

Populations of *D. gallinae* infesting French layer farms show a strong homogeneity in mt-Co1 sequences, if compared with some other populations

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Within genus *Dermanyssus*, the Poultry Red Mite *D. gallinae* is pest in layer farms. It is also present in wild avifauna, but proliferates mainly in farms. The causes of its prevalence and its spread remain unclear. Commercial flaws, environmental conditions, exchanges between different bird species may structure populations within this species. The aim of present study is to investigate the diversity of populations within *D. gallinae* using a mitochondrial gene. Indeed, this species seems to be composed of several different lineages on the basis of a mitochondrial protein coding gene region. A fragment of the cytochrome oxidase1 gene (mt-Co1) has been sequenced in more than 50 populations of *D. gallinae*, sampled from farms and wild birds in France and in some European countries. 29 different haplotypes have been found, only 5 of which was found in French layer farms and 4 in some other European countries' layer farms, all different from French haplotypes. Phylogenetic and network analyses allowed identification of several different clusters and observation of some patterns. At the European level (inter-country), a single haplotype per sample (but few samples investigated), with until 5% divergence from French farm samples. Some more samples would be needed to exploring phylogeographic patterns at this level. At the French level (intra country), no geography-correlated population structure has been revealed. One haplotype is characteristic and strongly recurrent in French layer farms, independently of their type. Each of the four other haplotypes found in French layer farms have been encountered only once. Some few "amateur" hen houses and chicken farms have been sampled and provided all haplotypes which differ from layer farms, with up to 6% divergence. Among samples from France, until 12% divergence between some populations from wild avifauna and from non-galliform breeding facilities have been noted. Among samples from French layer farms, up to 5% divergence have been noted. On the whole, not all *D. gallinae* lineages are present in layer farms, but only some very close to each another, which suggests that there might have been some adaptive evolution processes allowing these mites to infest farms and that their dissemination might be correlated to commercial flaws. Moreover, present data also suggest that there are almost no exchanges of red mites between wild and domestic birds.

Keywords: poultry red mite, populations, molecular phylogeography