

Hybridization between introduced *Torymus sinensis* and indigenous *T. beneficus*, parasitoids of *Dryocosmus kuriphilus*

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Hybridization between introduced parasitoid *Torymus sinensis* and indigenous congener *T. beneficus* has attracted attention since *T. sinensis* was first introduced and released to control *Dryocosmus kuriphilus* in chestnut orchards in Japan because the biological control would fail if the hybrids were sterile. Such apprehension disappeared as the damage caused by *D. kuriphilus* decreased. Since the initial introduction of *T. sinensis*, however, morphologically intermediate individuals between the two *Torymus* species have appeared in the field. This has led to investigation of the hybridization in the form of examining the non-target effect of biological control in recent years. Molecular markers have been used for hybridization surveys in the field not only because *T. sinensis* and *T. beneficus* are exceedingly similar morphologically but also because at least two emergence types (early- and late-spring) are recognized in *T. beneficus*, for which emergence periods are not defined clearly. Our surveys show that the hybridization between *T. sinensis* and early-spring *T. beneficus* occurred at low frequency (ca. 1%). On the other hand, the hybrid F₁s between *T. sinensis* and late-spring *T. beneficus* were detected at higher frequency (ca. 20%). Furthermore, individuals with the F₁ genotype were detected even after *T. sinensis* displaced *T. beneficus* and were the dominant species, which suggests that hybrids (including descendants of F₁) interbreed successively with *T. sinensis*.

References

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- Yara, K. (2006) Identification of *Torymus sinensis* and *T. beneficus* (Hymenoptera: Torymidae), introduced and indigenous parasitoids of the chestnut gall wasp *Dryocosmus kuriphilus* (Hymenoptera: Cynipidae), using the ribosomal ITS2 region. *Biol. Control* 36: 15–21.
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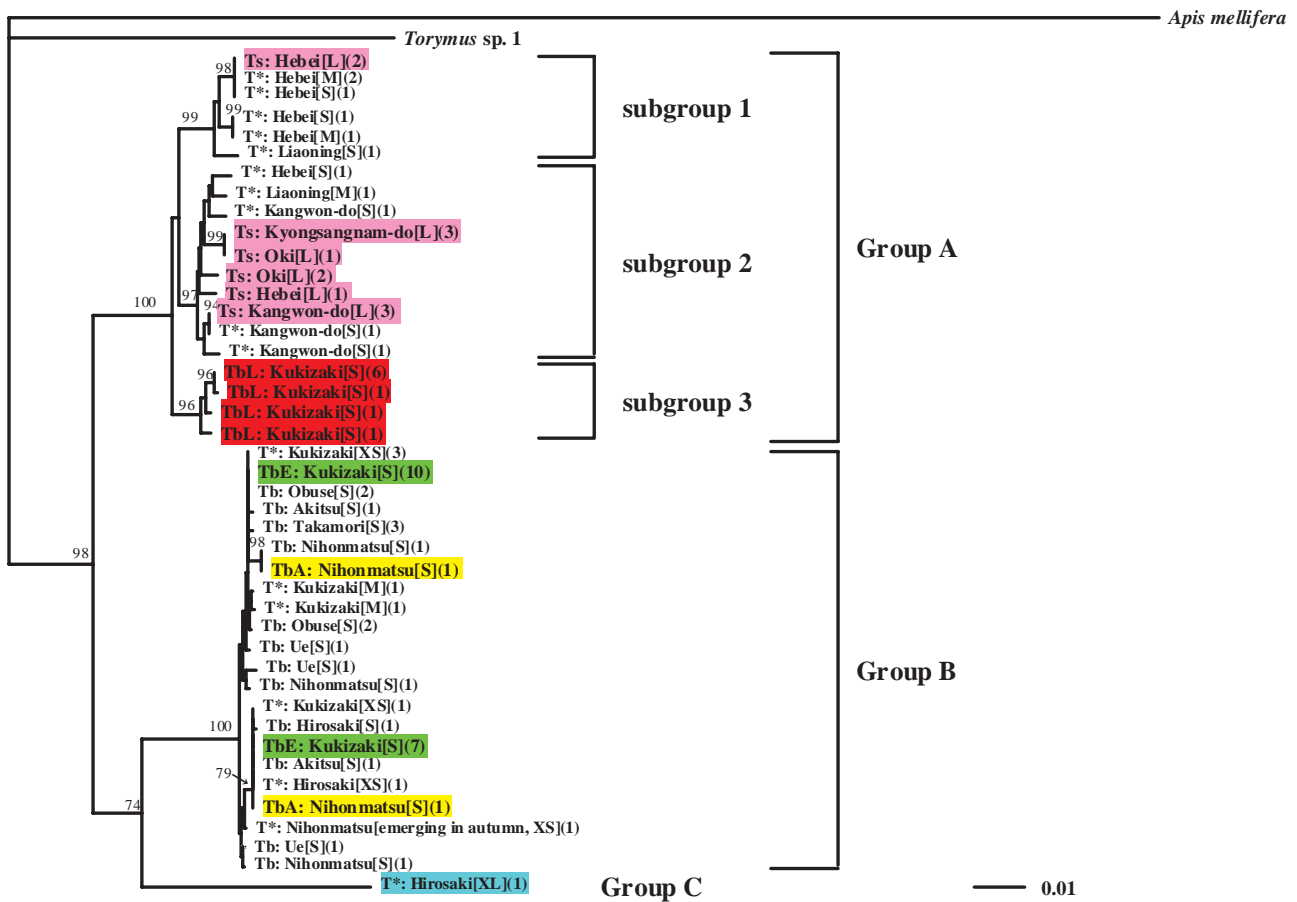
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Withered galls of *Dryocosmus kuriphilus* at the research site of Yara *et al.* (2007), Obuse, Nagano Prefecture on Mar. 6, 2006.



A chestnut orchard in Obuse, Nagano Prefecture on Mar. 6, 2006. This is another research site of Yara *et al.* (2007).



Phylogenetic tree inferred from 1129 bp sequences of the mitochondrial COI gene of *Torymus* spp. using the neighbor-joining method. *Apis mellifera* and *Torymus* sp. 1 were used as outgroups. The abbreviations for each species and strain are as follows Ts: *Torymus sinensis* (highlighted in pink), TbE: early-spring strain of *T. beneficus* (highlighted in green), TbL: late-spring strain of *T. beneficus* (highlighted in red), TbA: autumn strain of *T. beneficus* (highlighted in yellow), Tb: *T. beneficus* emerging in spring (strain unidentified), T*: unidentified *Torymus*. One unidentified *Torymus* from Hirosaki with the XL- category O/T ratio (ratio of the ovipositor sheath length to the thorax length, a morphological index to *Torymus* spp.) is highlighted in blue. O/T categories are indicated in square brackets. The numbers of specimens are given in parentheses. Bootstrap probabilities (500 replicates) are provided on each branch when they are greater than 70%. The scale of distances is shown under the tree (Yara, 2004).