The microbiome of New World vultures

Vultures are scavengers that fill a key ecosystem niche, in which they have evolved a remarkable tolerance to bacterial toxins in decaying meat. Here we report the first deep metagenomic analysis of the vulture microbiome. Through face and gut comparisons of 50 vultures representing two species, we demonstrate a remarkably conserved low diversity of gut microbial flora. The gut samples contained an average of 76 operational taxonomic units (OTUs) per specimen, compared with 528 OTUs on the facial skin. Clostridia and Fusobacteria, widely pathogenic to other vertebrates, dominate the vulture's gut microbiota. We reveal a likely faecal-oral-gut route for their origin. DNA of prey species detectable on facial swabs was completely degraded in the gut samples from most vultures, suggesting that the gastrointestinal tracts of vultures are extremely selective. Our findings show a strong adaption of vultures and their bacteria to their food source, exemplifying a specialized host-microbial alliance.