

On some approaches for estimating local species richness of parasitoid Hymenoptera

О некоторых подходах к оценке локального видового богатства паразитических перепончатокрылых (Hymenoptera)

V.E. Gokhman

В.Е. Гохман

Botanical Garden, Moscow State University, Moscow 119234 Russia. E-mail: vegokhman@hotmail.com.
Ботанический сад Московского государственного университета, Москва 119234 Россия.

Key words: hymenopterous parasitoids, local species richness, taxonomic revision, molecular characters, DNA barcoding, chromosomes, karyotypes, faunistic survey.

Ключевые слова: паразитические перепончатокрылые, локальное видовое богатство, таксономическая ревизия, молекулярно-генетические признаки, ДНК-баркодинг, хромосомы, кариотипы, фаунистический обзор.

Abstract. Main approaches for estimating local species richness of parasitoid Hymenoptera, i.e. methods of classical taxonomy, certain modern techniques as well as surveys of regional faunas are discussed and compared. Additions of newly recorded species to local inventories due to faunistic studies usually exceed those resulting from taxonomic revisions either fully based on morphological characters or also using chromosomal, molecular and/or similar ones. Nevertheless, the use of DNA barcoding and other modern techniques will undoubtedly revolutionize both local and global studies of parasitoid faunas.

Резюме. В работе обсуждаются и сравниваются основные подходы к оценке локального видового богатства паразитических перепончатокрылых: методы классической таксономии, различные современные методики, а также обзоры региональных фаун. Пополнение локальных списков вновь зарегистрированными видами за счет фаунистических исследований обычно превышает таковое, являющееся результатом таксономических ревизий, которые целиком основаны на морфологических особенностях, а также используют наряду с этим хромосомные, молекулярно-генетические и/или им подобные признаки. Тем не менее, использование ДНК-баркодинга и других современных методов, несомненно, революционизирует как локальные, так и глобальные исследования фаун паразитоидов.

Introduction

Parasitic wasps are one of the most diverse, taxonomically complicated and economically important groups of insects, which currently includes far more than 70 thousand described species [Rasnitsyn, 1980; Aguiar et al., 2013]. However, various estimates of local species richness of parasitoid Hymenoptera can strongly differ in terms of the number of recorded species both in the temperate zone and in the tropics [Rodriguez et al., 2013; Tselikh, 2014]. Moreover, these estimates are often based on external morphology [Quicke, 1997] de-

spite an increasing advent of the so-called modern methods in systematics, i.e. molecular, chromosomal and analogous approaches [Heraty, 2003; Gokhman, 2009].

As far as newly described species are concerned, additions of these taxa can result from taxonomic studies, including generic revisions and descriptions of separate species. In turn, these works are either entirely based on morphology or can include data obtained by modern techniques. On the other hand, extensive research using contemporary methods in systematics (e.g. DNA barcoding) as well as detailed surveys of regional faunas also can substantially increase the number of recorded species [Quicke, 2015]. In the present paper, I am going to review and compare these sources of local species estimates in more detail.

This paper is dedicated to the 70th anniversary of an outstanding Russian entomologist, Professor Arkadiy S. Lelej, who has made an enormous contribution to the taxonomic and faunistic study of the order Hymenoptera in many territories including the Russian Far East [Lelej, 2012].

Methods of classical taxonomy

Taxonomic treatments can change the existing species estimates in a number of ways. For example, my restricted experience of worldwide taxonomic revisions of a few relatively small parasitoid genera shows that most of these studies can only moderately increase, if at all, the number of known species [Gokhman, 1994; Baur et al., 2014]. However, a revision of another moderate-sized genus, *Trachyarus* Thomson (Ichneumonidae), has approximately doubled the number of its species in the Palaearctic region [Gokhman, 2007]. Nevertheless, many of them were mostly or entirely restricted to less studied territories, such as the mountain ranges of Central Europe or the Russian Far East, from which many other parasitoid species were described

during the last few decades (see e.g. [Kostjukov, 1995; Belokobylskij, Tobias, 2007]). In addition, Elzinga et al. [2011] showed that molecular data obtained from individuals of several *Trachyarus* species did not confirm morphology-based species borderlines, although no formal taxonomic change was made since that publication. The data presented in this chapter, together with many analogous studies, therefore suggest that generic revisions and descriptions of separate species usually lead to a relatively slow increase in the amount of local species records.

At first glance, this continuous accumulation of species numbers due to taxonomic treatments must be the predominating source of addition to local species lists, because, at least in theory, only these studies can adequately and reliably describe the existing biodiversity. However, in reality we usually observe the reverse pattern (at least in the better-studied temperate zone), i.e. a strong increase in the number of previously described species due to faunistic research [Quicke, 2015], as opposed to any recent taxonomic study. This can be explained by the fact that revision of a poorly studied but potentially speciose taxon is usually very difficult, time-consuming and subject to obvious flaws, and therefore studies of that kind are relatively rare (but see e.g. [Kostjukov, 1995]).

Studies using modern techniques

Since «host races» or «strains» are widespread in parasitoid Hymenoptera [Clarke, Walter, 1995], it is particularly important to know whether these «races» represent either subpopulations of the same species or different, although often cryptic, species. To distinguish between these possibilities, environmentally independent characters (e.g. DNA and/or karyotype structure) must be studied. For example, a few years ago [Baur et al., 2014] we were able to describe a cosmopolitan synanthropic species, *Anisopteromalus quinarius* Gokhman et Baur, 2014 (Pteromalidae), which was initially differentiated on the basis of karyotypic study from a presumably well-known and also cosmopolitan *A. calandrae* (Howard, 1881) with a similar biology. Moreover, as soon as the presence of the two separate species was established, many interspecific differences in morphology, DNA structure, life-history strategies etc. immediately began to come to light (reviewed in [Baur et al., 2014]). Furthermore, an analogous situation was later revealed in *Lariophagus distinguendus* (Förster, 1841) complex from the same family, in which two separate species were initially detected on the basis of molecular study [König et al., 2015], also supported by differences in the chromosome number and other karyotypic features of those parasitoids [Gokhman, 2015]. Moreover, since chromosomal characters can be treated as morphological in a broad sense [Gokhman, 2009], the latter data are crucial because a thorough study of external morphology failed to distinguish between different species of the *L. distinguendus* complex

[König et al., 2015]. In this case, karyotypic information therefore provided the first direct morphological support of the presence of cryptic species. It is also worth noting that even crossing experiments are not always able to reveal the true nature of the taxa under analysis, because, for example, members of some populations that belong to different species of the *L. distinguendus* complex can produce hybrid offspring under certain circumstances. Nevertheless, hybrid individuals will be immediately recognized due to their intermediate chromosome number and specific karyotype structure.

Both above-mentioned complexes of cryptic species, i.e. *A. calandrae* and *A. quinarius* as well as *L. distinguendus* s.l., were supposed to have relatively broad host ranges. However, a detailed investigation has shown that each of these complexes contained different species, which preferred to attack either beetles of the family Dryophthoridae and a few similar taxa, or members of the family Anobiidae [Baur et al., 2014; König et al., 2015]. Recently, a rapidly increasing amount of analogous papers mainly based on the results of molecular research [Zhang et al., 2011; Chesters et al., 2012; Derocles et al., 2016] also demonstrates that many examined parasitoid species with wide host ranges are in fact complexes of cryptic species. These results suggest that situations of this kind can be far more widespread than it was supposed before. This is especially true for endoparasitoids and/or tropical groups which generally tend to have narrower host ranges [Quicke, 2015]. Specifically, DNA barcoding along with information on bionomics of different populations of apparently the same polyphagous morphospecies, *Apanteles leucostigmus* (Ashmead, 1900) (Braconidae), from a particular area of Costa Rica showed that their studied individuals actually belonged to at least 36 putatively undescribed monophagous or strictly oligophagous species [Smith et al., 2008]. Furthermore, another molecular and bionomic study [Kenyon et al., 2015] demonstrated that each of the three examined morphospecies of the genus *Horismenus* Walker (Eulophidae) in the southern USA and Mexico also harboured at least one cryptic species.

An approach based on extensive molecular research and subsequent morphological description of taxa revealed during that study (the main components of the so-called turbo-taxonomy [Riedel et al., 2013]; also see below) therefore can substantially increase the number of described species, especially in tropical regions, which are heavily understudied in this respect despite their high biodiversity. For example, 176 and 186 new species of the braconid genera *Aleiodes* Wesmael and *Apanteles* Förster were respectively described during two recent studies of that kind [Butcher et al., 2012; Fernández-Triana et al., 2014]. On the other hand, a relatively low sampling effort followed by a DNA barcoding study has recently led to the discovery of 177 likely undescribed morphospecies of tropical orthocentrine Ichneumonidae [Veijalainen et al., 2012], thus putting into doubt the presumed prevalence of ichneumonid species in the temperate zone. Nevertheless, molecular research,

together with morphological and bionomic information, can reveal and delimit new species within taxonomically difficult groups inhabiting temperate regions as well, as in the *Eupelmus urozonus* Dalman, 1820 complex (Eupelmidae), in which eleven new species were described [Al khatib et al., 2014].

DNA studies also help establishing identity of conspecific individuals collected in different geographical areas. This is also of considerable significance because situations of that kind seem to be relatively frequent. For example, Petrović et al. [2013] discovered that an effective aphid parasitoid, *Lysiphlebus orientalis* Starý et Rakhshani, 2010 (Braconidae), which has been recently described from northwest China, was also found in Europe, presumably due to an accidental introduction; the taxonomic identity of European specimens of *L. orientalis* was confirmed by DNA barcoding. What is perhaps more important, molecular data can help matching males and females or different forms of the same parasitoid; however, in these cases the overall number of recorded species can slightly decrease. For instance, both morphological and molecular data were successfully used to match males and females of different *Philotrypesis* Förster species (Pteromalidae) [Zhou et al., 2012]. Furthermore, molecular evidence confirmed that both *Scambus planatus* (Hartig, 1838) and *S. ventricosus* (Tschek, 1871) (Ichneumonidae) were in fact seasonal forms of *S. calobatus* (Gravenhorst, 1829) [Shaw et al., 2011]. A similar study has also shown that morphologically different specimens from a few locations in North Finland belonged to the same newly described species, *Meteorus acerbiavorus* Belokobylskij, Stigenberg et Vikberg, 2011 (Braconidae) [Stigenberg et al., 2011].

Surveys of regional faunas

Interestingly, both above-mentioned complexes of cryptic species of the family Pteromalidae found in the genera *Anisopteromalus* Ruschka and *Lariophagus* Crawford, represent cosmopolitan synanthropic taxa. In each case, additional species could be either newly described or restored from synonyms. This situation indicates our insufficient ability to recognize cryptic taxa even within apparently well-known groups of parasitoids. Moreover, both *Anisopteromalus* and *Lariophagus* are absent from the recent catalogue of insects of the Russian Far East [Tselikh, 2012] which is supposed to have the best studied Hymenoptera fauna of Russia [Lelej et al., 2015] despite worldwide distribution and synanthropic way of life of the most widespread members of these genera. Nevertheless, two *Lariophagus* species (but not *L. distinguendus* itself) were included into the subsequent list of Pteromalidae of the above-mentioned territory [Tselikh, 2014]. Furthermore, only 91 species that belonged to 56 genera of Pteromalidae were recorded in the preceding study [Tselikh, 2012]. Surprisingly enough, as much as 105 genera and 260 species of this family were found in the Russian Far East just two years later [Tselikh, 2014]. Moreover,

about 160 species from this list were recorded for the first time in Russia. However, only nine species were already described or going to be described as new to science in the latter study. An analogous situation was reported by Fernández-Triana [2010] who added 50% species to the list of the subfamily Microgastrinae (Braconidae) of Canada and Alaska which now contains 225 species; again, only eight new species were described. Furthermore, several independent estimates suggested that the real number of species in the latter case would be at least doubled in the future [Fernández-Triana, 2010]. Nevertheless, similar estimates indicate that the global species richness of this subfamily (which, of course, includes tropical regions) is probably 8 to 20 times more than the current number of described species [Rodríguez et al., 2013]. Anyway, curves displaying accumulation of the number of species based on DNA barcoding (or, to be precise, the number of MOTUs, i.e. molecular operational taxonomic units) of Microgastrinae versus an increase in the number of sampled specimens show no sign of saturation for all listed regions, both tropical and temperate [Smith et al., 2013]. These data demonstrate that regional studies of parasitoid faunas (as opposed to taxonomic descriptions) remain the principal source of newly recorded species within local inventories, at least in the temperate zone. On the other hand, considerable amounts of originally described species of parasitic wasps also can be included into regional surveys of certain temperate faunas in some exceptional cases (see e.g. [Kostjukov, 1995; Belokobylskij, Tobias, 2007]).

Conclusion

All accumulated information suggests that amounts of newly recorded species added to local inventories due to faunistic studies usually exceed those resulting from taxonomic revisions either fully based on morphological characters or also using chromosomal, molecular and/or similar ones. Nevertheless, the use of DNA barcoding and other modern techniques will undoubtedly revolutionize both local and global studies of parasitoid faunas in the future due to high resolution and reliability of these methods, although these techniques do have certain restrictions [Klopfstein et al., 2016]. Turbo-taxonomy can therefore rapidly increase the number of species discovered in the tropics, but morphologically distinct new species still can be revealed within temperate faunas as well (see e.g. [Baur, 2015]).

Acknowledgements

I am very grateful to Prof. Alexandr P. Rasnitsyn (Paleontological Institute, Russian Academy of Sciences, Moscow, Russia) and Dr. Sergey A. Belokobylskij (Zoological Institute, Russian Academy of Sciences, Saint Petersburg, Russia) for providing useful discussion. The present study was partly supported by a research grant from the Russian Foundation for Basic Research (No. 15-04-07709).

References

- Aguiar A.P., Deans A.R., Engel M.S., Forshage M., Huber J.T., Jennings J.T., Johnson N.F., Lelej A.S., Longino J.T., Lohrmann V., Mikó I., Ohl M., Rasmussen C., Taeger A., Yu D.S.K. 2013. Order Hymenoptera // *Zootaxa*. Vol.3703. No.1. P.51–62.
- Al khatib F., Fusu L., Cruaud A., Gibson G., Borowiec N., Rasplus J.-Y., Ris N., Delvare G. 2014. An integrative approach to species discrimination in the *Eupelmus urozonus* complex (Hymenoptera, Eupelmidae), with the description of 11 new species from the Western Palaearctic // *Systematic Entomology*. Vol.39. P.806–862.
- Baur H. 2015. Pushing the limits — two new species of *Pteromalus* (Hymenoptera, Chalcidoidea, Pteromalidae) from Central Europe with remarkable morphology // *ZooKeys*. Vol.514. P.43–72.
- Baur H., Kranz-Baltensperger Y., Cruaud A., Rasplus J.-Y., Timokhov A.V., Gokhman V.E. 2014. Morphometric analysis and taxonomic revision of *Anisopteromalus* Ruschka (Hymenoptera: Chalcidoidea: Pteromalidae) — an integrative approach // *Systematic Entomology*. Vol.39. No.4. P.691–709.
- Belokobyl'skij S.A., Tobias V.I. 2007. [Subfamily Alysiinae (Braconidae). Group of genera related to *Aspilota*] // Lelej A.S. (ed.): *Opređelitel' nasekomykh Dal'nego Vostoka Rossii*. Vol.4. Pt.5. Vladivostok: Dal'nauka. P.9–133. [In Russian]
- Butcher B.A., Smith M.A., Sharkey M.J., Quicke D.L.J. 2012. A turbo-taxonomic study of Thai *Aleiodes* (*Aleiodes*) and *Aleiodes* (*Arcalaiodes*) (Hymenoptera: Braconidae: Rogadinae) based largely on COI barcoded specimens, with rapid descriptions of 179 new species // *Zootaxa*. Vol.3457. P.1–232.
- Chesters D., Wang Y., Yu F., Bai M., Zhang T.-X., Hu H.-Y., Zhu C.-D., Li C.-D., Zhang Y.-Z. 2012. The integrative taxonomic approach reveals host specific species in an encyrtid parasitoid species complex // *PLOS ONE*. Vol.7. No.5. e37655.
- Clarke A.R., Walter G.H. 1995. «Strains» and the classical biological control of insect pests // *Canadian Journal of Zoology*. Vol.73. P.1777–1790.
- Derocles S.A.P., Plantegenest M., Rasplus J.-Y., Marie A., Evans D.M., Lunt D.H., Le Ralec A. 2016. Are generalist Aphidiinae (Hym. Braconidae) mostly cryptic species complexes? // *Systematic Entomology*. Early View. DOI: 10.1111/syen.12160
- Elzinga J.A., Zwakhals K., Mappes J., Grapputo A. 2011. The parasitoid species complex associated with sexual and parthenogenetic *Naryciinae* (Lepidoptera: Psychidae): Integrating ecological and molecular analyses // *European Journal of Entomology*. Vol.108. P.635–650.
- Fernández-Triana J.L. 2010. Eight new species and an annotated checklist of Microgastrinae (Hymenoptera, Braconidae) from Canada and Alaska // *ZooKeys*. Vol.63. P.1–53.
- Fernández-Triana J.L., Whitfield J.B., Rodriguez J.J., Smith M.A., Janzen D.H., Hallwachs W.D., Hajibabaei M., Burns J.M., Solis M.A., Brown J., Cardinal S., Goulet H., Hebert P.D.N. 2014. Review of *Apanteles sensu stricto* (Hymenoptera, Braconidae, Microgastrinae) from Area de Conservación Guanacaste, northwestern Costa Rica, with keys to all described species from Mesoamerica // *ZooKeys*. Vol.383. P.1–565.
- Gokhman V.E. 1994. [Ichneumon flies of the genus *Baeosemus* (Hymenoptera, Ichneumonidae)] // *Zoologicheskij Zhurnal*. Vol.73. No.6. P.52–60. [In Russian]
- Gokhman V.E. 2007. Revision of the genus *Trachyarus* Thomson (Insecta, Hymenoptera, Ichneumonidae, Alomyini) // *Spixiana*. Vol.30. No.1. P.65–83.
- Gokhman V.E. 2009. *Karyotypes of parasitic Hymenoptera*. Dordrecht: Springer Science + Business Media B.V. XIII + 183 p.
- Gokhman V.E. 2015. Chromosomal analysis: an effective research tool in phylogenetics and taxonomy of parasitoid Hymenoptera // *Caucasian Entomological Bulletin*. Vol.11. No.1. P.71–73.
- Heraty J.M. 2003. Molecular systematics, Chalcidoidea and biological control // Ehler L.E., Sforza R., Mateille T. (eds): *Genetics, evolution and biological control*. Wallingford etc.: CABI Publishing. P.39–72.
- Kenyon S.G., Buerki S., Hansson C., Alvarez N., Benrey B. 2015. Uncovering cryptic parasitoid diversity in *Horismenus* (Chalcidoidea, Eulophidae) // *PLOS ONE*. Vol.10. No.9. e0136063.
- Klopfstein S., Kropf S., Baur H. 2016. *Wolbachia* endosymbionts distort DNA barcoding in the parasitoid wasp genus *Diplazon* (Hymenoptera: Ichneumonidae) // *Zoological Journal of the Linnean Society*. Early View. doi: 10.1111/zoj.12380
- Kostjukov V.V. 1995. [Subfamily Tetrastichinae (Eulophidae)] // Lehr P.A. (ed.): *Opređelitel' nasekomykh Dal'nego Vostoka Rossii*. Vol.4. Pt.2. Vladivostok: Dal'nauka. P.346–505. [In Russian]
- König K., Krimmer E., Brose S., Gantert C., Buschlüter I., König C., Klopfstein S., Wendt I., Baur H., Krogmann L., Steidle J.L.M. 2015. Does early learning drive ecological divergence during speciation processes in parasitoid wasps? // *Proceedings of the Royal Society*. Ser.B. Vol.282. 20141850.
- Lelej A.S. (ed.). 2012. [Annotated catalogue of insects of the Russian Far East]. Vol.1. Hymenoptera. Vladivostok: Dal'nauka. 635 p. [In Russian]
- Lelej A.S., Belokobyl'skij S.A., Kasparyan D.R., Proshchalykin M.Y. 2015. [Taxonomic diversity and distribution pattern of Hymenoptera from the Russian Far East] // *Evroaziatskii simposium po pereponchatokrylym nasekomym*. Tezisy dokladov. Nizhni Novgorod: Izdatel'stvo Nizhegorodskogo Universiteta. P.105–106. [In Russian]
- Petrović A., Mitrović M., Starý P., Petrović-Obradović O., Žikić V., Tomanović Ž., Vorbürger C. 2013. *Lysiphlebus orientalis* (Hymenoptera, Braconidae), a new invasive aphid parasitoid in Europe — evidence from molecular markers // *Bulletin of Entomological Research*. Vol.103. P.451–457.
- Quicke D.L.J. 1997. *Parasitic wasps*. London: Chapman & Hall. XVII + 470 p.
- Quicke D.L.J. 2015. *The braconid and ichneumonid parasitoid wasps: biology, systematics, evolution and ecology*. Chichester: John Wiley & Sons, Ltd. XV + 681 p.
- Rasnitsyn A.P. 1980. [Origin and evolution of hymenopterous insects] // *Trudy Paleontologicheskogo Instituta AN SSSR*. Vol.174. Moscow: Nauka. P.1–192. [In Russian]
- Riedel A., Sagata K., Suhardjono Y.R., Tänzler R., Balke M. 2013. Integrative taxonomy on the fast track — towards more sustainability in biodiversity research // *Frontiers in Zoology*. Vol.10. DOI: 10.1186/1742-9994-10-15
- Rodriguez J.J., Fernández-Triana J.L., Smith M.A., Janzen D.H., Hallwachs W., Erwin T.L., Whitfield J.B. 2013. Extrapolations from field studies and known faunas converge on dramatically increased estimates of global microgastrine parasitoid wasp species richness (Hymenoptera: Braconidae) // *Insect Conservation and Diversity*. Vol.6. P.530–536.
- Shaw M.R., Jennings M.T., Quicke D.L.J. 2011. The identity of *Scambus planatus* (Hartig, 1838) and *Scambus ventricosus* (Tschek, 1871) as seasonal forms of *Scambus calobatus* (Gravenhorst, 1829) in Europe (Hymenoptera, Ichneumonidae, Pimplinae, Ephialtini) // *Journal of Hymenoptera Research*. Vol.23. P.55–64.
- Smith M.A., Fernández-Triana J.L., Eveleigh E., Gómez J., Guclu C., Hallwachs W., Hebert P.D.N., Hrcek J., Huber J.T., Janzen D., Mason P.G., Miller S., Quicke D.L.J., Rodriguez J.J., Rougerie R., Shaw M.R., Várkonyi G., Ward D.F., Whitfield J.B., Zaldívar-Riverón A. 2013. DNA barcoding and the taxonomy of Microgastrinae wasps (Hymenoptera, Braconidae): impacts after 8 years and nearly 20000 sequences // *Molecular Ecology Resources*. Vol.13. P.168–176.
- Smith M.A., Rodriguez J.J., Whitfield J.B., Deans A.R., Janzen D.H., Hallwachs W., Hebert P.D.N. 2008. Extreme diversity of tropical parasitoid wasps exposed by iterative integration of natural history, DNA barcoding, morphology, and

- collections // Proceedings of the National Academy of Sciences of the USA. Vol.105. No.34. P.12359–12364.
- Stigenberg J., Vikberg V., Belokobylskij S.A. 2011. *Meteorus acerbiavorus* sp.nov. (Hymenoptera, Braconidae), a gregarious parasitoid of *Acerbia alpina* (Quensel) (Lepidoptera, Arctiidae) in North Finland // Journal of Natural History. Vol.45. No.21–22. P.1275–1294.
- Tselikh E.V. 2012. [Family Pteromalidae] // Lelej A.S. (ed.): Annotirovannyi katalog nasekomych Dalnego Vostoka Rossii. Vol.1. Hymenoptera. P.150–161. [In Russian]
- Tselikh E.V. 2014. [Chalcid flies of the family Pteromalidae (Hymenoptera, Chalcidoidea) of the Russian Far East]. Avtoreferat diss... kand. biol. nauk. Saint Petersburg. 23 p. [In Russian]
- Veijalainen A., Wahlberg N., Broad G.R., Erwin T.L., Longino J.T., Sääksjärvi I.E. 2012. Unprecedented ichneumonid parasitoid wasp diversity in tropical forests // Proceedings of the Royal Society. Ser.B. Vol.279. P.4694–4698.
- Zhang Y.-Z., Si S.-L., Zheng J.-T., Li H.-L., Fang Y., Zhu C.-D., Vogler A.P. 2011. DNA barcoding of endoparasitoid wasps in the genus *Anicetus* reveals high levels of host specificity (Hymenoptera: Encyrtidae) // Biological Control. Vol.58. P.182–191.
- Zhou M.-J., Xiao J.-H., Bian S.-N., Li Y.-W., Niu L.-M., Hu H.-Y., Wu W.-S., Murphy R.W., Huang D.-W. 2012. Molecular approaches identify known species, reveal cryptic species and verify host specificity of Chinese *Philotrypesis* (Hymenoptera: Pteromalidae) // Molecular Ecology Resources. Vol.12. P.598–606.

Поступила в редакцию 29.03.2016