

A comparative study of the fecal microbiota of grey seal pups and yearlings - a marine mammal sentinel species

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Abstract

Grey seals (*Halichoerus grypus*) can act as sentinel species reflecting the condition of the environment they inhabit. Our previous research identified strains of pathogenic *Campylobacter* and *Salmonella*, originating from both human and agricultural animal hosts, on rectal swabs from live grey seal (*Halichoerus grypus*) pups and yearlings on the Isle of May, Scotland, UK. We examined rectal swabs from the same pup (n=90) and yearling (n=19) grey seals to gain further understanding into the effects of age-related changes (pup versus yearling) and three different natal terrestrial habitats on seal pup fecal microbiota. DNA was extracted from a subset of rectal swabs (pups n=23, yearlings n=9) using an optimized procedure, and the V4 region of the 16S rRNA gene was sequenced to identify each individual's microbiota. Diversity in pup samples was lower (3.92 ± 0.19) than yearlings (4.66 ± 0.39) although not significant at the p=0.05 level (p = 0.062) but differences in the composition of the microbiota were (p < 0.001). Similarly, differences between the composition of the microbiota from pups from three different terrestrial habitats (PH, RR, and TS) were highly significant (p < 0.001). Pairwise tests showed significant differences between all three habitats: PH vs TS (p = 0.019), PH vs RR (p = 0.042) and TS vs RR (p = 0.020). This preliminary study suggests a general trend, that seal microbiomes are modified by both age and, in pups, different terrestrial habitats. Furthermore, knowledge of the microbiota species present has the potential to be used in determining the environmental quality index.

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