Parasites of the genus *Nosema*, *Crithidia* and *Lotmaria* in the honeybee and bumblebee populations: a case study in India

V.Y. Vavilova1, I. Konopatskaia1,2, S.L. Luzyanin3, M. Woyciechowski4, A.G. Blinov1,5

1 Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia
2 Novosibirsk State University, Novosibirsk, Russia
3 Institute of Biology, Ecology and Natural Resources, Kemerovo State University, Kemerovo, Russia
4 Institute of Environmental Sciences, Jagiellonian University, Krakow, Poland
5 Institute of Systematics and Ecology SB RAS, Novosibirsk, Russia

The populations of honeybees and bumblebees have been decreasing around the world in the recent decades. A variety of pathogens and parasites, including bacteria, fungi, protozoa, nematodes, mites and insects play significant role in honeybee and bumblebee colonies loss. Parasites of the genus *Nosema* (Microsporidia: Nosematidae) and the genera *Crithidia* and *Lotmaria* (Kineto plastida: Trypanosomatidae) have a significant negative impact on honeybee and bumblebee colonies. Recent studies of nuclear DNA markers of these parasites allowed to describe new species and genetic variants. The aim of this study was to investigate the Microsporidia (*Nosema* spp.) and Trypanosomatidae (*Crithidia* spp. and *Lotmaria passim*) prevalence and genetic diversity in honeybee and bumblebee populations of Indian territories that haven't been studied before. In total 119 specimens of 4 honeybee and 5 bumblebee species were analyzed in this study. The prevalence of parasites in honeybee and bumblebee populations of the two Indian states (Jammu and Kashmir, Karnataka) were identified using PCR with primers specific for the ribosomal RNA genes cluster of *Nosema*, *Crithidia* and *Lotmaria* species. Co-infection by microsporidian and trypanosomatid parasites was detected in several honeybee and bumblebee specimens from Jammu and Kashmir state. Comparative analysis of ribosomal RNA genes sequences showed that honeybee samples from India studied were infected by *N. bombi*, *N. ceranae* and *L. passim*. Bumblebee populations were infected by *Nosema D*, *Crithidia bombi* and *Crithidia expoeki*. No honeybee's specimen with trypanosomatid infection was found in Karnataka state. For the first time *N. bombi* infection was detected in the honeybee population. The studies of distribution of microsporidia and trypanosomatid parasites among the honeybee and bumblebee populations all over the World were summarized and supplemented.

Key words: honeybees; bumblebees; infection; ribosomal RNA genes; *Nosema* spp.; *Crithidia* spp.; *Lotmaria passim*.

В последние десятилетия наблюдается резкое снижение численности пчел медоносных и шмелей на территории большинства стран мира. Вклад в снижение численности данных опылителей вносят различные паразитические организмы (бактерии, грибы, простейшие, нематоды, клещи и насекомые). Паразиты рода *Nosema* (Microsporidia: Nosematidae) и родов *Crithidia* и *Lotmaria* (Kineto plastida: Trypanosomatidae) оказывают значительное негативное влияние на численность медоносных пчел и шмелей. В недавних исследованиях, проведенных с использованием ядерных ДНК-маркеров, были описаны новые виды и генетические варианты данных паразитов. Целью настоящей работы являлось установление уровня зараженности медоносных пчел и шмелей микроспоридиями (*Nosema* spp.) и трипаносоматидами (*Crithidia* spp. и *Lotmaria passim*), а также изучение генетической вариабельности этих паразитов на ранее не исследованной территории Индии. В работе проанализировано 119 образцов из четырех видов медоносных пчел и пяти видов шмелей. Уровни зараженности популяций пчел и шмелей паразитическими организмами на территории двух штатов (Джамму и Кашмир, Карнатака) были определены с помощью полимеразной цепной реакции с праймерами, специфичными к кластеру генов рибосомной РНК *Nosema*, *Crithidia* и *Lotmaria*. Совместное заражение популяций медоносных пчел и шмелей микроспоридиями и трипаносоматидами было зафиксировано на территории штата Джамму и Кашмир. В результате сравнительного анализа нуклеотидных последовательностей кластер генов рибосомной РНК *Nosema*, *Crithidia* и *Lotmaria* установлено, что в популяциях медоносных пчел на территории Индии были представлены *N. bombi*, *N. ceranae* и *L. passim*. Популяции шмелей были поражены микроспоридиями *Nosema D* и трипаносоматидами *Crithidia bombi* и *Crithidia expoeki*.
Microsporidia of the genus *Nosema* (Microsporidia: Nosematidae) and trypanosomatid parasites of the genera *Crithidia* and *Lotmaria* (Kinetoplastida: Trypanosomatidae) have a negative impact on the honeybees and bumblebees colonies’ fitness (Schmid-Hempel, 2001; Brown et al., 2003; Higes et al., 2008; Hornitzky, 2008; Yourth et al., 2008; Ravoet et al., 2013).

*Nosema* and *Tubulinosema* species represent the obligate intracellular spore forming organisms that are related to the Fungi (Han, Weiss, 2017). Two microsporidium species, *Nosema ceranae* (Fries et al., 1996) and *Nosema apis* (Zander, 1909), are known to infect honeybees. *Nosema bombi* is another parasite belonging to the phylum Microsporidia which is widespread in the bumblebee populations (Fantham, Porter, 1914). Analysis of standard nuclear DNA markers of *N. bombi* in bumblebee colonies from USA, Russia, China and several European countries revealed new genetic variants of the parasite (Fries et al., 2001; Tay et al., 2005; Szentgyörgyi et al., 2011; Cordes et al., 2012; Li et al., 2012; Vavilova et al., 2015). Three new *Nosema* variants (A, B, and C) isolated from bumblebees in China were suggested to be genetic variants of *N. ceranae* (Li et al., 2012; Vavilova et al., 2015). All detected genetic variants of *Nosema* species did not receive the status of separate species.

Another microsporidium species *Tubulinosema pampeana* (Microsporidia: Tubulinosomatidae) was described for the first time in *Bombus araratus* individuals from Argentina (Plischuk et al., 2015). Currently, there are no cases of *T. pampeana* infections in other regions.

*Crithidia* and *Lotmaria* species are the protozoan flagellated trypanosomatid parasites of honeybees and bumblebees. For a long time *Crithidia mellificae* (Langridge, McGhee, 1967) was the only Trypanosomatidae species described for the *Apis mellifera* and it was poorly investigated. Recent identification of several DNA markers of the American honeybees parasites revealed their high genetic diversity (Cox-Foster et al., 2007; vanEngelsdorp et al., 2009; Runckel et al., 2011; Corman et al., 2012). After detailed analysis of trypanosomosis stains the *C. mellificae SF* was redesignated as *Lotmaria passim*. Therefore at the moment two stains of *C. mellificae* (designated as ATCC 30254 and ATCC 30862) and two stains of *Lotmaria passim* (designated as BRL and SF) for honeybee populations are described (Schwarz et al., 2015). Trypanosomatid *Crithidia bombi* (Lipa, Triggiani, 1988) infecting bumblebees is highly researched (Schmid-Hempel, Reber Funk, 2004; Meeus et al., 2010; Schmid-Hempel, Tognazzo, 2010). Microsatellite data showed that several *C. bombi* genotypes circulate in bumblebee populations from Switzerland, Argentina and Chile (Schmid-Hempel, Reber Funk, 2004; Schmid-Hempel et al., 2011, 2014). Recently two new *Crithidia* species, *Crithidia expoeki* and *Crithidia mexicana*, have been identified in bumblebees from North America and Mexico, respectively (Schmid-Hempel, Tognazzo, 2010; Gallot-Lavallée et al., 2016).

Microsporidian and trypanosomatid parasites described above have a negative impact on the honeybees and bumblebees fitness. The parasites cause the rapid honeybees and bumblebees loss at both individual and colony levels (Schmid-Hempel, 2001; Brown et al., 2003; Higes et al., 2008; Hornitzky, 2008; Yourth et al., 2008; Ravoet et al., 2013).

Thus, investigation of these parasites in host populations from new geographical regions allows to characterize new genetic variants and describe it’s specific distribution. Despite the high importance of honeybees and bumblebees for the economy of India no studies of their parasites have been performed so far. In this study the diversity of *Nosema, Crithidia*, and *Lotmaria* parasites from honeybees and bumblebees in an unexplored regions of India, states Jammu and Kashmir and Karnataka were analyzed.

### Materials and methods

#### Sample collection, DNA extraction, PCR amplification, and sequencing.

80 samples of honeybee species (*A. cerana, A. dorsata, A. florea* and *A. mellifera*) were collected in two Indian states (Jammu and Kashmir, Karnataka) in May and June, 2007, respectively (Fig. 1, Table). 39 bumblebee specimens of *B. asiaticus, B. lucorum, B. ryufosfasciatus, B. simillimus* and *B. trifasciatus* species were collected in Jammu and Kashmir state in May, 2007 (see Fig. 1, Table).

All samples were obtained by entomological sweep nets, identified to the species level in the field and preserved in 70 % ethanol. Total DNA were extracted from abdomens of the specimens fixed in ethanol using DNeasy Blood and Tissue Kit (QIAGEN) according to the manufacturer’s protocol.

The standard sets of primers and PCR conditions were used for PCR amplification of small subunit ribosomal RNA (SSU rRNA), internal transcribed spacer (ITS) and large subunit ribosomal RNA (LSU rRNA) genes of *Nosema* spp. and *Tubulinosema* spp. (Tay et al., 2005; Szentgyörgyi et al., 2011) and 18S rRNA genes of *Crithidia* spp. and *L. passim* (Meeus et al., 2010; Arismendi et al., 2016). Polymerase chain reactions (PCR) were performed in 20 µl volume containing 0.1 µg of genomic DNA, 10 mM Tris-HCl (pH 8.9), 1 mM (NH₄)₂SO₄, 1.5 mM MgCl₂, 200 µM of each of four dNTPs, 0.5 µM primers, and 2.5 units of Taq DNA polymerase. The PCR products were analyzed in 1.2 % agarose gel electrophoresis and extracted from gel with a QIAquick Gel Extraction Kit (QIAGEN). From 40 ng to 200 ng of each PCR product...
**Fig. 1.** Map of Indian states with collection sites designation. Collection sites are correlated with the Table.

<table>
<thead>
<tr>
<th>Indian state</th>
<th>Site Coords.</th>
<th>Species of genus</th>
<th>Specimen number</th>
<th>Number of infected specimens (positive results of PCR) Nosema spp./Tubilinosema spp.</th>
<th>Crithidia spp./Lotmaria passim</th>
</tr>
</thead>
<tbody>
<tr>
<td>Jammu and Kashmir</td>
<td>1 34°08'50.2&quot; N, 74°53'01.2&quot; E</td>
<td><em>Apis cerana</em> Fabricius, 1793</td>
<td>4 2/0</td>
<td>0/2</td>
<td><em>Apis mellifera</em> Linnaeus, 1758</td>
</tr>
<tr>
<td></td>
<td>2 34°01'57.2&quot; N, 74°21'50.5&quot; E</td>
<td><em>A. cerana</em></td>
<td>2 0/0</td>
<td>0/0</td>
<td></td>
</tr>
<tr>
<td></td>
<td>3 33°32'09.2&quot; N, 75°14'57.8&quot; E</td>
<td><em>A. cerana</em></td>
<td>1 0/0</td>
<td>0/0</td>
<td></td>
</tr>
<tr>
<td></td>
<td>4 33°07'38.1&quot; N, 75°22'19.2&quot; E</td>
<td><em>A. mellifera</em></td>
<td>5 0/0</td>
<td>0/1</td>
<td></td>
</tr>
<tr>
<td></td>
<td>6 32°59'38.0&quot; N, 75°42'10.9&quot; E</td>
<td><em>A. cerana</em></td>
<td>7 0/0</td>
<td>0/0</td>
<td></td>
</tr>
<tr>
<td></td>
<td>7 32°43'07.4&quot; N, 75°51'59.1&quot; E</td>
<td><em>A. cerana</em></td>
<td>2 0/0</td>
<td>0/0</td>
<td></td>
</tr>
<tr>
<td>Karnataka</td>
<td>9 13°01'09.0&quot; N, 77°34'07.0&quot; E</td>
<td><em>A. cerana</em></td>
<td>6 1/0</td>
<td>0/0</td>
<td></td>
</tr>
<tr>
<td></td>
<td>10 12°53'05.8&quot; N, 77°28'21.5&quot; E</td>
<td><em>A. mellifera</em></td>
<td>5 0/0</td>
<td>0/0</td>
<td></td>
</tr>
<tr>
<td></td>
<td>11 12°01'07.4&quot; N, 76°06'06.6&quot; E</td>
<td><em>A. dorsata</em></td>
<td>2 1/0</td>
<td>0/0</td>
<td></td>
</tr>
<tr>
<td><strong>Total specimen number</strong></td>
<td></td>
<td></td>
<td>80 20/0</td>
<td>0/10</td>
<td></td>
</tr>
<tr>
<td>Jammu and Kashmir</td>
<td>1 34°08'50.2&quot; N, 74°53'01.2&quot; E</td>
<td><em>Bombus simillimus</em> Smith, 1852</td>
<td>8 0/0</td>
<td>2/0</td>
<td></td>
</tr>
<tr>
<td></td>
<td>2 34°01'57.2&quot; N, 74°21'50.5&quot; E</td>
<td><em>Bombus asiaticus</em> Morawitz, 1875</td>
<td>2 0/0</td>
<td>1/0</td>
<td></td>
</tr>
<tr>
<td></td>
<td>3 33°07'38.4&quot; N, 75°22'19.5&quot; E</td>
<td><em>Bombus lucorum</em> Linnaeus, 1761</td>
<td>1 0/0</td>
<td>0/0</td>
<td></td>
</tr>
<tr>
<td></td>
<td>4 33°05'09.9&quot; N, 75°19'49.2&quot; E</td>
<td><em>Bombus rufofasciatus</em> Smith, 1852</td>
<td>1 0/0</td>
<td>0/0</td>
<td></td>
</tr>
<tr>
<td></td>
<td>5 32°57'11.1&quot; N, 75°43'31.5&quot; E</td>
<td><em>B. asiaticus</em></td>
<td>16 0/0</td>
<td>7/0</td>
<td></td>
</tr>
<tr>
<td></td>
<td>8 32°57'11.1&quot; N, 75°43'31.5&quot; E</td>
<td><em>B. trifasciatus</em></td>
<td>3 0/0</td>
<td>0/0</td>
<td></td>
</tr>
<tr>
<td><strong>Total specimen number</strong></td>
<td></td>
<td></td>
<td>39 4/0</td>
<td>12/0</td>
<td></td>
</tr>
</tbody>
</table>
Parasites of the genus *Nosema*, *Crithidia* and *Lotmaria* in the honeybee and bumblebee populations: a case study in India

V.Y. Vavilova, I. Konopatskaia, S.L. Luzyanin
M. Woyciechowski, A.G. Blinov

Fig. 2. Prevalence of *Nosema* spp. (a), *Crithidia* spp. or *L. passim* (b) infection and co-infection of all parasites (c) in honeybee and bumblebee populations from Jammu and Kashmir and Karnataka states.

Bars represent confidence intervals defined by chi-square test ($p = 0.95$) in STATISTICA. The studied parasites were characterized by low host-specificity; thus, their prevalence was calculated as percentage of the infected specimens to the total number of honeybee or bumblebee specimens in each sampling site.

**Prevalence and discussion**

**Prevalence of parasite infection in honeybee and bumblebee populations**

We studied 80 honeybee and 39 bumblebee specimens collected in two Indian states. *Nosema* spp. were detected by PCR amplification with primers specific to SSU rRNA sequence. *Nosema* spp. were discovered in 20 honeybee specimens from all investigated honeybee species and 4 bumblebee specimens of *B. trifasciatus*. The prevalence of *Nosema* spp. in honeybee populations was 25 and 24 % in Jammu and Kashmir, and Karnataka states, respectively (Fig. 2, a). In Jammu and Kashmir state the prevalence of *Nosema* spp. in bumblebee population was 10 %.

The trypanosomatid parasites were identified by PCR amplification with primers specific to 18S rRNA sequence in 10 honeybee and 12 bumblebee specimens. *A. cerana*, *A. dorsata*, *A. mellifera*, *B. asiaticus*, *B. simillimus* and *B. trifasciatus* species were infected. In Jammu and Kashmir state the prevalence of trypanosomatid parasites was 16 and 31 % in honeybee and bumblebee populations, respectively (Fig. 2, b). No infected honeybee specimens were found in Karnataka state.

Co-infection by *Nosema* spp. and one of the trypanosomatid parasites (*Crithidia* spp. or *L. passim*) was detected in 6 honeybee (*A. cerana* and *A. mellifera*) and 2 bumblebee (*B. trifasciatus*) specimens in Jammu and Kashmir state (Fig. 2, c).

**Genetic diversity of *Nosema* spp. in honeybee and bumblebee populations**

Comparative analyses of the SSU rRNA sequences of *Nosema* spp. Totally, we obtained 24 nucleotide sequences of *Nosema* spp. SSU rRNA gene from honeybees and bumblebees (see Table). The results of the comparative analysis showed that 13 out of 20 sequences from honeybee specimens were identical to *N. bombi* SSU rRNA sequences (KF002566, HG321391, KF188769, JN872234, and JN872233). *N. bombi* was described for bumblebees only. The remaining 7 sequences were identical to SSU rRNA of *N. ceranae* (KF640602, JX205150). Previously *Nosema* species were considered to be the host specific parasites. *N. apis* infected only the European honeybee *A. mellifera*, while *N. ceranae* was a specific parasite for the Asian honeybee *A. cerana* (Smith, 2012). In the recent years *N. ceranae* was identified in *A. mellifera* and some bumblebee species in the different parts of the world. Moreover, some stains of *N. ceranae* are predicted to replace *N. apis* in populations of *A. mellifera* honeybees (Chen, Huang, 2010;...
Comparative and phylogenetic analyses of SSU rRNA, ITS2 and partial LSU rRNA sequences from Nosema spp. To expand information about Nosema D we obtained SSU rRNA, ITS2, and partial LSU rRNA sequences for four B. trifasciatus specimens. Sequences of Vairimorpha spp., N. bombi, N. ceranae, N. apis, and Nosema sp. from Pieris rapae from GenBank, as well as the obtained sequences were used for phylogenetic analysis. Sequences of several Tubulinosema species were taken as an outgroup. Phylogenetic tree built by the NJ method is presented in Fig. 3.

The phylogenetic tree was divided on outgroup and three clusters (see Fig. 3). The outgroup was presented by sequences of T. pampeana, which were described as parasite of B. araratus from South America and two parasites of Drosophila spp. (T. ratisbonensis and T. kingi). The first cluster (I) consists of sequences of N. bombi WS2 and N. bombi WS3 that were previously described in populations of bumblebee from West Siberia (Vavilova et al., 2015). The second cluster (II) includes two clades. The sequences of N. bombi previously identified from the Europe, USA and West Siberia formed the first clade (Tay et al., 2005; Sokolova et al., 2010; Szentgyörgyi et al., 2011). The second clade consists of the newly identified Nosema D sequences. The third cluster (III) is also split into two clades. Sequence of N. apis, obtained from A. mellifera apiary specimens in New Zealand (Gatehouse, Malone, 1998), is in the first clade of the third cluster. The second clade of this cluster consists of sequences of several Vairimorpha spp. from Bombyx mori and Manayunkia speciosa (Liu et al., 2012; Malakauskas et al., 2015); sequences of N. ceranae from Taiwan honeybees (Huang et al., 2007); and sequence of unspecified Nosema from Pieris rapae (Chen et al., 2012).

Thus, the analysis of complete SSU rRNA, ITS2 and partial LSU rRNA gene sequences confirmed that Nosema D is a genetic variant of N. bombi and distributed in the bumblebee populations at least in China and India.

Genetic diversity of Crithidia spp. and Lotmaria passim in honeybee and bumblebee populations

Comparative analyses of the 18S rRNA sequences of Crithidia spp. and Lotmaria passim. We obtained 10 and 12 nucleotide sequences of 18S rRNA gene of trypanosomatid parasites in honeybees and bumblebees, respectively.
Parasites of the genus *Nosema*, *Crithidia* and *Lotmaria* in the honeybee and bumblebee populations: a case study in India

V.Y. Vavilova, I. Konopatskaia, S.L. Luzyanin, M. Woyciechowski, A.G. Blinov

948

**Ecological and population genetics**

**Vavilov Journal of Genetics and Breeding • 2017 • 21 • 8**

Fig. 4. Alignment of partial 18S rRNA gene sequences of *C. bombi*, *C. expoeki* and *C. mellificae/L. passim* specified from honeybee and bumblebee specimens in this study.

Nucleotide positions are indicated according to *Crithidia fasciculata* sequence (Y00055) of full-length rRNA gene cluster.

Fig. 5. World map of microsporidian and trypanosomatid distributions across the honeybee and bumblebee populations.

* Nosema D, which was determined in bumblebee populations from China (Li et al., 2012) and from India (the present study).

(see Table). The results of comparative analysis showed that nine of infected bumblebee specimens refer to *C. expoeki* (KM980187) and three others refer to *C. bombi* (FN546181, KM980184, KM980185). The distinguish between *C. bombi* and *C. expoeki* sequences amounted five nucleotide substitutions (Fig. 4).

All ten 18S rRNA gene sequences were identical and they could belong to either *C. mellificae* or *L. passim* parasites. Sequences of *C. mellificae/L. passim* differ in 4 and 3 nucleotide substitutions from *C. bombi* and *C. expoeki*, respectively (see Fig. 4). Using the primers for 18S rRNA specific to *L. passim* and to *C. mellificae* (Arismendi et al., 2016) on the next
step, we proved that all the obtained sequences belonged to *L. passim* (KJ713378, KM980188, KT252553, KX953206).

Summarizing the data about microsporidian and trypanosomatid parasites in honeybee and bumblebee population from India, we identified that two *A. cerana* and one *A. mellifera* specimens were co-infected by *N. ceranae* and *L. passim*; three specimens of *A. mellifera* were infected by both *N. bombi* and *L. passim*. Co-infection by *Nosema D* and *C. expoeki* in bumblebee populations was established in two *B. trifasciatus* specimens. No cases of *Nosema D* and *C. bombi* co-infection were found in this study.

Co-infection by *N. ceranae* and *L. passim* was also previously established in honeybee samples from Switzerland (Trütscher et al., 2017). Infection of both *N. ceranae* and *C. mellificae* parasites was described for honeybees from Belgian apiaries (Ravoet et al., 2013) (see Fig. 4). Nevertheless, sequences of *C. mellificae* 18S rRNA, identified by Ravoet et al. (2013), were identical for *C. mellificae* and *L. passim*. Thus, these data should be clarified. Gallot-Lavallée et al. (2016) investigated co-infection by *Nosema spp.* and *Crithidia spp.* in the bumblebee populations from Mexico and established the cases of shared parasite infection (Fig. 5). However, species of *Nosema* and *Crithidia* genera found in infected bumblebee samples were not specified. Our data about co-infection of honeybee and bumblebee specimens by microsporidia and trypanosomatid parasites coincide with previously described studies. For the first time *N. bombi/L. passim* and *N. bombi/C. expoeki* co-infection were detected.

**Geographic distribution of Nosema spp., Crithidia spp., and L. passim in honeybee and bumblebee populations**

The results of this study supplement the knowledge of the distribution of microsporidia parasites among the honeybee and bumblebee populations all over the world (see Fig. 5).

African parasites of genus *Nosema* (*N. apis* and *N. ceranae*) are widely distributed in honeybee populations. Joint presence of these parasites was described in numerous studies (Table S1 in the Supplementary material). Nevertheless, there are cases in the several countries such as Indonesia, Israel, Kenya and Zimbabwe of honeybee infections by *N. apis* only (see Table S1). Presence of *N. ceranae* only was established in the honeybee’s population from countries of Latin America (except Brazil), several European countries, Iran, Mongolia, Saudi Arabia and Vietnam (see Table S1). In this study, we discovered that honeybee populations were infected by *N. ceranae*. There were no cases of *N. apis* presence. Presence of *N. bombi* parasite in honeybee specimens was detected for the first time (see Fig. 5).

*N. bombi* is widespread in the natural and commercial bumblebee populations of North and South America, Eurasia and New Zealand (Gallot-Lavallée et al., 2016; Brown, 2017). Several *N. bombi* genetic variants (*WS1, WS2 and WS3*) were described in Siberian bumblebee populations (Vavilova et al., 2015). Four new *Nosema* variants (A, B, C and D) were isolated from bumblebees in China (Li et al., 2012). The microsporidian parasite, *T. pampeana*, was described in bumblebee populations from Argentina (Plischuk et al., 2015). In the recent decades the cases of bumblebee infections by apian parasites *N. ceranae* (Argentina, China, Colombia, Mexico, UK and Uruguay), *N. apis* (Mexico and UK) and other *Nosema* species (Chile, China and Mexico) have been described (Gallot-Lavallée et al., 2016; Brown, 2017). We established the presence of *Nosema D* in bumblebee population from Jammu and Kashmir state (India). *Nosema D* was previously described by (Li et al., 2012) (see Fig. 5).

Presence of two trypanosomatid parasites, *C. mellificae* and *L. passim*, was indicated in honeybee populations globally. *C. mellificae* was found in honeybee specimens from Australia, Belgium, USA and Spain (Table S2). *L. passim* infections were described for honeybees from Belgium, Japan, Serbia and Switzerland (see Table S2). In this study distribution of *L. passim* in Indian honeybee populations were established (see Fig. 5). There were no cases of honeybee infection by *C. mellificae*.

The cases of trypanosomatid infections were determined in commercial and native populations of bumblebees on the territories of North and South America and Eurasia. *C. bombi* is the most common trypanosomatid parasite that infects bumblebees from Argentina, Belgium, Chile, Germany, Italy, Russia, Switzerland and UK (Table S3). The second species *C. expoeki* is presented in Mexican and Swiss bumblebee populations (Schmid-Hempel, Tognazzio, 2010; Gallot-Lavallée et al., 2016). Bumblebee infection by *C. mexicana* was indicated in Mexico (Gallot-Lavallée et al., 2016). Both *C. bombi* and *C. expoeki* are distributed among bumblebee populations from India (see Fig. 5).

Thus, in this study the prevalence of *Nosema, Crithidia* and *Lotmaria* parasites in honeybee and bumblebee populations of Jammu and Kashmir and Karnataka states were identified. In addition, co-infection by Microsporidia and Trypanosomatidae parasites was identified in several honeybee and bumblebee specimens from Jammu and Kashmir state. Honeybee and bumblebee specimens from India studied were infected by several microsporidian parasites (*N. bombi, N. ceranae* and *Nosema D*). Trypanosomatid parasites of *C. bombi, C. expoeki* and *L. passim* species were detected in honeybee and bumblebee populations. Moreover, for the first time *N. bombi* infection was detected in the honeybee population. Thus, further investigations are required to determine distribution of microsporidia and trypanosomatid parasites among the honeybee and bumblebee populations all over the World.

**Acknowledgments**

The study was supported by the project 0324-2016-0008 from the Russian State Budget.

**Conflict of interest**

The authors declare no conflict of interest.

**References**


