

Phylogenetic relationship between *Dermanyssus gallinae* populations in European countries based on mitochondrial CO1 gene sequences

M. MARANGI¹, C.J. DE LUNA², M.A. CAFIERO³, A. CAMARDA⁴, S. LE BOUQUIN⁵, A. GIANGASPERO¹ and O.A.E. SPARAGANO²

¹Dipartimento PrIME, Università di Foggia, Italy;

²School of Agriculture, Food and Rural Development, Newcastle University, Newcastle upon Tyne, NE1 7RU, UK;

³Istituto Zooprofilattico Sperimentale della Puglia e Basilicata, Italy;

⁴Dipartimento di Sanità pubblica e Zootecnia, Università di Bari, Italy;

⁵Unité EBEAC, AFSSA - BP 53 - F 22 440 PL.

E-mail: m.marangi@unifg.it

Phylogenetic analysis of *Dermanyssus gallinae* mites originating from UK, France and Italy was performed using partial amplification of the mitochondrial CO1 gene by PCR. A genetic tree based on the mitochondrial DNA sequences was constructed to assess whether the mites showed diverged lineages. Moreover, intra variations between each farm and inter variations between all the farms were studied. Mites were all collected from poultry farms keeping birds in cages. Results indicated that UK samples showed the greatest genetic variability if compared to the other European farms (36.5% to French farms and 33.9% to Italian farms). Interestingly, the UK populations were linked to one of the French population highlighting North-South genetic transitions in European red mite populations. Intra farm variations between samples (21.4% for French farms and 17.3% for Italian farms) also highlighted the diversity between regional populations possibly due to different chemical strategies used in each country. This paper also discusses the transitions and transversions observed at sequence levels and its implications at farm level.

Keywords: phylogeny, *Dermanyssus gallinae*, population diversity