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Social and ecological effects on the genome: lessons from baboons and rhesus macaques

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The social environment can have profound effects on individual fitness in primate societies. However, the mechanistic basis for these effects is not well understood. Part of the answer may lie in changes that occur at the level of the genome. I will present three vignettes illustrating work in my lab aimed at investigating this possibility. To study the effects of social status, we experimentally manipulate dominance rank in captive female macaques. In this context, dominance rank leads to pervasive changes in gene regulation, such that relative rank can be predicted based on gene expression signatures alone. Sensitivity to dominance rank is particularly great for cells and genes involved in innate immunity. To understand its evolutionary significance, we also investigate gene regulatory variation in wild baboons. Here, we have tested the hypothesis that environmental variation drives epigenetic changes in DNA methylation. In baboon males, resource availability is significantly associated with DNA methylation levels, and we have shown that some of these differences drive variation in gene expression levels using experimental transfection assays. Interestingly, a persistent signature of resource limitation, but not resource abundance, can be detected in these data, suggesting limits to the plasticity of resource-associated methylation patterns. Finally, we also study the impact of social relationships on the "extended genome" encoded by the gut microbiome. Our results show that social group membership and social network structure predict gut microbiome composition in the baboons. These patterns are not explained by diet, kinship, or environmental exposure. Instead, social relationships appear to directly affect microbiome transmission, with potentially important ramifications for individual health and the evolution of group living.