Deciphering microbial landscapes of fish eggs to mitigate emerging diseases Irene de Bruijn^{*1}, Yiying Liu¹, Allison Jack², Keith Drynan³, Albert Hendrik van den Berg⁴, Even Thoen⁵, Vladimir Sandoval-Sierra⁶, Ida Skaar⁷, Pieter van West⁴, Menno van der Voort², Rodrigo Mendes⁸, Mark Mazzola⁹, Jos Raaijmakers¹

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Animals and plants are increasingly suffering from diseases caused by fungi and oomycetes. These emerging pathogens are now recognised as a global threat to biodiversity and food security. Among oomycetes, *Saprolegnia* species cause significant declines worldwide in farmed and natural populations of freshwater fish and amphibians. This disease, referred to as Saprolegniosis, is characterised by filamentous white/grey patches on the fish skin and gills, and cotton-like growth on fish eggs. Fish eggs have an immature adaptive immune system and depend on nonspecific innate defences to ward off pathogens. Here, meta-taxonomic analyses revealed that Atlantic salmon eggs are home to diverse fungal, oomycete and bacterial communities. While virulent *Saprolegnia* isolates were found in all salmon egg samples, a low incidence of Saprolegniosis was strongly correlated with a high richness and abundance of specific commensal Actinobacteria, with the genus *Frondihabitans* (Microbacteriaceae) effectively inhibiting attachment of *Saprolegnia* to salmon eggs may provide new sustainable means to mitigate emerging diseases.