

RESEARCH ARTICLE

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Family matters: skin microbiome reflects the social group and spatial proximity in wild zebra finches

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Abstract

Background: So far, large numbers of studies investigating the microbiome have focused on gut microbiota and less have addressed the microbiome of the skin. Especially in avian taxa our understanding of the ecology and function of these bacteria remains incomplete. The involvement of skin bacteria in intra-specific communication has recently received attention, and has highlighted the need to understand what information is potentially being encoded in bacterial communities. Using next generation sequencing techniques, we characterised the skin microbiome of wild zebra finches, aiming to understand the impact of sex, age and group composition on skin bacteria communities. For this purpose, we sampled skin swabs from both sexes and two age classes (adults and nestlings) of 12 different zebra finch families and analysed the bacterial communities.

Results: Using 16S rRNA sequencing we found no effect of age, sex and family on bacterial diversity (alpha diversity). However, when comparing the composition (beta diversity), we found that animals of social groups (families) harbour highly similar bacterial communities on their skin with respect to community composition. Within families, closely related individuals shared significantly more bacterial taxa than non-related animals. In addition, we found that age (adults vs. nestlings) affected bacterial composition. Finally, we found that spatial proximity of nest sites, and therefore individuals, correlated with the skin microbiota similarity.

Conclusions: Birds harbour very diverse and complex bacterial assemblages on their skin. These bacterial communities are distinguishable and characteristic for intraspecific social groups. Our findings are indicative for a family-specific skin microbiome in wild zebra finches. Genetics and the (social) environment seem to be the influential factors shaping the complex bacterial communities. Bacterial communities associated with the skin have a potential to emit volatiles and therefore these communities may play a role in intraspecific social communication, e.g. via signalling social group membership.

Keywords: Family-specific, Social group, Bacterial communities, Nestling, Avian olfaction, Olfactory communication, Relatedness, Social environment, Microbiota

Background

While most studies investigating the microbiome of birds have focused on gut microbiota, e.g. [1], only a few have addressed the microbiome of the skin, such as the facial skin [2], brood patch [3, 4], neck region [5] and uropygial gland [3, 5, 6]. However, feathers and skin act as barriers between the bird and its environment and are thus

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