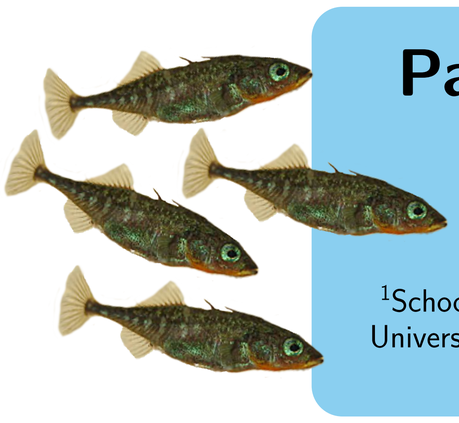

Parasite infection alters methylation inheritance in the three-spined stickleback

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Background

Parasites influence the evolution of resistance and tolerance mechanisms in their hosts. Infection experiment using three-spined stickleback fish (*Gasterosteus aculeatus*) by the nematode *Camallanus lacustris* showed that paternal infection were associated with both cost and benefit for offspring tolerance[1]. We speculated DNA methylation was an underlying mechanism of these phenotypic differences between infected and uninfected fish[2].

Aim: Understanding the mechanisms of phenotypic plasticity within and across generations, focusing on DNA methylation. Identifying which of the DNA methylations linked to parasite infection can be inherited by the next generation.

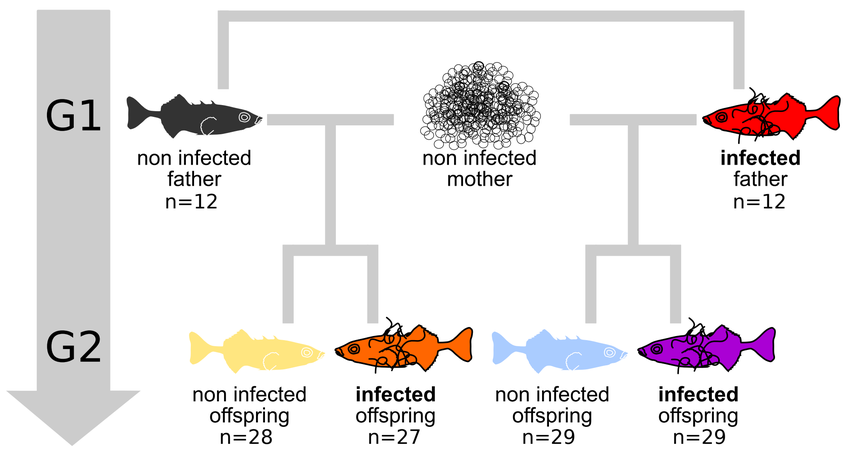

Fig. 1: Experimental design

Material & methods

1. **Experimental design: G0 generation** from natural lake population -> **G1 generation** of full-sib fish families. In vitro fertilisation of G1 gravid female serving as egg donor with G1 male from another family, repeated in brother pairs within each male family (1 from G1 "treatment" group and 1 from G1 "control" group) -> **G2** (Fig.1). Infection of G1 & G2 with *C. lacustris* larvae through copepod ingestion
2. **Data processing:** Methylome sequencing: Reduced Representation Bisulfite Sequencing (RRBS) single-end reads of 100bp long, Illumina HiSeq 2500. Alignment on a European gynogen genome[3] and methylation call with BSBolt. Downstream analyses with Methylkit.

Preliminary results

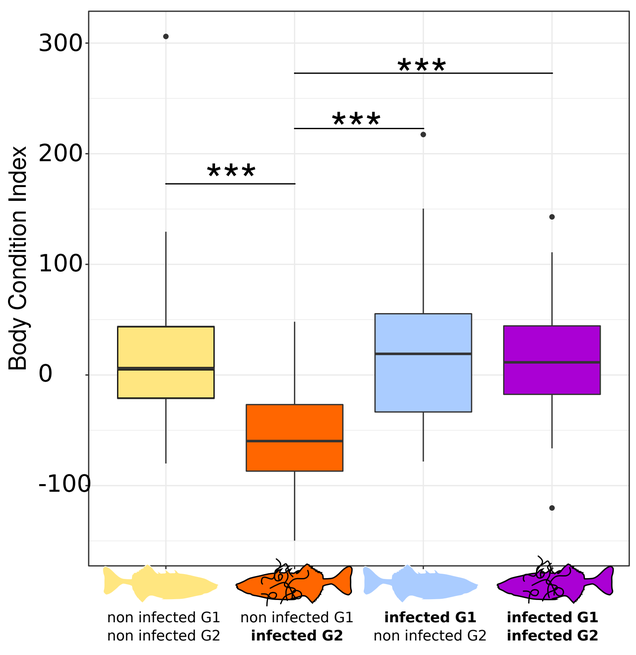

Fig. 2: Paternal treatment effect on offspring body condition

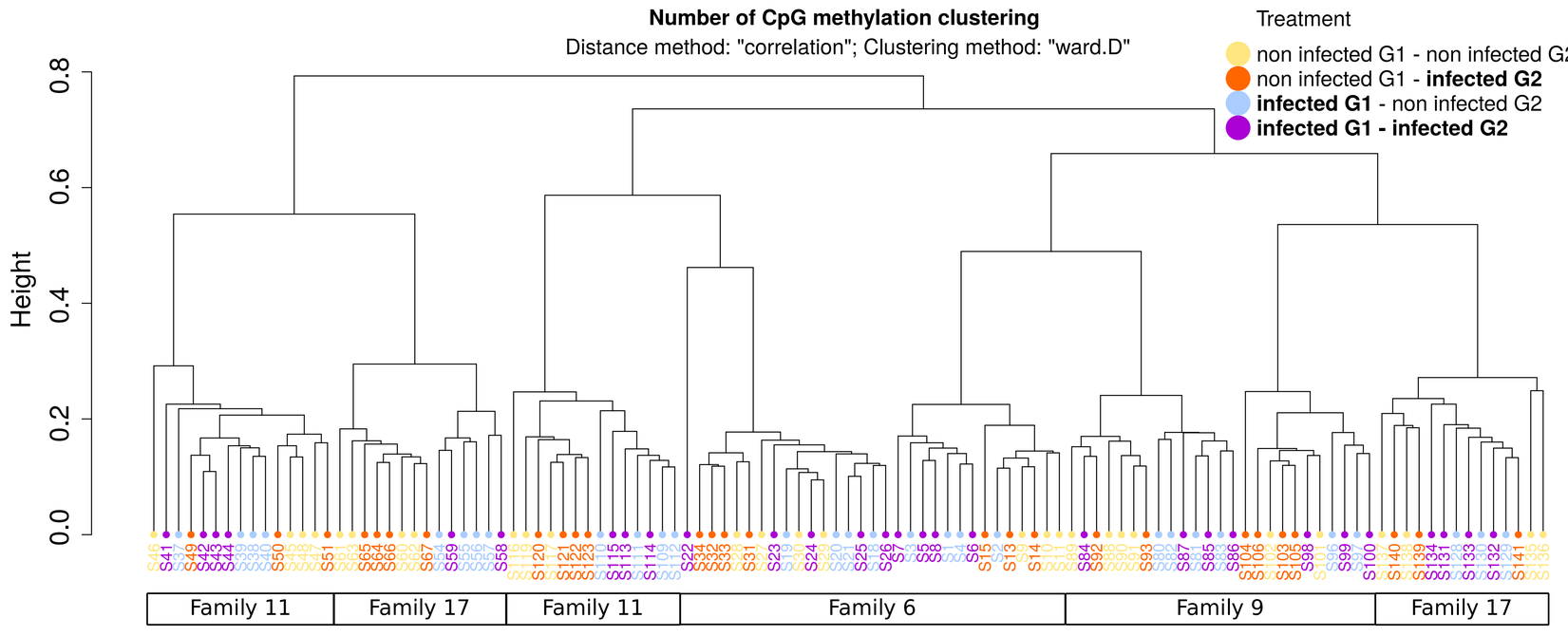

Fig. 3: Hierarchical clustering of individual fish CpG methylation

Paternal treatment affects body condition: infected offspring from non infected fathers show a decrease in body condition after infection; this drop is absent in infected offspring from infected fathers (Fig.2)[1]

Offspring methylomes cluster by family and paternal treatment: within family subgroups, the paternal treatments seem to play a stronger role in clustering than the treatment of offspring itself (Fig.3)

Perspective

1. Compare Differentially Methylated Sites (DMS), hypo and hypermethylation, between offspring groups:
   (a) **Tests of parental effect:**
   comparisons of (G1 non infected-G2 non infected vs G1 infected-G2 non infected), and (G1 non infected-G2 infected vs G1 infected-G2 infected)
   (b) **Tests of offspring exposure:**
   comparisons of (G1 non infected-G2 non infected vs G1 non infected-G2 infected) and (G1 infected-G2 non infected vs G1 infected-G2 infected)
2. Identification of genes and genes networks (method: WGCNA) involved

References

[1]Kaufmann, J., Lenz, T. L., Milinski, M., & Eizaguirre, C. (2014). Experimental parasite infection reveals costs and benefits of paternal effects. Ecology Letters; [2]Sagonas, K., Meyer, B. S., Kaufmann, J., Lenz, T. L., Häsler, R., & Eizaguirre, C. (2020). Experimental parasite infection causes genome-wide changes in DNA methylation. Molecular Biology and Evolution; [3]Thornburn et al., in prep.

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