2100 m a.s.l. .............. *T. alpestre*
2 Eye very large: EL / CS = 0.218 ± 0.005, EW / CS = 0.159 ± 0.003. Distance between outer margins of spines very small and spines short: SPWI / CS = 0.237 ± 0.010, SPST / CS = 0.171 ± 0.008. Petiole and postpetiole narrow: PEW / CS = 0.297 ± 0.009, PPW / CS = 0.391 ± 0.011. Petiole short: PEL / CS = 0.219 ± 0.005. Ridges frontal antennal fossae wider apart: RTI / CS = 0.417 ± 0.010. Stickman-like or reticulate microstructure on first gastral tergite pronounced: MC1TG = 20.57 ± 1.85. Number of postoculo-temporal costae and costulae moderate: POTCos = 6.76 ± 2.12. Discriminant D1 (error 0.0% in 34 workers): 164.05 * SPWI / CS + 95.81 * PEL / CS - 53 < 0. Thermophilic. ..........................

3 Sculpture on head and mesosoma reduced and large parts smooth and shiny. Very few postoculo-temporal costae and costulae: POTCos = 2.14 ± 1.21. Lateral face of propodeum anterior propodeal stigma often smooth: Ppss = 95.6 ± 36.1. Eye large: EL / CS = 0.211 ± 0.009, EW / CS = 0.156 ± 0.006. Postpetiole narrow: PPW / CS = 0.382 ± 0.013. Mesosoma short: ML / CS = 1.103 ± 0.018. Hind femur short: HFL / CS = 0.770 ± 0.011. Discriminant D2 (error 7.8% in 51 workers and 0.0% in 379 nest means of Italian species): 3.606 * PPW + 27.209 * POTCos + 6.072 * PEL + 1.375 * PhnHL - 11.221 * EYE - 886 < 0. Thermophilic. .......................... T. hungaricum

4 Balkans only. Scape very short: SLd / CS = 0.730 ± 0.013. Petiole and mesosoma short: PEL / CS = 0.215 ± 0.002, ML / CS = 1.121 ± 0.014. Sculpture on large parts of head and mesosoma pronounced, but often distinct smooth and shiny area on lateral face of propodeum anterior the propodeal stigma: Ppss = 73.6 ± 16.6. Number of postoculo-temporal costae and costulae small to moderate: POTCos = 5.95 ± 0.53. Discriminant D3 (error 0.0% in 15 workers): 5.405 * SLD + 6.028 * PEH + 8.718 * PEL - 5.216 * CS - 5.462 * PEW - 4.074 * PLSP - 53 < 0. Thermophilic. .......................... T. breviscapus sp.n.

5 Sculpture well developed, number of postoculo-temporal costae and costulae large, smooth area on lateral face of propodeum anterior propodeal stigma small: POTCos = 10.53 ± 1.75, Ppss = 16.9 ± 5.3. Eye larger: EL / CS = 0.202 ± 0.006, EW / CS = 0.153 ± 0.004. Discriminant D4 (error 3.7% in 81 workers and 0.0% in 447 nest means of staerckei): 13.144 * ML + 89.666 * dAN + 304.936 * POTCos + 123.574 * EYE + 57.722 * PLST + 106.414 * MC1TG - 40.588 * MtpW - 50.045 * CW - 21.122 * RTI - 46.477 * PLSP - 2800 > 0. Thermophilic. ........................... T. staerckei sp.n.

6 Stickman-like or reticulate microsculpture on first gastral tergite moderate: MC1TG = 15.93 ± 2.35. Distance between antennal fossae larger: dAN / CS = 0.300 ± 0.005. Mesosoma longer: ML / CS = 1.188 ± 0.025. Smaller: CS = 746 ± 57. Discriminant D5 (error 12.2% in 81 workers and 0.0% in 41 nest means): 58.624 * MtpW + 58.287 * CL + 84.382 * CW - 57.153 * ML - 51.265 * PPW - 159.873 * dAN - 28593 < 0. Often natural habitats. ............................ T. staerckei stat.n.

7 Kyrgyzstan. ............................. T. indocile

8 Stickman-like or reticulate microsculpture on first gastral tergite pronounced: MC1TG = 21.67 ± 2.68. Distance between antennal fossae smaller: dAN / CS = 0.280 ± 0.007. Mesosoma shorter: ML / CS = 1.158 ± 0.020. Larger: CS = 834 ± 56. D3 > 0 (error 0.0% in 84 workers). Often in anthropogenically influenced, vegetation-free, and even concreted habitats, but also rocky natural habitats. ............................ T. immigra stat.n.
0.005, EW / CS = 0.152 ± 0.004. Postocular distance smaller: PoOc / CS = 0.387 ± 0.006. Discriminant D6 (error 8.3% in 84 workers and 2.5% in 40 nest means): 3.348 * CL + 23.130 * POTCos + 9.953 * EW + 2.235 * PPW + 3.313 * PLST + 19.914 * MC1TG - 1.869 * SPWI - 4.364 * MW - 3.172 * PoOc - 1.967 * PPL - 3.243 * PLSP - 0.047 * ALT - 1295 * 0. Thermophilic. In Europe < 1000 m a.s.l. Often in anthropogenically influenced, vegetation-free, and even concreted habitats, but also rocky natural habitats. .......... T. immigrans stat.n.

- Stickman-like or reticulate microsculpture on first gastral tergite reduced: MC1TG = 13.71 ± 2.73. Number of postoculo-temporal costae and costulae often smaller, POTCos = 7.74 ± 1.96. Distance between outer margins of spines larger: SPWI / CS = 0.288 ± 0.019. Eye smaller: EL / CS = 0.195 ± 0.007, EW / CS = 0.146 ± 0.005. Postocular distance larger: PoOc / CS = 0.398 ± 0.010. D6 < 0 (error 0.7% in 717 workers and 0.3% in 349 nest means of T. alpestris, T. caespitum, T. indocile, T. caesiacum, and T. impurum). .............................................. 9

9 Iberian Peninsula, mainland western France, Balearic Islands, Corsica, Sardinia, British Channel Islands. .................................................. 10

- Mainland eastern France, Switzerland, Austria, mainland Italy, Sicily, Balkans (incl. Slovenia and Romania). > 900 m a.s.l. .................................................. 11

- Mainland eastern France, Switzerland, Austria, mainland Italy, Sicily, Balkans (incl. Slovenia and Romania). < 900 m a.s.l. ........................................ 13

- Benelux, Germany, Poland, Czechia, Slovakia, Hungary. ........................................ 13

- Eastern Europe, Caucasus. ........................................ 16

10 Mesosoma shorter and narrower: ML / CS = 1.131 ± 0.023, MW / CS = 0.627 ± 0.010. Postocular distance larger: PoOc / CS = 0.408 ± 0.010. Longest hair on frontal lateral corner of pronotum shorter: PnHL / CS = 0.244 ± 0.023. Discriminant D7 (error 7.1% in 56 workers and 0.0% in 28 nest means of impurum western clade): 3.518 * HFL + 2.918 * ML + 6.601 * MW + 4.883 * dAN + 2.229 * PnHL - 4.404 * CS - 3.962 * SLd - 24.810 * POTCos - 5.711 * PEL - 11.518 * MSP - 5.995 * SPST - 9.220 * MC1TG + 22.761 * LAT + 0.109 * ALT - 215 < 0. ......................... T. impurum

- Mesosoma longer and wider: ML / CS = 1.164 ± 0.023, MW / CS = 0.643 ± 0.013. Postocular distance smaller: PoOc / CS = 0.397 ± 0.009. Longest hair on frontal lateral area of pronotum longer: PnHL / CS = 0.272 ± 0.021. D7 > 0 (error 4.5% in 132 workers and 1.5% in 65 nest means of T. alpestris, T. caespitum, and T. indocile in the region defined in 9a). ........................................... 14

11 Petiole wider, distance between outer margins of propodeal spines larger: PEW / CS = 0.334 ± 0.011, SPWI / CS = 0.303 ± 0.021. Petiole higher: PEH / CS = 0.356 ± 0.009. Longest hair on frontal lateral area of pronotum shorter: PnHL / CS = 0.248 ± 0.025. Distance between antennae fossae smaller: dAN / CS = 0.281 ± 0.006. Discriminant D8 (error 4.5% in 88 workers and 0.0% in 44 nest means of T. alpestris in the region defined in 9-11): 2.810 * ML + 5.130 * PPW + 1.876 * SPWI + 4.863 * PnOc + 1.182 * Ppss - 2.349 * Mpw - 2.908 * MW - 2.565 * SLd - 8.968 * POTCos - 1.265 * PnHL - 4.676 * MSP - 0.186 * ALT + 109 > 0. ... 12

- Petiole narrower, distance between outer margins of propodeal spines smaller: PEW / CS = 0.322 ± 0.011, SPWI / CS = 0.282 ± 0.017. Petiole lower: PEH / CS = 0.346 ± 0.009. Longest hair on frontolateral corner of pronotum larger: PnHL / CS = 0.276 ± 0.020. Distance between antennal fossae larger: dAN / CS = 0.288 ± 0.007. D8 < 0 (error 4.5% in 222 workers and 0.9% in 111 nest means of T. caespitum and T. indocile in the region defined in 9-11). ........................................... 13

12 Sculpture on dorsum of petiole and postpetiole often less developed; interspaces between the stronger rugae and rugulae frequently smooth or with faint microsculpture. Dorsum of postpetiole often with shiny areas. Rugae and rugulae on paramedian and lateral areas of dorsal postpetiole weaker and with more longitudinal orientation. Pigmentation of mesosoma varying from brown to black. Longest hair on frontolateral corner of pronotum shorter: PnHL / CS = 0.248 ± 0.023. Postpetiole wider: PPW / CS = 0.424 ± 0.011. Eye wider: EW / CS = 0.146 ± 0.004. Discriminant D9 (error 6.8% in 88 workers and 2.3% in 44 nest means in the region defined in 9b): 3.370 * ML + 5.764 * PPW + 11.408 * EYE + 4.184 * PEL + 4.097 * PPL + 3.508 * Ppss - 3.533 * PoOc - 6.001 * CW - 2.123 * SLd - 20.511 * POTCos - 3.151 * MPSP + 0.135 * ALT + 270 > 0. .................. T. alpestris

- Sculpture on dorsum of petiole and postpetiole often more developed; interspaces between stronger rugae and rugulae with fine transverse or reticulate microsculpture. Dorsum of postpetiole often rather dull; shiny areas can occur, but only on small patch on dorsomedian postpetiole. Rugae and rugulae on paramedian and lateral areas of dorsal postpetiole coarser and semicircular. Mesosoma in adult workers usually light to dark brown, never black. Longest hair on frontolateral corner of pronotum longer: PnHL / CS = 0.260 ± 0.026. Postpetiole narrower: PPW / CS = 0.411 ± 0.012. Eye narrower: EW / CS = 0.142 ± 0.004. D9 < 0 (error 5.2% in 96 workers and 2.1% in 48 nest means in T. impurum eastern clade). .................... T. impurum

13 Sculpture on dorsum of petiole and postpetiole often more developed; interspaces between stronger rugae and rugulae with fine transverse or reticulate microsculpture. Dorsum of postpetiole often rather dull; shiny areas can occur, but only on small patch on dorsomedian postpetiole. Rugae and rugulae on paramedian and lateral areas on dorsum of postpetiole coarser and semicircular. Mesosoma usually light to dark brown, never black. Distance between antennae fossae smaller: dAN / CS = 0.278 ± 0.006. Eye shorter: EL / CS = 0.189 ± 0.006. Discriminant D10 (error 3.1% in 96 workers and

- Sculpture on dorsum of petiole and postpetiole often less developed; interspaces between stronger rugae and rugulae frequently smooth or with only suggested microsculpture. Dorsum of postpetiole often with shiny areas. Rugae and rugulae on paramedian and lateral areas on dorsum of postpetiole weaker and with more longitudinal orientation. Pigmentation of mesosoma varying from brown to black. Distance between antennae fossae larger: dAN = 0.288 / CS ± 0.006. Eye longer: EL / CS = 0.196 ± 0.006. D10 < 0 (error 4.0% in 277 workers and 0.7% in 138 nest means of European *T. caespitum* eastern clade and European *T. indocile*). ..... 17

14 Maximum distance between outer margins of propodeal spines larger: SPWI / CS = 0.301 ± 0.017. Petiole and postpetiole higher: PEH / CS = 0.360 ± 0.010, PPH / CS = 0.373 ± 0.011. Discriminant D11 (error 1.9% in 54 workers and 0.0% in 277 workers and 0.7% in 138 nest means of European *T. caespitum* eastern clade and European *T. indocile*). ..... 17

15 Mainland France (excl. Pyrenees), British Channel Islands. .......................................................... 17

16 Caucasus only. Distance between frontal carinae and antennal fossae smaller: FL / CS = 0.382 ± 0.008, dAN / CS = 0.283 ± 0.005. Distance between propodeal stigma and dorsocaudal end of propodeal lobe smaller: PLST / CS = 0.252 ± 0.008. Discriminant D12 (error 0.0% in 32 workers): 4.043 * SPWI + 5.776 * CL + 4.686 * PPH + 1.199 * Pps - 11.585 * MCTG - 3.593 * PwW - 3.318 * FL - 4.665 * PreOc - 1.017 * PnHL - 6.289 * MPSP - 3.502 * PLST + 14.909 * LAT + 0.227 * ALT - 1870 > 0. > 1000 m a.s.l. ... *T. caespitum* sp.n.

- Distance between frontal carinae and antennal fossae larger: FL / CS = 0.391 ± 0.008, dAN / CS = 0.289 ± 0.006. Distance between propodeal stigma and dorsocaudal end of propodeal lobe larger: CL / CS = 0.262 ± 0.008. D12 < 0 (error 0.8% in 122 workers and 0.0% in 37 nest means of *T. caespitum* and *T. indocile* in the region defined in 9-16). .......................................................... 17

17 Hind femur and scape longer: HFL / CS = 0.826 ± 0.023, SLd / CS = 0.779 ± 0.014. Mesosoma longer and metapleuron wider: ML / CS = 1.179 ± 0.021, MtpW / CS = 0.504 ± 0.012. Postpetiole longer: PPL / CS = 0.169 ± 0.008. Longest hair on frontolateral corner of pronotum longer: PnHL / CS = 0.279 ± 0.020. Larger: CS = 770 ± 47. Sculpture on head and mesosoma developed. Discriminant D13 (error 3.3% in 242 workers and 0.8% in 121 nest means of *T. caespitum* eastern clade): 4.272 * CS + 3.883 * CL + 7.783 * dAN + 4.929 * PEH + 2.350 * Pps + 4.209 * MPSP + 8.733 * MCTG - 6.570 * MtpW - 7.246 * PoOc - 7.085 * FL - 3.367 * RTI - 3.459 * SLd - 10.625 * PPL + 247 < 0. ........................................... *T. caespitum* eastern clade and European *T. indocile*). ..... 17

18 Head longer: CL / CW = 1.012 ± 0.007. Posttemporal distance larger: PoOc / CS = 0.405 ± 0.010. Distance between antennal fossae smaller: dAN / CS = 0.278 ± 0.009. Eye smaller: EL / CS = 0.195 ± 0.008. EW / CS = 0.145 ± 0.004. Propodeal spines shorter: SPST / CS = 0.185 ± 0.007. Discriminant D14 (error 23.1% in 52 workers, and 4.2% in 24 *T. caespitum* nest means from Iberia): 6.532 * CW + 10.326 * SPST + 8.118 * PLSP - 17.560 * PoOc - 19.893 * PreOc + 1195 < 0. ... *T. caespitum* eastern clade and European *T. indocile*). ..... 17

Key to males of the *Tetramorium caespitum* complex

This dichotomous key considers Europe (incl. Caucasus and Ural) and Kyrgyzstan. The male genital morphology remains unknown for *Tetramorium fusciclava* stat.n. and *T. breviscapus* sp.n., which are endemic to Italy and the Balkans, respectively. Figures S3 - 5 show typical examples of paramere structure; for further examples, see Figure S1; "n" is always the number of nests investigated.

1 Ventral view: one or two corners visible on ventral paramere lobe (Fig. S3a - d, arrows). Posterior view: no distinct emargination between paramere lobes (Fig. S4a - d, A arrows); *caespitum*-like form. ..... 2

- Ventral view: no corner but rounded ends on ventral paramere lobe (Fig. S3e - h, arrows). Anterior view: distinct division of ventral and dorsal lobe by
deep emargination between paramere lobes (Fig. S4e - h, A arrows); *imparum*-like form.  

2 Ventro-posterior view: ventral paramere lobe with two corners, > 87 µm apart (101 ± 16; n = 8) (here in posterior view: Fig. S4d, B arrow). Often in anthropogenically influenced, vegetation-free, and even concreted habitats. In Europe nesting < 1000 m a.s.l. ................................. T. immigrans stat.n.

- Ventro-posterior view: ventral paramere lobe has one corner or two corners, < 87 µm apart (here in posterior view: Fig. S4a - c, B arrow). All regions and habitats. ................................................................. 3

3 Posterior view: two sharp corners on ventral paramere lobe (Fig. S4c, B arrow, n = 5). Corner between ventral and dorsal lobe often missing or small and positioned more ventral (Fig. S4c, C arrow). In Europe rare and < 51° N. ............................. T. indocile

- Posterior view: usually one corner on ventral paramere lobe (Fig. S4a - b, B arrows, n = 41). Corner between ventral and dorsal lobe often large and positioned more median (Fig. S4a, b, A arrows), but sometimes missing or small. .................. T. caespitum (whole Europe) and ..................... T. hungaricum (Pannonian zone, Balkans, Eastern Europe)

4 Posterior view: sharp corner at end of ventral paramere lobe (Fig. S4f, B arrow, n = 2). Caucasus only. Nesting > 1000 m a.s.l. .................. T. caucasicum sp.n.

- Posterior view: rounded margin at end of ventral paramere lobe (Fig. S4e, g, h, B arrows). .................. 5

5 Lateral view: paramere length < 991 µm (n = 11). Posterior view: dorsal and ventral paramere lobes often longer and narrower (Fig. S4e). Dorsal view: dorsal paramere lobe often longer and sharp-ended (Fig. S5a, A arrow). Nesting > 900 m a.s.l. ... T. alpeste

- Lateral view: paramere length > 1014 µm (n = 21). Posterior view: dorsal and ventral paramere lobes often shorter and wider (Fig. S4g, h). Dorsal view: dorsal paramere often shorter and with round end (Fig. S5b, c, A arrow). Nesting < 2000 m a.s.l. .... 6

6 Dorsal or posterior view: ventral paramere lobe with distinct corner between lobe top and emargination with dorsal paramere lobe (Fig. S4g, C arrow; Fig. S5b, B arrow, n = 3). Pannonian zone, Balkans, Eastern Europe, Central Asia. .... T. staerckeii sp.rev.

- Dorsal or posterior view: ventral paramere lobe without corner between lobe top and emargination with dorsal paramere lobe (Fig. S4h, C arrow; Fig. S5c, B arrow, n = 18). Iberia, Western Europe, Central Europe, Balkans, Anatolia. .................. T. impurum

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