MicroResist

The influence of snail host microbiome in trematode parasite resistance

DURATION
15/12/2019 - 15/03/2024

BUDGET
319 940 €

PROJECT DESCRIPTION

Gastropod-borne diseases (GBDs) affect more than 300 million people worldwide but also lead to economic losses and mortality in livestock. Schistosomiasis is one of the most prevalent tropical infections in Africa, affecting almost 200 million people in Sub-Saharan Africa.

Despite the availability of adequate tools for diagnosis and treatment, and the concerted control efforts to date, schistosomiasis continues to (re-) emerge with unexpected distributions and unprecedented intensities. The realization that mass drug treatment alone does not suffice to control the disease, renewed the focus on snail control. Such control measures are focussed on eliminating local snail populations. Not only do these products kill other aquatic life such as fish and amphibians, but by killing snails and other organisms they also remove important links from the ecosystem. The snail immune response to infection is influenced by host genetic factors, by abiotic environmental factors like temperature, and by biotic factors like the microbiota associated with the snail host, which is increasingly being recognized as an important player. Studies on microbiota of gastropod snails are however very rare, despite their medical importance. Moreover, studies concentrate on single infection experiments while in nature vector species are usually infected by multiple parasites.

In this project we want to pave the way for new sustainable biocontrol strategies in combating neglected tropical diseases by generating novel baseline and experimental data on the microbiota of gastropod snail hosts through 16S metabarcoding on naturally infected gastropods (museum collections) and experimentally infected snails. More specifically, the objectives of this project are 1) to characterize the microbiome of selected gastropod species that act as host for schistosomiasis and fasciolosis in Africa and test the impact of the phylogeny, geography and infection status, 2) to test the short- and long-term temporal variation in the microbiome of selected gastropod species with multiple infections and 3) to conduct experimental analysis to disentangle causation and correlation for the relationships found in work packages 1 and 2. Such Disentanglement will be attempted through a transplant experiment. We selected *Bulinus truncatus* from Senegal as organism for this experiment as it has a different susceptibility towards *Schistosoma haematobium* within the same river system, with populations from the Lower Senegal River Valley being resistant to infection, in contrast to populations 40 km away in the Middle Valley. Four *Bulinus truncatus* genotypes (two susceptible and two resistant) will be used as gut microbiome donors for four other (two susceptible and two resistant) genotypes (see Fig. 1 for a visualization of the experimental set-up).

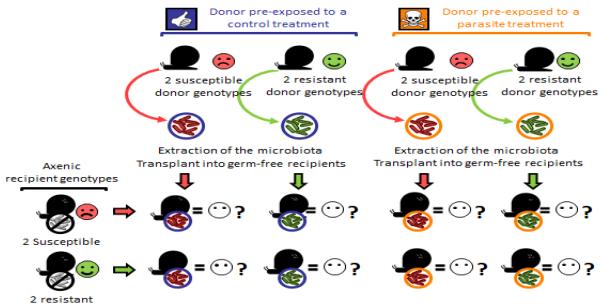

Figure 1: Deciphering how genotype and gut microbiota interact to drive resistance to parasitic infections through gut microbiota transplants in Bulinus truncatus. Donor snail populations from either susceptible (S1 and S2; red) or resistant (R1 and R2; green) genotypes will be exposed to either S. haematobium for several generations or without exposure (blue and orange colour, respectively). From each combination, microbiota are isolated and inoculated in axenic genotypes (S3, S4, R3 and R4) for each factorial combination.

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The recipient genotypes are first made axenic or microbiome-free through a protocol described by Chernin in 1957 to eliminate any potential priority effects. Knowledge of microbes that can promote resistance, allows the engineering of beneficial microbial communities, effectively eliminating the need for detrimental molluscicides. This could lead to sustainable and environmentally friendly snail control strategies based on the exploitation of natural resources. For example, the microbiota's capacity to influence vector susceptibility has been exploited in the control of malaria by introducing microbiota-based-control strategies. These include the use of entomopathogens to decrease vector populations or the introduction of competence-limiting bacteria and fungi into mosquito populations. Another option is paratransgenesis; transgenesis of a vector symbiont to eliminate a pathogen from a vector population.

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LINKS

https://www.kuleuven-kulak.be/nl/onderzoek/key-areas/onderzoeksgroepen/aquatische-biologie2/data/persoonlijke-paginas/Ruben_Schols

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