

## *Dirofilaria* and *Wolbachia* in mosquitoes (Diptera: Culicidae) in central European Russia and on the Black Sea coast

Elena Shaikovich<sup>1,\*</sup>, Anna Bogacheva<sup>2</sup>, and Ludmila Ganushkina<sup>3</sup>

<sup>1</sup> Vavilov Institute of General Genetics, Russian Academy of Sciences, Moscow 119991, Russia

<sup>2</sup> Moscow State University, Moscow 119234, Russia

<sup>3</sup> Martynovskiy Institute of Medical Parasitology, Tropical and Vector-Borne Diseases, Sechenov First Moscow State Medical University, Moscow 119435, Russia

Received 5 October 2018, Accepted 4 January 2019, Published online 15 January 2019

**Abstract** – *Dirofilariasis* is endemic in Russia, as well as in many other European countries. The aim of this study was to assess the ability of mosquitoes to transfer *Dirofilaria immitis* and *Dirofilaria repens* in regions with temperate and subtropical climates. The possible impact of the symbiotic bacterium *Wolbachia* on *Dirofilaria* transmission was also investigated. 5333 female mosquitoes were collected at 11 points in central European Russia and on the Black Sea coast during the period 2013–2017. Out of 20 mosquito species examined, 14 were infected with *D. repens* and 13 with *D. immitis*. Both species of *Dirofilaria* were found in different climatic regions. The total *Dirofilaria* spp. estimated infection rate (EIR) in the central part of Russia varied from 3.1% to 3.7% and, in the southern region, from 1.1% to 3.0%. The highest estimated infection rate was found in *Anopheles messeae*, the lowest in *Culex pipiens*. The greatest epidemiological danger was represented by *Aedes aegypti*, *Ae. geniculatus*, *An. messeae* and *Ae. communis*. Six out of 20 mosquito species were infected with *Wolbachia*. Pools of *Aedes albopictus*, *Cx. pipiens* and *Coquillettidia richiardii* were simultaneously infected with *Dirofilaria* and *Wolbachia*. After checking mosquitoes individually, it was found that there was no development of *Dirofilaria* to the infective larval stage in specimens infected with *Wolbachia*. Twenty-two *Dirofilaria*-infective pools were *Wolbachia*-free and only two mosquito pools were *Wolbachia*-infected. The potential for transmission of *Dirofilaria* in mosquito species naturally uninfected with the symbiotic bacterium *Wolbachia* is higher than in species infected with the bacterium.

**Key words:** mosquitoes, *Dirofilaria repens*, *Dirofilaria immitis*, *Wolbachia pipiens*.

**Résumé** – *Dirofilaria* et *Wolbachia* chez les moustiques (Diptera: Culicidae) en Russie centrale et sur la côte de la Mer Noire. La dirofilariose est endémique en Russie, ainsi que dans de nombreux autres pays européens. L'objectif de ce travail était d'étudier la capacité des moustiques à transférer *Dirofilaria immitis* et *Dirofilaria repens* dans les régions à climat tempéré et subtropical. L'impact possible de la bactérie symbiotique *Wolbachia* sur la transmission de *Dirofilaria* a également été étudié. 5333 moustiques femelles ont été collectés en 11 points en Russie centrale et sur la côte de la mer Noire au cours de la période 2013–2017. Sur les 20 espèces de moustiques examinées, 14 étaient infectées par *D. repens* et 13 par *D. immitis*. Les deux espèces de *Dirofilaria* ont été trouvées dans différentes régions climatiques. Le taux total d'infection estimé des *Dirofilaria* spp. dans la partie centrale de la Russie variait de 3,1 à 3,7 % et de 1,1 à 3,0 % dans le sud. Le taux d'infection estimé le plus élevé a été observé chez *Anopheles messeae* et le plus faible chez *Culex pipiens*. Le plus grand danger épidémiologique était représenté par *Aedes aegypti*, *Ae. geniculatus*, *An. messeae* et *Ae. communis*. Six espèces de moustiques sur 20 étaient infectées par *Wolbachia*. Des pools d'*Aedes albopictus*, *Cx. pipiens* et *Coquillettidia richiardii* étaient infectés simultanément par *Dirofilaria* et *Wolbachia*. Après avoir examiné les moustiques individuellement, il a été trouvé que les *Dirofilaria* ne se sont pas développés au stade larvaire infectant chez les spécimens infectés par *Wolbachia*. Vingt-deux pools infectés par *Dirofilaria* étaient indemnes de *Wolbachia* et seulement deux pools de moustiques étaient infectés par *Wolbachia*. Le potentiel de transmission de *Dirofilaria* chez les espèces de moustiques naturellement non infectées par la bactérie symbiotique *Wolbachia* est plus élevé que chez les espèces infectées par la bactérie.

\*Corresponding author: [elenashaikovich@mail.ru](mailto:elenashaikovich@mail.ru)

## Introduction

Dirofilariasis is a vector-borne disease common in many countries on various continents [27, 42, 44, 60]. Sources of infection for mosquitoes are infected dogs, less often cats and wild canines (wolves, foxes, etc.). *Dirofilaria immitis* and *Dirofilaria repens* are transmitted by culicid mosquito species belonging to the *Culex*, *Aedes*, *Ochlerotatus*, *Anopheles*, *Coquilletidia*, *Armigeres* and *Psorophora* genera [42, 58, 69]. Vectors ingest microfilariae during a blood meal on an infected host. In mosquito Malpighian tubules, microfilariae develop to the third stage larvae (L3) [34]. The season for *Dirofilaria* transmission in the central part of Russia begins in late May to early June [26]. In order for the larvae to develop to L3, a sum of temperatures of 130 degrees-day [27] is necessary. L3 reach the salivary glands and proboscis from where they are transferred while feeding to another host [34, 43]. However, development of larvae to the infective stage does not always occur; *Dirofilaria* remain in the Malpighian tubules and do not undergo further development or are encapsulated by the immune system of mosquitoes, and may also die within a few hours of entering the intestine of a mosquito [18, 34]. Thus, only mosquitoes in which development has progressed to the third stage larvae (L3) can be considered epidemiologically competent vectors, and the larvae, infective.

*Dirofilaria* infection is endemic in Russia. Two species of *Dirofilaria* (*D. immitis* and *D. repens*) have been identified in humans [54, 63]. Prior to 2014, *D. repens* infection was detected in 850 people living permanently in 42 regions of the Russian Federation [54]. The first case of *D. immitis* was detected in 2015 in the Moscow region; an immature female was removed from a 14-month-old child [63]. The dirofilariasis zone in the north of the European part of Russia has advanced to 58° N [4, 10].

In Russia, mosquitoes infected with *Dirofilaria* have previously been investigated in the southern regions (Astrakhan, Rostov, Krasnodar Krai and Republic of Adygea) and the estimated infection rate (EIR) was 1.0%–14.0% [2, 24, 35]. Even though dirofilariasis is a concern in Russia, many areas have not been sufficiently studied. Also, there are no data on the species of mosquito that are potential vectors of dirofilarial worms. Identification of mosquitoes in all cases was conducted only to the genera level: *D. immitis* and *D. repens* have been detected in the *Culex*, *Aedes* and *Anopheles* genera and the EIR was established as 1.9%–7.0%, 2.3%–6.7%, and 0.6%–3.4%, respectively [2, 24, 35].

An endosymbiotic, maternally inherited bacterium, *Wolbachia pipientis* (Rickettsiales: Rickettsiaceae), hereafter *Wolbachia*, infects filarial nematodes and many insects, including some mosquito species. *Wolbachia* is required for the development and survival of filarial nematodes [61], whereas its symbiotic relationship with mosquitoes is largely parasitic [65]. Among the culicid mosquito species, *Culex pipiens*, *Cx. quinquefasciatus* and *Ae. albopictus* are known to be infected with *Wolbachia* [32, 67] and considered as vectors for *Dirofilaria* [13–15, 28, 45, 50, 69]. However, it was found that *Culex pipiens* f. *molestus* from Madeira, Portugal was unable to support the full development of *D. immitis*, both in nature and after experimental infection with *D. immitis* [29].

In continental Portugal, *Cx. pipiens* were found to be infected with *D. immitis*, but were not potentially infective; filarial DNA was detected only in the abdomen and not in thorax-head samples [25]. However, *D. immitis* microfilariae development to the L3 stage has recently been found in the thorax-head of one *Cx. pipiens* f. *pipiens* from Spain [9]. The hypothesis concerning the influence of *Wolbachia* on the transmission of *Dirofilaria* by *Cx. pipiens* mosquitoes in nature requires further confirmation, particularly in view of the limited number of infected specimens [9] and the absence of 100% *Wolbachia* infection of *Cx. pipiens* in nature [22, 56]. There are only three studies that have focused on investigating simultaneous infection with native *Wolbachia* and *Dirofilaria* in mosquitoes from natural populations [22, 23, 51]. Therefore, the effect of co-infection with native *Wolbachia* on mosquito vector competence for *Dirofilaria* remains unclear.

Prior to clarifying whether naturally occurring *Wolbachia* has any influence on filarial susceptibility or the development of *Dirofilaria* to the infective stage in the vectors, it is necessary to understand *Wolbachia*-mosquito interactions, which mosquito species are infected with the bacterium, the variability of bacterial strains, and the frequency with which *Wolbachia* occurs in mosquito populations.

The objectives of the current study were to examine mosquito fauna and to identify mosquito species that can potentially transmit filarial worms in rural and urban localities in the central part of European Russia compared with the Black Sea resorts, and to evaluate epidemiologically dangerous mosquito species in which larvae develop to the infective (L3) stage. All mosquito species were screened to determine their *Wolbachia* infection status.

## Materials and methods

### Mosquito sampling and taxa discrimination

Mosquitoes were captured in the Tula region, Nizhny Novgorod region, Moscow region and on the Black Sea coast (Fig. 1, SM1). The climate in the studied regions in the central part of the country is moderately continental with clear seasonality; the average temperature in July is +19 °C, and in January –10 °C. At the resorts of the Black Sea coast, the climate is mild Mediterranean and subtropical with average temperatures in July of +24 °C and in January +3 °C. Collection of mosquitoes in the central part of Russia was conducted throughout the warm season in 2013–2017, and in the southern part for one month at each point in 2012–2013 and 2016. Exact locations and months of gathering are presented in SM1.

Sampling locations in the Tula, Nizhny Novgorod and Moscow regions were typical areas for a large number of dogs to be found (gardens of private houses, forests and parks) and natural forests as far as 6–8 km from rural and urban areas. At one of the sampling points in the Moscow region (#5 Fig. 1), there was a kennel for stray dogs; this was located in the immediate vicinity of the forest where mosquito collections took place. To compare the infection rate of mosquitoes in urban and rural areas, we collected mosquitoes near human habitations and in forests.



**Figure 1.** Map of mosquito sample sites and *Dirofilaria* infection rates (EIRs). EIR values for total *D. immitis* and *D. repens* are indicated in red. The exact names and geographical coordinates of the places of collection #1–11 are presented in SM1.

Mosquito collection sites in the south were located in human settlements in a resort area. At the recreation centre “Priboi” (#11 Fig. 1), lakes and ponds are located at a distance of 200–500 m from the collection site and flying mosquito imagoes were observed here. On the Black Sea coast of the Caucasus (#8, 9, 10 Fig. 1) in Anapa, Tuapse and in Sochi, mosquitoes were collected in both urban and rural areas.

At all collection sites, the mosquitoes were captured using a suck tube by human landing during the most active attacking period from 6 pm to 9 pm several times during each month. After trapping, the mosquitoes were frozen at  $-19^{\circ}\text{C}$  for 20–30 min and, afterwards, were identified using taxonomic keys [31]. The specific name of the tribe Aedini is presented according to the studies of Wilkerson et al. [66]. Identification of the *molestus* and *pipiens* forms of *Cx. pipiens* and *Cx. torrentium* was conducted genetically using a PCR-RFLP assay, based on the DNA variability of the *COI* gene, as described previously [55, 56]. Representatives of *Anopheles maculipennis* complex were identified using an ITS2 PCR-RFLP [47].

### Molecular *Dirofilaria* spp. screening

The collected mosquitoes were grouped according to species, collection site and year; there were up to six specimens/pool, usually five. The thorax-head and abdomen of each mosquito in the group were dissected and formed the pool. In some cases, individual thorax-heads were analysed. DNA extraction was performed using the DIAAtom™ DNA Prep kit (Isogen, Russia). Extraction was conducted separately for the abdomens and

thorax-heads in order to determine infected and infective mosquito specimens, respectively. For the PCR analysis, we used 5333 female mosquitoes which were divided into 1095 pools. Each pool was tested separately to identify *D. immitis* and *D. repens* using the following primers: DIR-3: F-5′-CCGGTA-GACCATGGCATTAT-3′ and DIR-4: R-5′-CGTCTTGGACGTTTGGTTA-3′ for the *D. repens* DNA repeat region [64] and COIintF – 5′-TGATTGGTGGTTTTGGTAA-3′ and COIintR – 5′-ATAAGTACGAGTATCAATATC-3′ for detection of the *COI* gene in the mtDNA of *D. immitis* [46]. The PCR was run on a GeneAmpR PCR System 2700 thermal cycler (Applied Biosystems, USA) with a GenPak PCR MasterMix Core PCR kit (Isogen, Russia) for amplification, according to the manufacturer’s instructions. PCR was performed in 25- $\mu\text{l}$  reaction mixtures, containing 1.5 mM of  $\text{MgCl}_2$ , 10 pmol of each primer and 20–50 ng of mosquito genomic DNA. PCR protocols were as follows: primary denaturing at  $94^{\circ}\text{C}$  for 5 min and then 48 cycles of  $94^{\circ}\text{C}$  for 30 s, annealing at  $50^{\circ}\text{C}$  for 30 s and extension at  $72^{\circ}\text{C}$  for 60 s, and a final extension at  $72^{\circ}\text{C}$  for 5 min for *D. repens*; primary denaturing at  $94^{\circ}\text{C}$  for 5 min and then 30 cycles of  $94^{\circ}\text{C}$  for 1 min,  $50^{\circ}\text{C}$  for 2 min and  $72^{\circ}\text{C}$  for 3 min, and final extension for 5 min at  $72^{\circ}\text{C}$  for *D. immitis*. Negative and positive controls were used in each PCR analysis to avoid false-positive results. The positive control used in the study was obtained from adult *D. repens* isolated from a dog. The presence of filarial DNA was confirmed using 1.5% agarose gel electrophoresis. Resulting amplicon sizes were 656 bp for *D. immitis* and 246 bp for *D. repens*.

### Calculation of the infection rates

Minimum infection rates (MIRs) were calculated using the following standard formula: (number of positive mosquito pools)/(total number of mosquitoes tested)  $\times$  100 [13]. Estimated infection rates (EIRs) were calculated using the following formula:  $1 - (1 - x/m)^{1/k}$  [20], where  $x$  is the number of positive pools,  $m$  is the number of pools tested, and  $k$  is the pool size. In the text, all EIRs are given per 100 specimens. Corresponding 95% confidence intervals (95% CIs) were calculated by the modified Wald method, using GraphPad Scientific software. EIR values with corresponding 95% CIs were calculated for all analysed pools per mosquito and *Dirofilaria* species. Host effectiveness was determined as the number of infectious mosquito pools with L3 larvae as a proportion of the total number of mosquitoes studied  $\times$  100.

### Molecular *Wolbachia* screening

*Wolbachia* infection was detected in a sub-sample of 2926 individuals (633 pools) of 20 mosquito species by PCR with an Encyclo PCR kit (Evrogen, Russia), using the *wsp*-specific primers *wsp*-81F and *wsp*-691R [8]. In cases where *Dirofilaria* DNA was detected in pooled abdomens from the mosquitoes, pools of abdomens and individual thorax-heads were tested for *Wolbachia* infection. In other cases, pooled mosquito thorax-heads were analysed. The PCR fragments were purified from agarose gel with a Clean-Up Extraction Kit (Evrogen, Russia) and were sequenced using the BigDye Termination kit 3.1

(Applied Biosystems, USA) in order to distinguish *Wolbachia* of mosquito and of filarial nematode origins. Sequences of the *Wolbachia* *wsp* locus were deposited in GenBank under numbers [MF989984–MF989989](#).

To distinguish between two strains of *Wolbachia* in *Ae. albopictus*, multi-primer PCR was used [70]; primers 383F and 183F were paired with *wsp*-691R to allow the separation of *wAlbA* and *wAlbB* *Wolbachia* strains from *Ae. albopictus*. For the *wAlbA* strain, a fragment size of 379 bp was found and, for the *wAlbB* strain, an amplicon length of 501 bp was found.

The *wPip* infections in *Cx. pipiens* were genotyped in a subsample of 24 individuals representative of *Dirofilaria*-positive pools and assigned to the *wPip*-II and *wPip*-IV groups, using PCR-RFLP assays based on two *wPip* markers, *ank2* and *pk1*, as previously described [3, 56].

## Results

### *Dirofilaria* spp. infection in mosquitoes

The collected mosquitoes included 20 species; 16 species were in the central part of Russia and seven species on the Black Sea coast. The most abundant mosquito species in the temperate climate region was determined to be *Ae. cantans*. In the subtropical climate on the Black Sea coast, the most abundant sampled mosquito species was *Ae. albopictus*, followed by *Cx. pipiens* and *Cx. modestus* (Table 1). Filarial DNA was found in 15 species belonging to four genera with the total EIR for both *Dirofilaria* infections calculated as 2.71 (95% CI, 2.18–3.03) (Table 2). The highest EIR values occurred with the species *An. messeae*, *Ae. aegypti*, *Ae. geniculatus* and *Ae. cataphylla*, and were estimated as 8.67, 5.33, 4.85 and 4.12, respectively (Table 2). *D. repens* infected 14 of 15 mosquito species (EIR = 1.17, 61 positive pools) and *D. immitis* 13 species (EIR = 1.47, 76 positive pools). Both *Dirofilaria* species were found in one pool of *Ae. cantans* (twice), *Ae. geniculatus* (once), *Cx. pipiens* (once), *Ae. intrudens* (once) and *Cq. richiardii* (once). More than one abdomen pool positive with *D. repens* was detected from *Ae. cantans*, *Ae. cataphylla*, *Ae. intrudens* and *Ae. geniculatus*; with *D. immitis* from *Ae. cantans*, *Ae. intrudens*, *Ae. communis*, *Ae. albopictus*, *Cx. pipiens*, *Ae. geniculatus*, *Cq. richiardii*, *Cx. modestus* and *Ae. cinereus* (Table 2).

If we compare infection in the abdomen with the thorax-head, *D. immitis* DNA was detected in 5.75% of tested abdomen pools and 1.37% of tested thorax-head pools. *D. repens* was found in 4.66% of tested abdomen pools and in 1.74% of tested thorax-head pools. The species *Ae. cantans*, *Ae. geniculatus*, *Ae. communis* and *Cx. modestus* had more than one positive thorax-head pool (15, 5, 4 and 2 pools, respectively). *Ae. cantans*, *Ae. communis* and *Ae. vexans* had *Dirofilaria* in the abdomen and in the thorax-head in the same pools. In four species, *Ae. cataphylla*, *Ae. leucomelas*, *Ae. excrucians* and *Ae. cinereus*, microfilariae were only found in the abdomen, with EIR values of 1.51–4.12 (Table 2).

The EIR results for *Dirofilaria* in mosquitoes from specific collection sites are presented in an additional file (SM2). In the Nizhny Novgorod region (Fig. 1 #3), EIRs for *D. repens* and

*D. immitis* were 1.23 and 1.92, respectively. In the Tula region (Fig. 1 #1), EIRs for *D. repens* and *D. immitis* were 1.78 and 1.82, respectively. In the Moscow region (Fig. 1 #6, 7), the EIR for *D. repens* was 1.63 and for *D. immitis* 1.97, in a dog kennel in the forest near Moscow (Fig. 1 #5) infected mosquitoes were not found. The first infected mosquitoes were recorded in May and the last in August–September. In the forest zones of the Nizhny Novgorod and Tula regions, with a sample of 525 specimens, no infected mosquitoes were found (SM2). At the resorts of the Caucasian Black Sea coast, in Anapa, Tuapse and Sochi (Fig. 1 #8, 9, 10), the rates of mosquito infection were much lower; EIR values were 0.32 for *D. repens* and 0.81 for *D. immitis*. However, at the recreation center “Priboi” (Fig. 1 #11), *D. repens* had an EIR of 0.99 and *D. immitis* 2.04; this is comparable to values in the central regions of Russia (Fig. 1).

### *Wolbachia* infection in mosquitoes

The presence of *Wolbachia* was found in six out of 20 studied mosquito species. 93% of all tested *Cx. pipiens* were infected with *Wolbachia*, followed by *Cq. richiardii* (68%), *Ae. albopictus* (56%), *Ae. cinereus* (37%), *Cx. modestus* (7%) and *Ae. cantans* (3%). Specific sample sites and screening results are presented in an additional file (SM3). Sequences of *Wolbachia* *wsp* genes from all six mosquito species demonstrated that all bacteria belonged to supergroups A or B, which were shared between arthropods (Table 3). No filarial bacteria were amplified. Two *Wolbachia* strains were present in studied *Ae. albopictus* (*wAlbA* and *wAlbB*), *wPip*-II in *Cx. pipiens* f. *pipiens* and *wPip*-IV in *Cx. pipiens* f. *molestus*. Based on the *wsp* gene sequence, *Wolbachia* strains in *Cq. richiardii*, *Ae. cinereus* and *Ae. cantans* differ from *wAlb* and *wPip*, so we named these *wCrich*, *wAcin* and *wOcan*, respectively ([pubmlst.org/wolbachia](http://pubmlst.org/wolbachia)).

A total of 90 *Dirofilaria* positive abdomen and thorax-heads pools were analyzed for simultaneous infection with *Wolbachia* (Table 3). Seventy five of the *Dirofilaria* positive pools (83%), including *Ae. cinereus*, *Ae. cantans* and *Cx. modestus*, were free from *Wolbachia*. Fifteen pools of *Ae. albopictus*, *Cx. pipiens* and *Cq. richiardii* (17%) were positive for both *Wolbachia* and at least one *Dirofilaria* species. *Dirofilaria* was found in 22 thorax-head pools of mosquitoes uninfected with *Wolbachia* and in two thorax-head pools which were positive for *Wolbachia*.

In order to investigate a possible association between the occurrence of *Wolbachia* and the development of *Dirofilaria* to the infective third larval stage (L3) within mosquitoes, we tested the thorax-heads of individual specimens from 12 pools: 25 individuals (five pools) of *Ae. albopictus*, 23 individuals (five pools) of *Cx. pipiens* (21 f. *pipiens* and two f. *molestus*), and 11 individuals (two pools) of *Cq. richiardii* (SM4). There was no possibility to study one pool of *Ae. albopictus* (collected in Sochi 2012) infected with *D. repens* and two pools of *Cx. pipiens* (collected in Tula 2014) – one infected with *D. repens* and one infected with *D. immitis* individually. The development of *D. immitis* to the infective stage (L3) was successful only in one thorax-head of *Wolbachia*-free *Cq. richiardii* (No. 11'-1, SM4), although a pool of five mosquito abdomens gave a

**Table 1.** Mosquito species composition and their collected numbers in studied regions.

No.	Mosquito species	Tula region	N. Novgorod region	Moscow region	Total in Central European Russia (%)	Black Sea coast Caucasus	Crimean peninsula, Priboi	Total in southern regions (%)
1	<i>Anopheles messeae</i> (Falleroni)	33	23	6	62 (1.44)	5	0	5 (0.48)
2	<i>Coquillettidia richiardii</i> (Ficalbi)	57	87	3	147 (3.42)	25	12	37 (3.57)
3	<i>Aedes (Stegomyia) albopictus</i> (Scuse)	0	0	0	0	366	0	366 (35.36)
4	<i>Aedes (Stegomyia) aegypti</i> (Linnaeus)	0	0	0	0	21	0	21 (2.03)
5	<i>Aedes (Aedes) cinereus</i> (Meigen)	144	93	22	259 (6.03)	0	0	0
6	<i>Aedes (Aedimorphus) vexans</i> (Meigen)	125	46	8	179 (4.16)	0	0	0
7	<i>Aedes (Finlaya) geniculatus</i> (Olivier)	200	3	0	203 (4.72)	0	0	0
8	<i>Aedes (Ochlerotatus) cantans</i> (Meigen)	1140	337	299	1776 (41.32)	0	0	0
9	<i>Aedes (Ochlerotatus) communis</i> (de Geer)	88	67	152	307 (7.14)	0	0	0
10	<i>Aedes (Ochlerotatus) punctor</i> (Kirby)	50	0	0	50 (1.16)	0	0	0
11	<i>Aedes (Ochlerotatus) intrudens</i> (Dyar)	156	282	44	482 (11.21)	0	0	0
12	<i>Aedes (Ochlerotatus) cataphylla</i> (Dyar)	218	13	5	236 (5.49)	0	0	0
13	<i>Aedes (Ochlerotatus) leucomelas</i> (Meigen)	62	0	0	62 (1.44)	0	0	0
14	<i>Aedes (Ochlerotatus) excrucians</i> (Walker)	34	7	27	68 (1.58)	0	0	0
15	<i>Aedes (Ochlerotatus) caspius</i> (Pallas)	0	0	0	0	140	6	146 (14.11)
16	<i>Aedes (Ochlerotatus) diantaeus</i> (Howard, Dyar & Knab)	0	117	11	128 (2.98)	0	0	0
17	<i>Aedes (Ochlerotatus) sticticus</i> (Meigen)	54	0	3	57 (1.33)	0	0	0
18	<i>Culex (Culex) pipiens</i> (Linnaeus)	270	9	0	279 (6.49)	70	167	237 (22.89)
19	<i>Culex (Culex) torrentium</i> (Martini)	3	0	0	3 (0.07)	0	0	0
20	<i>Culex (Barraudius) modestus</i> (Ficalbi)	0	0	0	0	0	223	223 (21.55)
	<b>Total</b>	2634	1084	580	4298 (100)	627	408	1035 (100)

positive signal for both *D. repens* and *D. immitis*. Neither *D. immitis* nor *D. repens* were found in other individual thorax-heads; parasites were found only in pooled abdomens.

## Discussion

### Mosquito species and *Dirofilaria* infection

The detection of infection with *D. repens* and *D. immitis* was tested in 5333 mosquitoes comprising 1095 pools and representing 20 species collected in geographically remote locations in a temperate and sub-tropical climate. This is the first large-scale study of the infection of mosquitoes in the European part of Russia involving identification of the mosquito species. The published results on mosquito infestation in Europe, including Turkey, in comparison with our data are presented in Table 4. Previously, *Ae. cataphylla*, *Ae. cinereus*, *Ae. excrucians*, *Ae. leucomelas*, *Ae. punctor* and *Ae. diantaeus* mosquitoes were studied in Europe for the presence of *Dirofilaria*,

but no positive samples were detected. In our study, infection with *Dirofilaria* was newly detected in the first four of these mosquito species. However, development of the larvae did not reach the infectious stage.

*Ae. intrudens* and *Ae. communis* were firstly studied here as vectors of *Dirofilaria*; their EIR values were 3.08 and 3.11, respectively. It should be noted that their epidemiological significance is confirmed by the presence of third-stage larvae in the thorax-heads. *Ae. intrudens* and *Ae. communis* host effectiveness was 0.41 and 1.3, respectively.

Special attention should be paid to *Ae. aegypti* mosquitoes, which were found in Russia on the Black Sea coast of the Caucasus in 2000 [53]. As far as we know, the infection of natural populations of *Ae. aegypti* has not been studied. Based on a small sample (21 females), the EIR of this species of mosquitoes was reported as 5.33.

In our study, the most abundant species of mosquito was *Ae. cantans* (1776 specimens out of 5333) with an infection rate that was not high; the EIR for *D. repens* was 1.63 and for

**Table 2.** Mosquito species and infection with *D. immitis* and *D. repens*.

Mosquito species	Number of indiv. mosquitoes	Number of pools	Average number of specimens per pool	Pools positive for <i>D. repens</i>			Pools positive for <i>D. immitis</i>			Total infection with either <i>D. immitis</i> and <i>D. repens</i>		
				Number of abdomen pools	Number of head-thorax pools	EIR (95% CI)	Number of abdomen pools	Number of head-thorax pools	EIR (95% CI)	MIR (%)	EIR (95% CI)	Host effectiveness** (%)
<i>An. messeae</i>	67	15	4.47	1	1	3.15 (0.21–10.86)	3	0	4.87 (1.03–12.87)	7.46	8.67 (2.86–16.68)	1.49
<i>Ae. aegypti</i>	21	4	5.25	0	1	5.33 (0.01–24.42)	0	0	0	4.76	5.33 (<0.01–24.42)	4.76
<i>Ae. geniculatus</i>	203	43	4.72	2	2	2.05 (0.59–5.13)	2	3	2.59 (0.9–5.8)	4.43	4.85 (2.23–8.33)	2.46
<i>Ae. cataphylla</i>	236	49	4.82	6	0	2.67 (1.04–5.56)	3	0	1.3 (0.26–3.85)	3.81	4.12 (1.91–7.19)	0
<i>Cq. richiardii</i>	184	40	4.6	2	0	1.11 (0.04–4.13)	3	1	2.27 (0.65–5.65)	3.26	3.47 (1.34–7.09)	0.54
<i>Cx. modestus</i>	223	45	4.96	3	0	1.38 (0.27–4.06)	2	2	1.86 (0.54–4.68)	3.14	3.35 (1.40–6.46)	0.89
<i>Ae. cantans</i>	1776	356	4.99	25(8*)	11(8*)	1.63 (1.08–2.28)	21(1*)	4(1*)	1.9 (0.9–2.01)	2.93	3.11 (2.23–3.83)	0.84
<i>Ae. communis</i>	307	64	4.79	3(1*)	1*	0.99 (0.2–2.97)	3	3	2.03 (0.8–4.3)	2.93	3.11 (1.47–5.56)	1.3
<i>Ae. intrudens</i>	482	98	4.92	4	1	1.06 (0.37–2.48)	8	1	1.94 (0.93–3.57)	2.9	3.08(1.69–4.86)	0.41
<i>Ae. vexans</i>	179	37	4.84	2	0	1.14 (0.04–4.24)	3(1*)	1*	1.73 (0.35–5.04)	2.79	2.96 (1.02–6.55)	0.56
<i>Ae. cinereus</i>	259	54	4.79	1	0	0.39 (<0.01–2.38)	4	0	1.59 (0.46–4.05)	1.93	2.01 (0.70–4.57)	0
<i>Ae. albopictus</i>	366	74	4.95	0	1	0.27 (<0.01–1.69)	5	0	1.4 (0.49–3.25)	1.64	1.69 (0.67–3.62)	0.27
<i>Ae. leucomelas</i>	62	13	4.77	0	0	0	1	0	1.66 (<0.01–9.41)	1.61	1.66 (<0.01–9.41)	0
<i>Ae. excrucians</i>	68	15	4.53	1	0	1.51 (<0.01–8.63)	0	0	0	1.47	1.51 (<0.01–8.63)	0
<i>Cx. pipiens</i>	516	104	4.96	1	1	0.39 (0.01–1.5)	5	0	0.99 (0.35–2.32)	1.36	1.39 (0.60–2.83)	0.19
<i>Ae. sticticus</i>	57	13	4.38	0	0	0	0	0	0	0	0	0
<i>Ae. caspius</i>	146	30	4.87	0	0	0	0	0	0	0	0	0
<i>Ae. punctor</i>	50	11	4.55	0	0	0	0	0	0	0	0	0
<i>Ae. diantaeus</i>	128	27	4.74	0	0	0	0	0	0	0	0	0
<i>Cx. torrentium</i>	3	3	1	0	0	0	0	0	0	0	0	0
Total	5333	1095	4.87	51(9*)	19(9*)	1.17 (0.89–1.47)	63(2*)	15(2*)	1.47 (1.14–1.78)	2.57	2.71 (2.18–3.03)	0.64
						MIR = 1.14			MIR = 1.43			

\* Inclusive pools, in which infection was detected in both abdomens and head-thorax pools;

\*\* Host effectiveness – proportion of infectious mosquitoes with L3 larvae in total number of studied mosquitoes (%).

**Table 3.** Positive pools for both *Dirofilaria* and *Wolbachia*. Bold, samples positive for *Wolbachia*.

Species	Pools positive for <i>D. repens</i> (inclusive heads)	Pools positive for <i>D. immitis</i> (inclusive heads)	Pools positive for <i>Wolbachia</i>	<i>Wolbachia</i> supergroup
<i>Ae. cinereus</i>	0	1	0	
<i>Ae. vexans</i>	1	0	0	
<i>Ae. geniculatus</i>	4 (2)	5 (2)	0	
<i>Ae. cantans</i>	26 (9)	9 (3)	0	
<i>Ae. cataphila</i>	1	0	0	
<i>Ae. intrudens</i>	2	6	0	
<i>Ae. communis</i>	3 (1)	1	0	
<i>Ae. excrucians</i>	1	0	0	
<i>Ae. aegypti</i>	(1)	0	0	
<b><i>Ae. albopictus</i></b>	<b>(1)</b>	<b>5</b>	<b>6</b>	<b>A and B</b>
<i>An. messeae</i>	2 (1)	2	0	
<b><i>Cq. richiardii</i></b>	<b>1</b>	<b>4 (1)</b>	<b>2</b>	<b>B</b>
<b><i>Cx. pipiens</i> s.l.</b>	<b>2(1)</b>	<b>4</b>	<b>7</b>	<b>B</b>
<i>Cx. modestus</i>	3	4 (2)	0	
Total	48 (16)	41 (8)	15	

*D. immitis* 1.39. Infection of *Cq. richiardii* mosquitoes with *D. immitis* (EIR = 2.27) is comparable to data from Serbia [37] and Slovakia [11]. However, in Moldova [58], mosquitoes of these three species were infected with *Dirofilaria* to a greater extent than in our results for Russia (Table 4). In our study, *Ae. strictus* mosquitoes were not infected, in contrast with data from Serbia, Slovakia and especially from Moldova. The epidemiological significance of *Ae. vexans*, widely distributed in Europe, as a vector of *Dirofilaria* was minor. Its infection rate in different countries varied from 0.03 to 1.68 (Table 4). In Russia, in the Nizhny Novgorod region, there were no infected mosquitoes of this species; in Tula, *D. repens* was found with EIR of 0.81 and *D. immitis* with EIR 2.52. In the Moscow region, of a small sample of three *Ae. vexans* females, one was infected with *D. repens*. The infection rate with *D. repens* in *Cx. modestus* and *Ae. geniculatus* was similar to infection of these mosquito species in Moldova [58]. The difference is that in our samples, both mosquito species were infected, not only with *D. repens*, but also with *D. immitis*.

In our study, the highest EIR value was found in *An. messeae*. Importantly, some *An. messeae* mosquitoes were collected in early May. The females that flew out after the winter diapause actively attacked both humans and dogs. In the Nizhny Novgorod region, 2 out of 12 females caught in May were infected with microfilariae. Somewhat different infection rates of this mosquito species were reported in Moldova (Table 4).

The lowest infection in our study was found in *Ae. albopictus* and *Cx. pipiens*. According to our data, *Ae. albopictus* mosquitoes were infected with *D. repens* with an EIR of 0.27 and with *D. immitis*, an EIR of 1.4. In Italy, *Ae. albopictus* infected with *D. repens* [13], with *D. immitis* [28, 41] and with both species [16] were found with MIR values ranging from 0.69 to 3.19 (Table 4). According to our results, *Cx. pipiens* mosquitoes were infected with *D. repens* with EIR 0.39 and with *D. immitis* EIR 0.99. A comparable frequency was recorded in Italy, Turkey, Portugal, Germany, Moldova and the Republic of Belarus (Table 4).

Differences in infection rates in the same mosquito species from different regions could be connected with ecological

factors, such as season, climate and geographical features, which are specific for each region [27], but also, perhaps to an even greater extent as shown by our results with *Ae. aegypti*, *Ae. cantans* and *Ae. vexans*, connected with the sample size.

### Infection in specific collection regions

When comparing the total infection of mosquitoes with *D. repens* and *D. immitis* by region (SM2), almost identical EIR results in the settlements of the Central region were noted, with some prevalence of mosquitoes infected with *D. immitis*. On the Black Sea coast of the Caucasus (Fig. 1 #8, 9, 10), mosquitoes were collected in a resort area where the number of dogs near our sample sites was negligible and the infection of mosquitoes was lower. Temperature is an important factor for the maintenance of dirofilariasis foci. However, the presence of definitive hosts (mainly domestic, office and stray dogs) basically determines one or another level of mosquito infection with *Dirofilaria*. This is confirmed by the absence of infection in mosquitoes collected in the forest at a distance of 8–10 km from settlements in the Nizhny Novgorod and Tula regions (Fig. 1, “forests” #2, 4). However, in the settlements (Fig. 1 #1, 3, 6, 7), mosquito infection was high >3%. Possible reasons for this are that circulation of the pathogen in the two woodlands does not occur, or wild canines are not affected by *Dirofilaria* or are affected to such a small extent that we could not discern infection by examining the mosquito vectors.

In the Moscow region, one point was studied in the immediate vicinity of the dog kennel (Fig. 1 #5), located in a woodland 2 km away from the nearest settlement. Infected mosquitoes were not found. In this kennel, the dogs were treated for different infections, including *Dirofilaria*, and the infection from wild animals did not occur or was extremely low.

### Host effectiveness

According to our findings, under similar conditions (temperature and the presence of definitive hosts), the effectiveness

**Table 4.** Published results about *Dirofilaria* in mosquito species in Europe, including Turkey, in comparison with data obtained in this study.

Species	N indiv./pools	<i>D. repens</i>	<i>D. immitis</i>	Host effectiveness	Country, references
<i>Cx. pipiens</i>	516/104	EIR = 0.39	EIR = 0.99	0.19	This study
<i>Cx. pipiens</i>	1108/412	MIR = 0.27	MIR = 0.27	0.27*	Italy 2002–2003 [12]
<i>Cx. pipiens</i> (s.l.)/ <i>torrentium</i>	2663/132	EIR = 0.88	EIR = 0.47		Moldova 2010–2016 [58]
<i>Cx. pipiens</i>	1595/1123		EIR = 0.50		Continental Portugal 2011–2013 [25]
<i>Cx. pipiens</i>	2589		MIR = 0.12	0.12*	Turkey 2008–2009 [69]
<i>Cx. pipiens</i>	37,865/835	MIR = 0.01*	MIR = 0.04*		Italy 2010 [38]
<i>Cx. pipiens</i>	5568/115	MIR = 0.02*	MIR = 0.18*		Serbia 2013 [37]
<i>Cx. pipiens complex</i>	2539/187	MIR = 0.28*			Slovakia 2015–2017 [11]
<i>Cx. pipiens/Cx. torrentium</i>	12,292/554		MIR = 0.02*		Germany 2011–2013 [36]
<i>Cx. pipiens</i>	136/11		EIR = 0.58		Belarus 2015 [59]
<i>Cx. pipiens</i>	666		MIR = 0.3*		Spain 2004–2006 [46]
<i>Cx. pipiens</i>	604		MIR = 0.17*	0.17*	Spain 2012–2013 [9]
<i>An. messeae</i>	67/15	EIR = 3.15	EIR = 4.87	1.49	This study
<i>An. maculipennis</i> s.l.	400/114		EIR = 3.12	1.25*	Continental Portugal 2011–2013 [25]
<i>An. maculipennis</i>	136/28	MIR = 1.47*			Slovakia 2015–2017 [11]
<i>An. maculipennis</i> s.l.	947/ 62	EIR = 4.91	EIR = 2.01		Moldova 2010–2016 [58]
<i>Ae. vexans</i>	179/37	EIR = 1.14	EIR = 1.73	0.56	This study
<i>Ae. vexans</i>	3179		MIR = 0.41	0.35*	Turkey 2008–2009 [70]
<i>Ae. vexans</i>	720/25		MIR = 0.14*		Italy 2010 [38]
<i>Ae. vexans</i>	405/19	MIR = 0.25*			Serbia 2013 [37]
<i>Ae. vexans</i>	12,042	MIR = 0.03			Czech Republic 2009–2011 [52]
<i>Ae. vexans</i>	314/ 33	EIR = 1.68			Moldova 2010–2016 [58]
<i>Ae. vexans</i>	1750/35	MIR = 0.06			Slovakia 2012 [7]
<i>Ae. vexans</i>	96/20		MIR = 1.04		Turkey 2008 [6]
<i>Ae. caspius</i>	146/30	EIR = 0	EIR = 0	0	This study
<i>Ae. caspius</i>	26/13	EIR = 22.64			Moldova 2010–2016 [58]
<i>Ae. caspius</i>	270/193		EIR = 3.73	1.48*	Continental Portugal 2011–2013 [25]
<i>Ae. caspius</i>	2264/92		MIR = 0.18*		Italy 2010 [38]
<i>Ae. caspius</i>	195/13		MIR = 0.5*		Serbia 2013 [37]
<i>Cq. richiardii</i>	184/40	EIR = 1.11	EIR = 2.27	0.54	This study
<i>Cq. richiardii</i>	34/7		MIR = 2.94*		Serbia 2013 [37]
<i>Cq. richiardii</i>	48/26		MIR = 2.08*		Slovakia 2015–2017 [11]
<i>Cq. richiardii</i>	19/11	EIR = 16.25			Moldova 2010–2016 [58]
<i>Ae. cantans</i>	1776/356	EIR = 1.63	EIR = 1.39	0.84	This study
<i>Ae. cantans</i>	15/5	EIR = 14.84			Moldova 2010–2016 [58]
<i>Ae. sticticus</i>	57/13	EIR = 0	EIR = 0	0	This study
<i>Ae. sticticus</i>	24/7	EIR = 4.43			Moldova 2010–2016 [58]
<i>Ae. sticticus</i>	120/7	MIR = 0.83*			Serbia 2013 [37]
<i>Ae. sticticus</i>	414/41	MIR = 0.24*	MIR = 0.24*		Slovakia 2015–2017 [11]
<i>Cx. modestus</i>	223/45	EIR = 1.38	EIR = 1.86	0.89	This study
<i>Cx. modestus</i>	203/25	EIR = 3.26			Moldova 2010–2016 [58]
<i>Ae. geniculatus</i>	203/43	EIR = 2.05	EIR = 2.59	2.46	This study
<i>Ae. geniculatus</i>	26/10	EIR = 7.45			Moldova 2010–2016 [58]
<i>Ae. albopictus</i>	366/74	EIR = 0.27	EIR = 1.4	0.27	This study
<i>Ae. albopictus</i>	2534/336	0	MIR = 3.19*	0.87*	Italy 2000–2002 [12, 13]
<i>Ae. albopictus</i>	436/436	MIR = 0.92*	MIR = 0.69*	1.15*	Italy 2002–2003 [16]
<i>Ae. albopictus</i>	528/98		MIR = 0.19*		Italy 2005 [41]
<i>Ae. albopictus</i>	175/35		MIR = 1.14	0.51*	Italy 2011 [28]

\*Number calculated based on the results published by the authors.

of mosquitoes as vectors of *Dirofilaria* was not the same. There were five species of mosquitoes, *Ae. punctor*, *Ae. diantaeus*, *Ae. sticticus*, *Ae. caspius* and *Cx. torrentium*, in which no infected samples were found. Absence of infection in *Ae. sticticus* and *Ae. punctor* was probably associated with a small sample size (57 and 50 mosquitoes, respectively). *Cx. torrentium* rarely attack people, and with our collection method, the sample size was only three mosquitoes. However, of particular interest is the reason for the absence of infection in *Ae. diantaeus* and *Ae. caspius*, which were collected in sufficient numbers

(117 and 146 mosquitoes) and not in the natural forests. Another interesting finding was the absence of infection in *Ae. diantaeus*, which were mainly collected in the Nizhny Novgorod region, where other mosquito species of the same biotope were infected (SM2). In contrast to our results, it was reported that *Ae. caspius* was infected with *D. repens* in Italy [38] and Moldova [58], with *D. immitis* in Serbia [37], Portugal [25] and Hungary, based on one positive sample of *D. repens* and *D. immitis* out of 267 collected mosquitoes from four species [71]. The absence of infection in *Ae. caspius* in our



collections may be explained by there being no infection or only slight infection at that particular collection point, since specimens of other species were also negative.

In four species (*Ae. leucomelas*, *Ae. cataphylla*, *Ae. cinereus* and *Ae. excrucians*), *Dirofilaria* were found only in the abdomens, indicating that its development did not reach an infective L3 stage (Table 2). Also, it should be highlighted that in three species of mosquitoes (*Ae. cantans*, *Ae. communis*, and *Ae. vexans*), there were positive signals for *Dirofilaria* simultaneously in the thorax-head and abdomen pools. This fact may indicate that mosquitoes could ingest the filariae at different times and repeatedly, and not all nematodes managed to complete the development cycle to become infective larvae and migrate to the front of the body. Similarly, it cannot be excluded that not all filariae reach the infectious stage due to possible defense mechanisms activated by host cells, such as encapsulation, melanization, and coagulation [12, 21, 34]. However, in all mosquito species, except *Ae. aegypti* where only one pool was infected, the percentage of positive thorax-head pools was lower compared to abdomen pools.

According to published research, the development of *Dirofilaria* to the infective stage (L3) was recorded in Europe in the mosquito species *Ae. caspius*, *An. maculipennis*, *Ae. vexans*, *Ae. geniculatus*, *Ae. albopictus*, and *Cx. pipiens* (Table 4). On the basis of our results, eleven mosquito species are epidemiologically dangerous, when *Dirofilaria* undergo development to L3 (Table 2). Of particular interest are the species *Ae. geniculatus*, *Ae. communis*, *Ae. intrudens*, *Ae. cantans* and *Cx. modestus*, in which L3 were found more than once. *Ae. aegypti*, *Ae. geniculatus*, *An. messeae* and *Ae. communis* have host effectiveness values ranging from 1.3 to 4.76. It should be noted that the efficacy of *Ae. aegypti* as a vector of *Dirofilaria* has been studied many times in laboratory conditions [34, 57, 62], where the microfilariae developed to third-stage larvae, but not in field-collected *Ae. aegypti*. In seven mosquito species, the host effectiveness was less than 1 (Table 2).

### **Wolbachia and Dirofilaria infection in individual mosquitoes**

Most mosquito species uninfected with *Wolbachia* showed higher epidemiological potential for *Dirofilaria* transmission in all studied regions (host effectiveness 0.41–4.76; EIR = 2.96–8.67, average EIR = 4.2). *Ae. cinereus* and *Cx. modestus* pools that had *Dirofilaria* were free from *Wolbachia* (Table 3).

*Dirofilaria* DNA was detected in abdomen pools of both *Wolbachia*-infected and uninfected mosquitoes. This result shows that *Wolbachia* does not prevent the acquisition of *Dirofilaria* by mosquitoes in nature. However, in eight thorax-head pools, *D. immitis* DNA was only detected in *Wolbachia*-uninfected mosquitoes. Moreover, after individual study of 11 thorax-heads from two *Wolbachia* positive *Cq. richiardii* abdomen pools, the *D. immitis* development was successful only in *Wolbachia*-free sample (Table SM4).

*D. repens* DNA in thorax-heads was found in 14 *Wolbachia*-uninfected and in only two *Wolbachia*-infected pools, in one of *Ae. albopictus* and in one of *Cx. pipiens*. We could

not study mosquitoes from these two pools individually, so it is impossible to determine whether all the individuals in pool were infected with the bacterium, and to what ecological form (f. *pipiens* or f. *molestus*) of *Cx. pipiens* they belonged. Therefore, our findings do not prove a clear influence of bacteria on the development of *Dirofilaria*.

Nevertheless, the ratio of *Dirofilaria*-infective mosquitoes is much higher in *Wolbachia*-free mosquito specimens than in *Wolbachia*-infected, 22:2. Differences in the effects of different strains of *Wolbachia* were not recorded. However, given the small sample size of *Dirofilaria*-infected mosquitoes, further investigation into whether *Wolbachia* is present in individual *Cx. pipiens* and *Ae. albopictus* mosquitoes carrying infective L3 stage larvae is required.

It is known that artificial bacterial transfer significantly increases the expression of immune genes, including those involved in the Toll and IMD immune pathways, enhances the mosquito's resistance to pathogens [5, 48, 49], and inhibits the development of filarial nematodes [1, 33]. In contrast, it has been shown that native *Wolbachia* does not affect the induction of host immune pathways [17, 39]. As a hypothesis, it could be proposed that there is a resource competition in the host for metabolites, because both *Dirofilaria* [19, 30] and *Wolbachia* [68] require them for their development. It should be noted that any *Wolbachia* anti-pathogen effect is dependent on bacterial density [40], so the development of microfilaria to the infective stage may differ in each mosquito. The study of simultaneous infection of individual mosquitoes with *Dirofilaria* spp. and a bacterial symbiont, taking into account *Wolbachia* density, will help us understand the mechanism of *Wolbachia* interference in the transmission of *Dirofilaria* by mosquitoes.

In conclusion, *Dirofilaria* were found in 15 mosquito species. This is the first study conducted in Russia examining the mosquito species as potential vectors of *D. immitis* and *D. repens*. Out of 1095 pools studied, there were 114 positive abdomen pools and 34 positive thorax-head pools. The ratio of infected pools to infective pools was 3.35:1. Mosquitoes in central temperate regions are able to spread *Dirofilaria* no less than mosquitoes in the southern regions. This indicates that the presence of infected dogs has a greater effect on the maintenance of foci of dirofilariasis than temperature. In the forests, the circulation of pathogens occurs with less intensity than in human settlements in rural and urban areas. For the first time in Europe, *Ae. aegypti*, *Ae. intrudens* and *Ae. communis* mosquitoes have been studied as *Dirofilaria* vectors, in which EIR values ranged from 3.08 to 5.33. Our data showed that *Ae. albopictus* and *Culex pipiens* s.l. are not the most important vectors of *Dirofilaria*. The greatest epidemiological danger was represented by *An. messeae*, *Ae. aegypti*, *Ae. geniculatus*, and *Ae. communis*. *Ae. cantans* might be added to this list given the considerable host effectiveness and the very high density.

**Acknowledgements.** We thank Vera Rakova and Ivan Patraman for the assistance in mosquito sampling and in carrying out certain molecular assays.

### **Conflict of interest**

There is no conflict of interests.

## Funding

This work was supported by the Russian Foundation of Fundamental Research [grant N 16-04-00091].

## Supporting information

**SM1.** Mosquitoes collected between 2013 and 2017. Information on the specificities and the coordinates of the sampling site, sampling date, total mosquito number and *Dirofilaria* screening results.

**SM2.** Mosquito infection with *Dirofilaria* spp. in specific sample sites. Information on the sampling date, mosquito species, pool size and *Dirofilaria* screening results.

**SM3.** Occurrence of *Wolbachia* in mosquito species. Information on the sampling region, mosquito number, pool size and *Wolbachia* screening results.

**SM4.** Comparison of simultaneous infection with *Wolbachia* and *Dirofilaria* individually.

Supplementary materials are available at <https://www.parasite-journal.org/10.1051/parasite/2019002/olm>.

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**Cite this article as:** Shaikevich E, Bogacheva A & Ganushkina L. 2019. *Dirofilaria* and *Wolbachia* in mosquitoes (Diptera: Culicidae) in central European Russia and on the Black Sea coast. *Parasite* 26, 2.



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