PARASITES AND PARASITOLOGY

FC-5

Severe eosinophilic dermatitis in Jersey cows infested with *Leptotrombidium* spp. (Acari: Trombiculidae)

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A serious outbreak of pruritic dermatitis was investigated in mid-October in an organic farming dairy herd with 21 Jerseys, three Bretonne pie noir and four crossed Abondance–Montbéliarde cows in south west France. Lactating cows (17) had permanent grazing access except for indoor milking times. Five 2-year-old and six 1-year-old heifers had been permanently kept in two different meadows, with no contact between them or with adults, since the beginning of the summer. No antiparasitic treatment had been administered for the previous five months. Severe and extensive lesions of alopecia, lichenification and crusting were observed on the jaws, dewlap, face, perineum, above the udder and distal limbs, associated with moderate pruritus. Only Jersey cows were affected (10 of 13 lactating cows and all three 2-year-old heifers) with various degrees of lesions severity. Heifers displayed more intense lesions than adults. Microscopic examination of deep skin scrapes showed numerous specimens of Trombiculidae larvae identified as *Leptotrombidium* spp. and no other ectoparasites. Histopathological examination of skin biopsy specimens included severe hyperplastic, superficial and deep perivascular, oedematous, eosinophilic dermatitis. Complete blood counts revealed mild to moderate eosinophilia. The final clinicopathological diagnosis was eosinophilic dermatitis suspected to be a consequence of Trombiculidae bites. The lesions completely self-resolved by the end of December. This case report emphasizes the need to include Trombiculidae in the differential diagnosis of bovine pruritic dermatoses. Finding lesions only in Jersey cows remained unexplained and could be hypothetically consistent with individual genetic susceptibility to develop hypersensitivity reactions, or other predisposing breed factors (e.g. feeding habits or skin characteristics).

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FC-6

Development of a quantitative PCR to evaluate accurately the treatment response of dogs with demodicosis

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Canine demodicosis is the result of an overpopulation of *Demodex* mites, normal inhabitants of most skin of mammals. There is no reliable method to quantify the number of *Demodex* mites present in the skin to provide accurate information about treatment response. The objective of this study was to develop a molecular technique to quantify the *Demodex* load in canine skin in order to evaluate the treatment response in dogs with demodicosis. For this purpose, a real-time quantitative (q)PCR was developed using primers that amplified a fragment of the *D. canis 18S rRNA* gene. Ten-fold dilutions of the DNA extracted from isolated mites were used to elaborate the standard curve. In addition, 44 skin biopsies (4 mm) obtained from nine canine cadavers and 18 skin biopsies from seven dogs with demodicosis in day (D)0 and D14, D35 and D56 post-treatment (Animal Welfare Committee, FCV-UNCPBA) were used to assess the number of mites in the skin of healthy dogs and of dogs with demodicosis. The skin biopsies of healthy dogs were negative in 38/44 samples and positive (>one mite) in the rest (6/44). However, in skin biopsies of diseased dogs the initial *Demodex* load was mostly >100 mites, decreasing to 50–100, 10–50 and 0–10 mites at D14, D35 and D56 post-treatment, respectively. The homology between the qPCR product and the *18S rRNA* gene was confirmed by DNA sequencing (GenBank KC010485 – *D. canis*). This simple technique could be a useful tool to evaluate accurately the response to treatment of dogs with demodicosis.

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