PREVALENCE OF BLOOD PARASITES IN FERAL PIGEONS (COLUMBA LIVIA) IN NORTHWEST ITALY

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Blood parasites have been subject of extensive research since the beginning of the 20th century. The presence of hemoparasites in birds is very common, and it is estimated that 68% of all bird species are susceptible to haemosporidians.

Feral pigeons (Columba livia) are widely distributed in the world. Their number is increasing, especially in urban areas. To authors’ best knowledge no data on pigeon hemoparasites distribution in Italy are available.

During the years 2010-2011, following the adoption of a regional animal containment programme, 51 Feral pigeons, from Piedmont Region (Northwest Italy) were captured and euthanized according to Italian National Bioethics Committee guidelines and subjected to a standard necropsy. Spleen was collected and frozen at -20°C for DNA amplification, as described by Hellgren et al. (2004) with some modifications. All positive samples were sequenced.

Out of the 51 Feral pigeons tested by nested PCR, 29.4% resulted positive for Haemoproteus/Plasmodium spp., and 15.7% for Leucocytozoon spp. A highly significant difference between the haemoparasites prevalence (p<0.001) was detected. The coinfection with both haemoparasites was very significant (p<0.01), and a greater relative risk (RR 7.2) to be infected by a second hemoparasite was recorded in already infected birds.

Regarding sex and age distribution of multiple infestation, associations were significant in males (p< 0.05; RR 11.0) and in adult birds (p< 0.05; RR 10.0).

DNA sequencing of the eight positive samples in nested PCR for Leucocytozoon spp. allowed to identify six different lineages: five of them were the same identified in Hooded crows investigated by the authors in the same area, the other was a new lineage in feral pigeons (L-AEM002). In two animals, two different lineages of Leucocytozoon were present at the same time. DNA sequencing of the 15 positive samples for Haemoproteus/Plasmodium spp. showed the presence of the already described haplotypes P-SGS1 and H-HAECOL1.

The significant differences in nested PCR detection of Haemoproteus/Plasmodium spp. and Leucocytozoon spp. infection may be due to variation in vector diversity and population size, and avian community composition, or to a greater susceptibility of pigeons to Leucocytozoon spp.

The finding of avian hematooza in pigeons implies the presence of ornithophilic vectors in Piedmont Region and the susceptibility of this species to infection.

Our results suggest that cross infection of feral pigeons with hemoparasites typical of other migratory or non migratory birds is possible, and should be further investigated and monitored.

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