Programme & Abstracts



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Feeding behaviour of Culicoides spp. (Diptera: Ceratopogonidae) on cattle and sheep in northeast Germany

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Culicoides spp. play an important role as vectors of several vector-borne pathogens such as bluetongue virus (BTV) and Schmallenberg virus (SV). The unexpected outbreak of bluetongue in Europe in 2006, its fast dissemination and the emergence of Schmallenberg disease in Europe had an enormous impact on livestock production (1,2). Although the importance of autochthonous Culicoides species in the dissemination of BTV and SV is generally recognized, many aspects of the ecology of native Culicoides species are still not fully understood, and there is a lack of information concerning their dispersal, vectorial capacity, feeding and host-seeking behaviour. In order to better understand the biology of Culicoides species in Central Europe, we performed a field study in northeast Germany which aimed to clarify the daily activity patterns, preferential landing and feeding sites and host feeding preferences of Culicoides spp. using cattle and sheep as baits.

The study was performed in July 2012 and was divided in three parts (A, B and C). In study A, 3545 Culicoides belonging to 13 species were collected from the vicinity of cattle and sheep over a 72h period using drop traps and backpack aspirators. We observed a bimodal pattern of activity, with peaks at dawn and dusk, although the highest midge activity was found around sunset (24% of the catches). By direct aspiration of midges from the body surface of cows and sheep in study B, we aimed to determine the preferential landing and feeding sites of Culicoides species. We collected 2024 Culicoides from four different body regions, whereby a high number of midges were collected from the lower body regions of cattle and sheep. This has implications for the use of topical (pour-on) insecticides to prevent midge bites, as their availability in the skin of different body regions may not be homogenous (3). Host feeding preferences of Culicoides were tested in study C where we collected midges using 2 drop traps placed at an intermediate distance of 10m with a cow or three sheep placed as baits inside. The origin of the host bloodmeal was confirmed by a PCR targeting the cytochrome B gene. In study C, 3710 Culicoides were collected, 83% of them from cattle and 17% from sheep. Nearly half (46.7%) of the midges collected from cattle were engorged, significantly more than sheep where 7.4% of the collected midges were engorged, which suggests that cattle are more attractive for Culicoides midges in comparison to sheep. All Culicoides species collected were morphologically identified, according to standard identification keys. Culicoides from the Obsoletus complex (C. obsoletus and C. scoticus) were the most common Culicoides species collected, followed by C. punctatus. Other species identified were C. dewulfi, C. chiopterus, C. pulicaris, C. lupicaris, C. pallidicornis, C. subfascipennis, C. achrayi, C. griseidorsum, C. subfagineus and C. stigma, the last two species described for the first time in Germany. Significantly more engorged C. chiopterus midges were collected from sheep in study C, suggesting a potential host preference of this species for sheep.

1. Conraths F, Peters M, Beer M 2013 Schmallenberg virus, a novel orthobunyavirus infection in ruminants in Europe: Potential global impact and preventive measures. New Zealand veterinary journal 61:63-67

2. Wilson AJ, Mellor PS 2009 Bluetongue in Europe: past, present and future. Philosophical transactions of the Royal Society of London Series

3. Stendel W, Hamel HD, Sieveking HU, Bruhne D 1992 Analytical determination of the distribution of flumethrin on the body surface of cattle following topical pour-on application. Veterinary parasitology 1992, 42(1-2):137-143.

Current knowledge of cryptosporidium at the wildlife livestock human the interface of the Kruger National Park

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Cryptosporidium spp. is an oocyst-forming apicomplexan protozoan, which infects a large number of animals and humans Putignani and March 1987 and ruminants are considered Putignani and Menichella 2010). Several species/genotypes have a relevant zoonotic potential and ruminants are considered as an important as as an important source of infection (Xiao and Feng 2008). In general, young individuals show higher rates of infection compared adults (Santin et al. 2004). O adults (Santín et al. 2004). Cryptosporidium infection has been demonstrated in a wide number of wild animals, which might contribute to environmental contribute to env Contribute to environmental contamination (Feng 2010). In sub-Saharan Africa, where HIV infections are the highest in the world, nigh rates of several Tripori 2008). However, nothing is high rates of severe and even fatal *Cryptosporidium* infection have been reported (Mor and Tzipori 2008). However, nothing is shown about the contraction of Southern Africa. thown about the epidemiology of this disease in a wildlife livestock interface context representative of Southern Africa.