**Supplementary Appendix A.** Materials and methods in the present study.Citations either in the reference section of the main article or are listed at the end of this appendix.

**Taxon sampling**

All *Eulecanium giganteum* and *E. kuwanai* specimens in this study were obtained from orchards, ornamental plants, and street trees from April 2011 to May 2013 in China. The *Eulecanium* species were collected from 19 sites located in 14 provinces. Their geographical distribution is shown in Fig. 2. Detailed information about locations, host plants, and collection dates are presented in Supplementary Appendix B and C. All adult females were initially classified according to dorsum morphology (wrinkled or smooth) in the post-reproductive stage. Reproductive-stage individuals and nymphs were not classified because identification could not be determined.

**DNA extraction, polymerase chain reaction (PCR) amplification, and sequencing**

The samples were placed in 95% ethanol and stored at -20 °C until DNA extraction. A total of 200 samples were used for molecular identification. Molecular identification has rarely been used in *Eulecanium* species, and only two COI sequences from *E. kunoense* were found in the GenBank database. We initially attempted to extract DNA from a whole adult female individual, but almost all trials failed to obtain sequences of the targeted region, as indicated by a mixed DNA sequencing signal (multiple peaks). Universal primers and non-target DNA interference by endoparasites, including some parasitoid wasps and moths, complicated the use of this approach. The adult Coccoidea females ranged from 1.0 to 18 mm in length; *E. giganteum* can grow up to approximately 18 mm in length (Ben-Dov and Hodgson 1997), providing enough space and nutrition for its parasitoids, *Beijinga utila* Yang (Lepidoptera: Heliodinidae) and *Blastothrix sericae* (Dalman) (Hymenoptera: Encyrtidae)*. Beijinga utila* and *Blastothrix sericae* are important parasitoids of *E. giganteum* with high parasitism rates (means of 37.8% and 39.8%, respectively) (Shen and Xie 1990; Liu and Liu 2005). Before DNA extraction, all individuals were examined for the presence of endoparasites, which were removed when detected. Genomic DNA was extracted directly from nymph individuals. For adult females, genomic DNA was extracted from a single egg or part of the derm. Total genomic DNA was isolated using the DNeasy Blood and Tissue Kit (Qiagen GmbH, Hilden, Germany) following the manufacturer’s instructions. After DNA extraction, some young adult females were slide mounted and identified according to their morphological characteristics and taxonomic keys (Tang 1991; Xie 1998; Wang 2001).

The barcode region of COI and the D2-D3 expansion segments of the 28S ribosomal gene were amplified in this study. For the COI gene, we used primers C1-1554F and C1-2342R (Deng *et al.* 2012) because of their good performance with Coccidae DNA; the PCR reaction volume and program were according to Deng *et al.* (2012). When amplifying the 28S ribosomal gene, we used the primers 28sF3633 (5'-TACCGTGAGGGAAAGTTGAAA-3') and 28b (Whiting *et al*. 1997). Polymerase chain reactions were performed using MightyAmp DNA polymerase version 2 (TaKaRa, Dalian, China). The 50-μL reaction volume included 25 μL 2× Buffer (Mg2+, dNTP plus), 10 pmol of each primer, 15 μL ddH2O, 1 μL MightyAmp DNA polymerase, and 5 μL DNA template. Polymerase chain reaction thermocycling of 28S rDNA was performed under the following conditions: an initial step of two minutes at 95 °C, then 35 cycles of 50 seconds at 94 °C, one minute at 60 °C, one minute at 72 °C, followed by five minutes at 72 °C. All products were visualised on a 1% agarose gel, and the most intense products were sequenced using BigDye v. 3.1 on the ABI3730xl DNA analyser (Applied Biosystems, Carlsbad, California, United States of America).

**Sequencing analyses**

The sequences were aligned using ClustalW in Bioedit version 7.05 (Hall 1999) using default parameters. Genetic distances were calculated with the K2P distance model (Kimura 1980), and neighbour-joining (NJ) trees (Saitou and Nei 1987) of the COI and 28S genes were reconstructed employing 1000 bootstrap replications in MEGA4 (Tamura *et al.* 2007). *Eulecanium cerasorum* (Cockerell) collected from Shanghai on *Acer buergerianum* Miquel (Sapindaceae) was selected as an outgroup. The “best close match” method was used to evaluate the accuracy of species assignments based on the barcode sequences in TaxonDNA (Meier *et al*. 2006). TaxonDNA is an effective tool to assess identification rates for DNA barcodes (Meier *et al*. 2006). This program sets a threshold value to test barcoding efficiencies and yields more perspicuous results. The threshold value is set according to a frequency distribution of all intraspecific pairwise distances. Below the threshold value, 95% of all intraspecific pairwise distances are identified (Meier *et al*. 2006). Queries with a barcode match below the threshold value are considered an identification success.

**Comparison of distribution and host ranges**

The distribution and host ranges are shown in Table 1. All host plant and distribution information of these two species were collected from the literature (Shinji 1935; Xie 1998; Wang 2001; Wang *et al.* 2013) and from our field surveys.

**References**

Hall, T.A. 1999. BioEdit: a user-friendly biological sequence alignment editor and analysis program for Windows 95/98/NT. Proceedings of the Nucleic Acids Symposium Series, **41**: 95–98.

Kimura, M. 1980. A simple method for estimating evolutionary rate of base substitutions through comparative studies of nucleotide sequences. Journal of Molecular Evolution, **16**: 111–120.

Liu, G.F. and Liu, Y.P. 2005. The biological characteristics and prevention of scale insects. Chinese Agricultural Science Bulletin, **21**: 349–351.

Meier, R., Shiyang, K., Vaidya, G., and Ng, P.K.L. 2006. DNA barcoding and taxonomy in Diptera: a tale of high intraspecific variability and low identification success. Systematic Biology, **55**: 715–728.

Saitou, N. and Nei, M. 1987. The neighbor-joining method: a new method for reconstructing phylogenetic trees. Molecular Biology and Evolution, **4**: 406–425.

Shen, S.Y. and Xie, X.X. 1990. Study on the bionomics of *Beijinga utila* Yang, an important natural enemy of scale insects belonging to *Eulecanium*. Scientia Silvae Sinicae, **26**: 30–38.

Tamura, K., Dudley, J., Nei, M., and Kumar, S. 2007. MEGA4: molecular evolutionary genetics analysis (MEGA) software version 4.0. Molecular Biology and Evolution, **24**: 1596–1599.

Wang, L., Wang, D.Y., and Yu, J.N. 2013. Preliminary prediction of potential geographic distribution areas for *Eulecanium giganteum* in Xinjiang using GARP modeling system. Xinjiang Agricultural Science, **50**: 2246–2253.

Whiting, M.F., Carpenter, J.C., Wheeler, Q.D., and Wheeler, W.C. 1997. The Strepsiptera problem: phylogeny of the holometabolous insect orders inferred from 18s and 28s ribosomal DNA sequences and morphology. Systematic Biology, **46**: 1–68.