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Transgenerational response to endocrine disruptor ingestion : phenotypic, genetic and epigenetic analyses in quail



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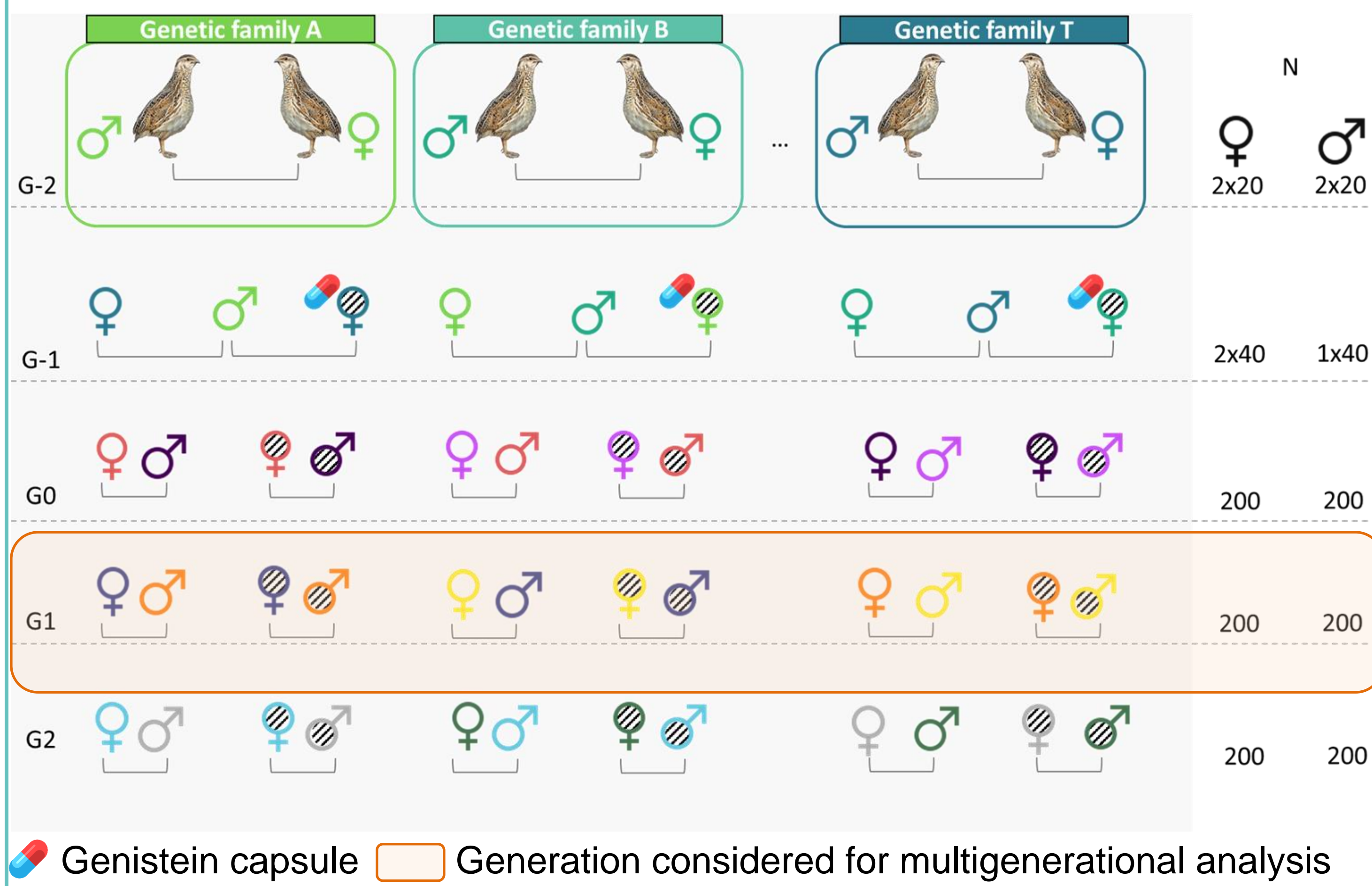
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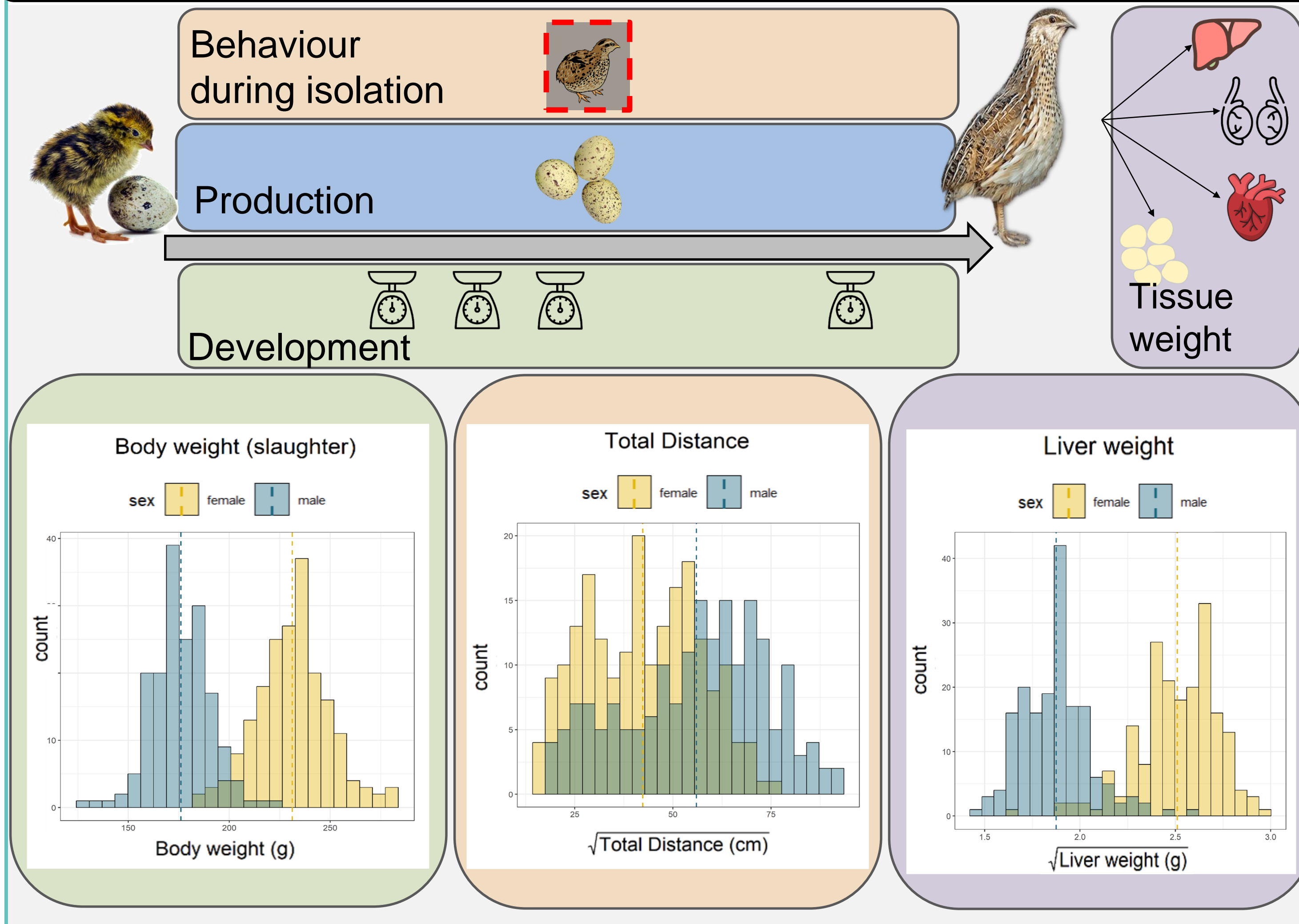
Typical evaluation of an offspring's phenotype usually focuses on the inheritance of parental alleles. However, variations across generations can also result from the **transmission of non-genetic factors**. Epigenetic marks like **DNA methylation** offer a dynamic molecular signature of an individual's history, as they can carry a memory of the individual's environmental past, and also of its parents. In this study, we aim to analyze the impact of an initial supplementation with an endocrine disruptor, genistein, on the phenotypes of subsequent generations. To better disentangle the complex **interplay between genetic and epigenetic effects**, a specific quail (*Coturnix japonica*) breeding plan was designed, where **mirror crosses** ensure a balanced genetic structure between epilines. By recording multiple phenotypes (development, breeding, production, behaviour), our goal is to investigate the **transgenerational inheritance** of an environmental effect through changes in DNA methylation profiles. Here, we present **preliminary results on phenotypic traits** two generations after the environmental disruption and thus, focus on **multigenerational inheritance**.

1 – Quail Breeding Design



40 initial matings (G-2) representing 20 families.
 G-1 females plain: genistein caps /30 days
 G-1 females empty: empty caps /30 days.
 Transgenerational effects can be assessed in G2. Before, we assess multigenerational effects.

2 – Phenotypes



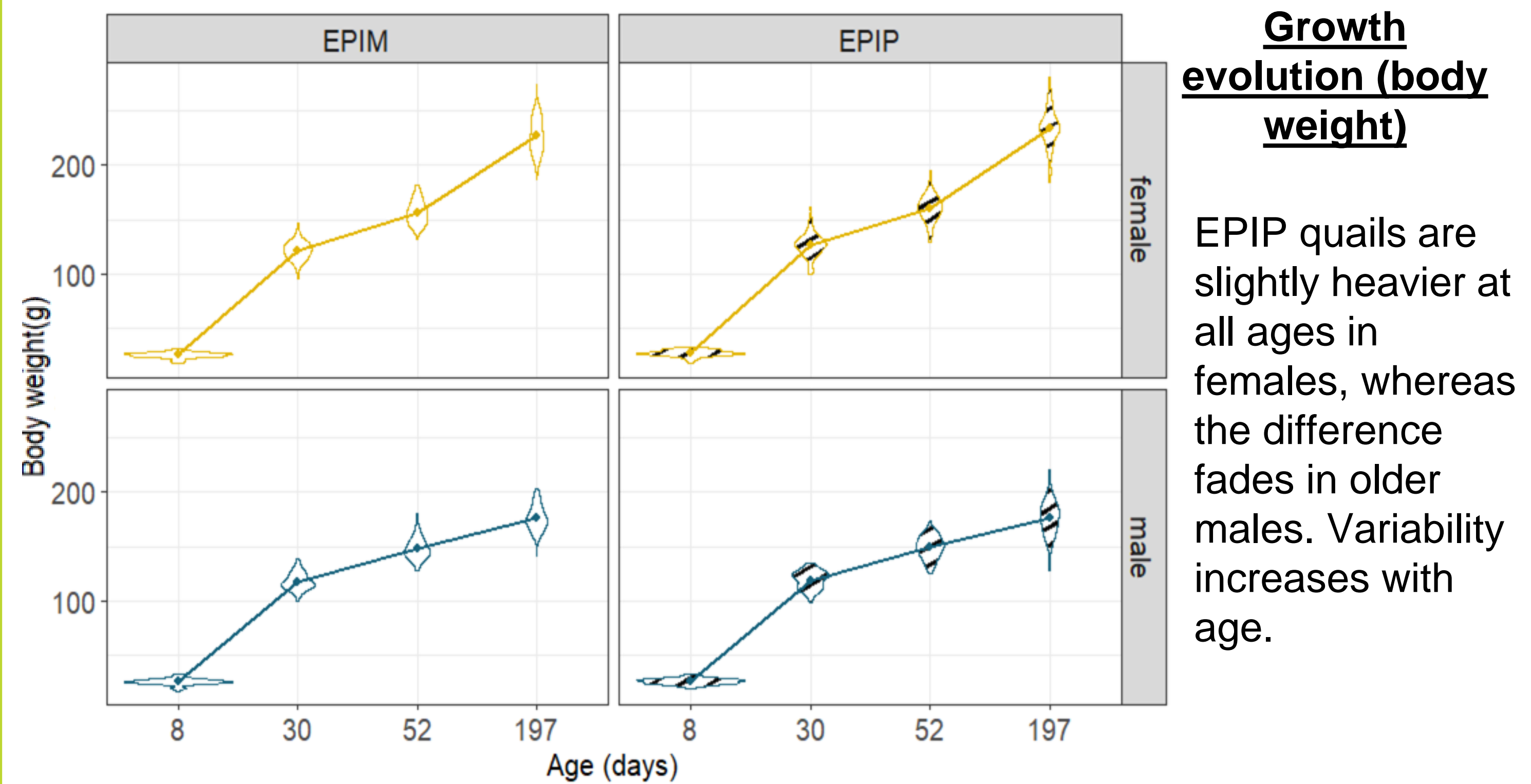
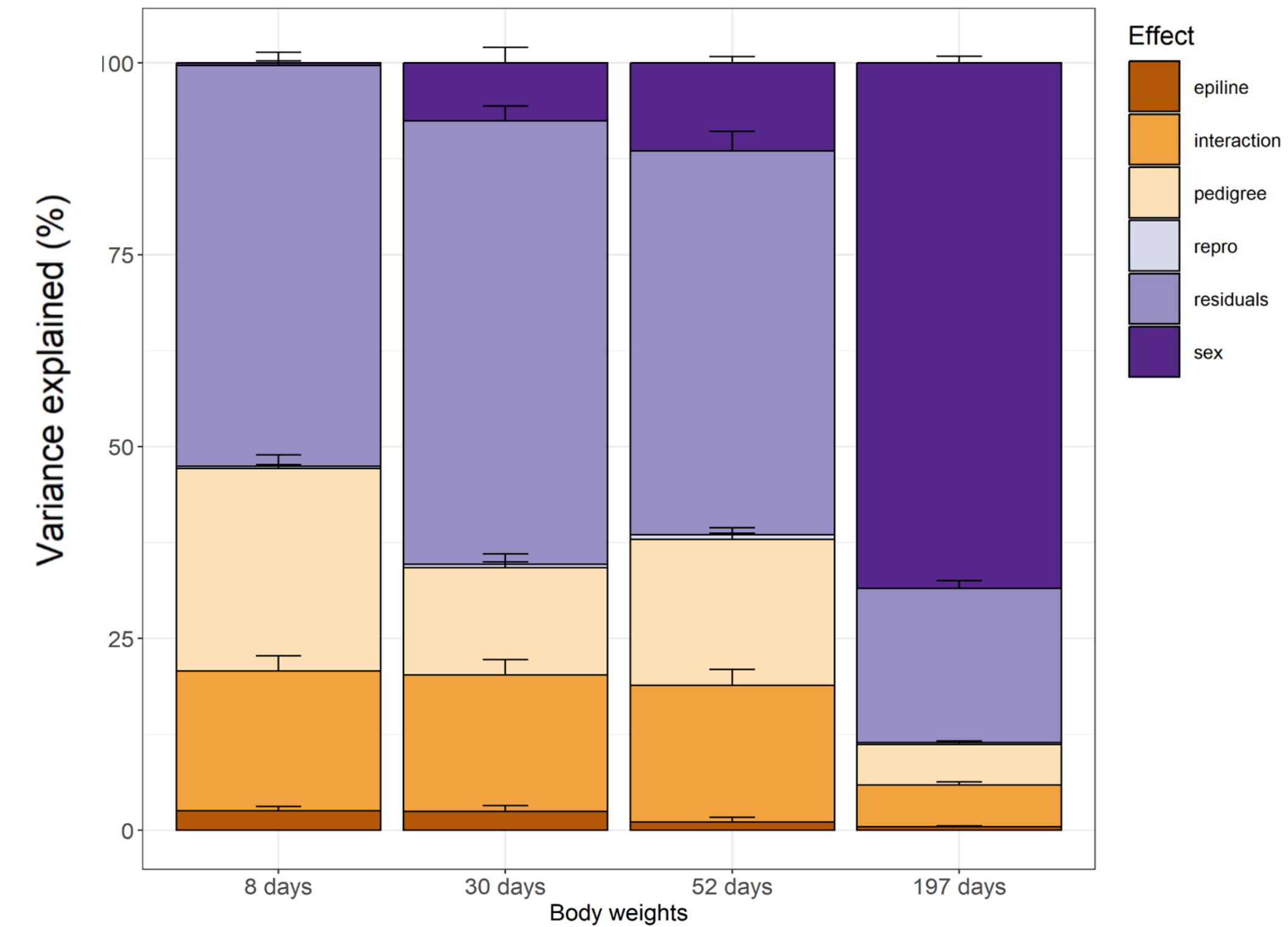
3 – Results: Influence of the epiline on development traits

Multiple linear regression:

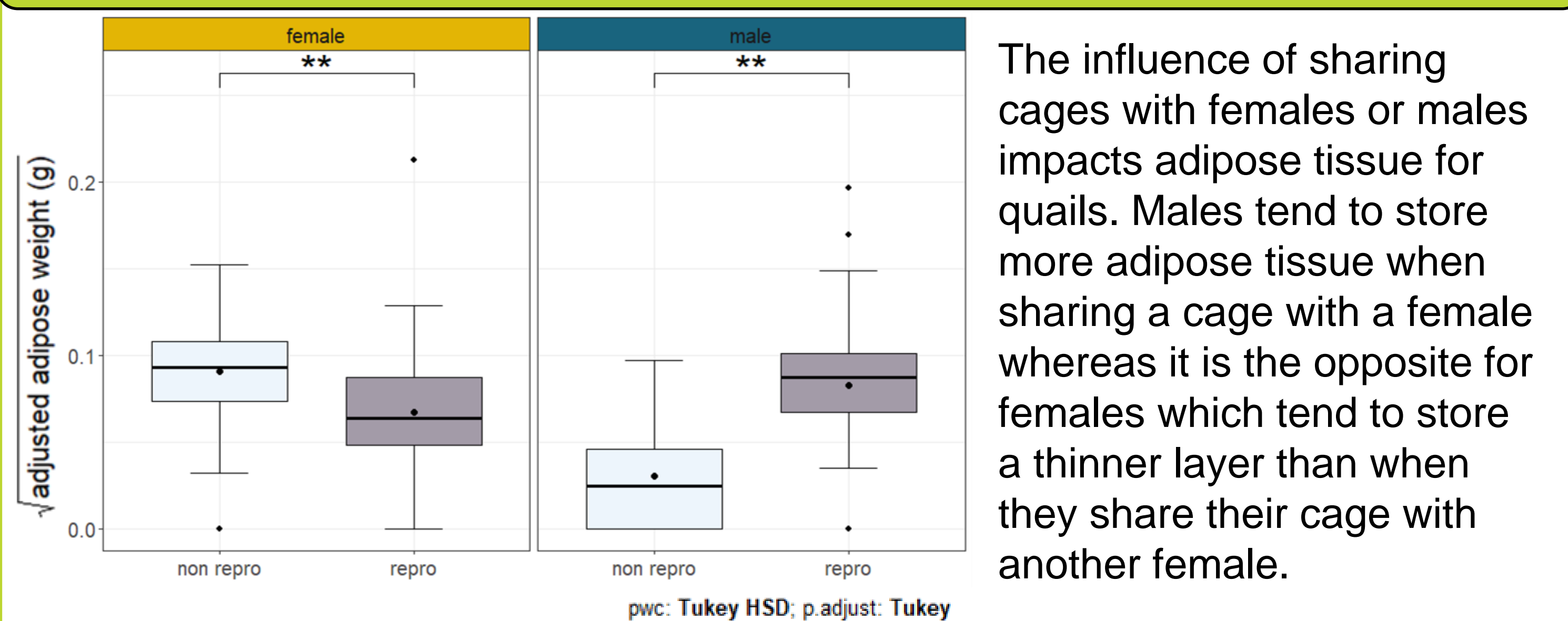
$$Y_{ij} = \text{Sex}_i + \text{Pedigree}_j + \text{Epiline}_k + \text{Repro}_l + \text{interaction}_{ijkl} + \epsilon_{ijkl}$$

Cross validation on 20% of dataset. Results across 5 kfolds.

The effect of epiline is stronger on phenotypes of young individuals. As quails grow, the variance explained by the epiline decreases, and the influence of sex becomes more important.



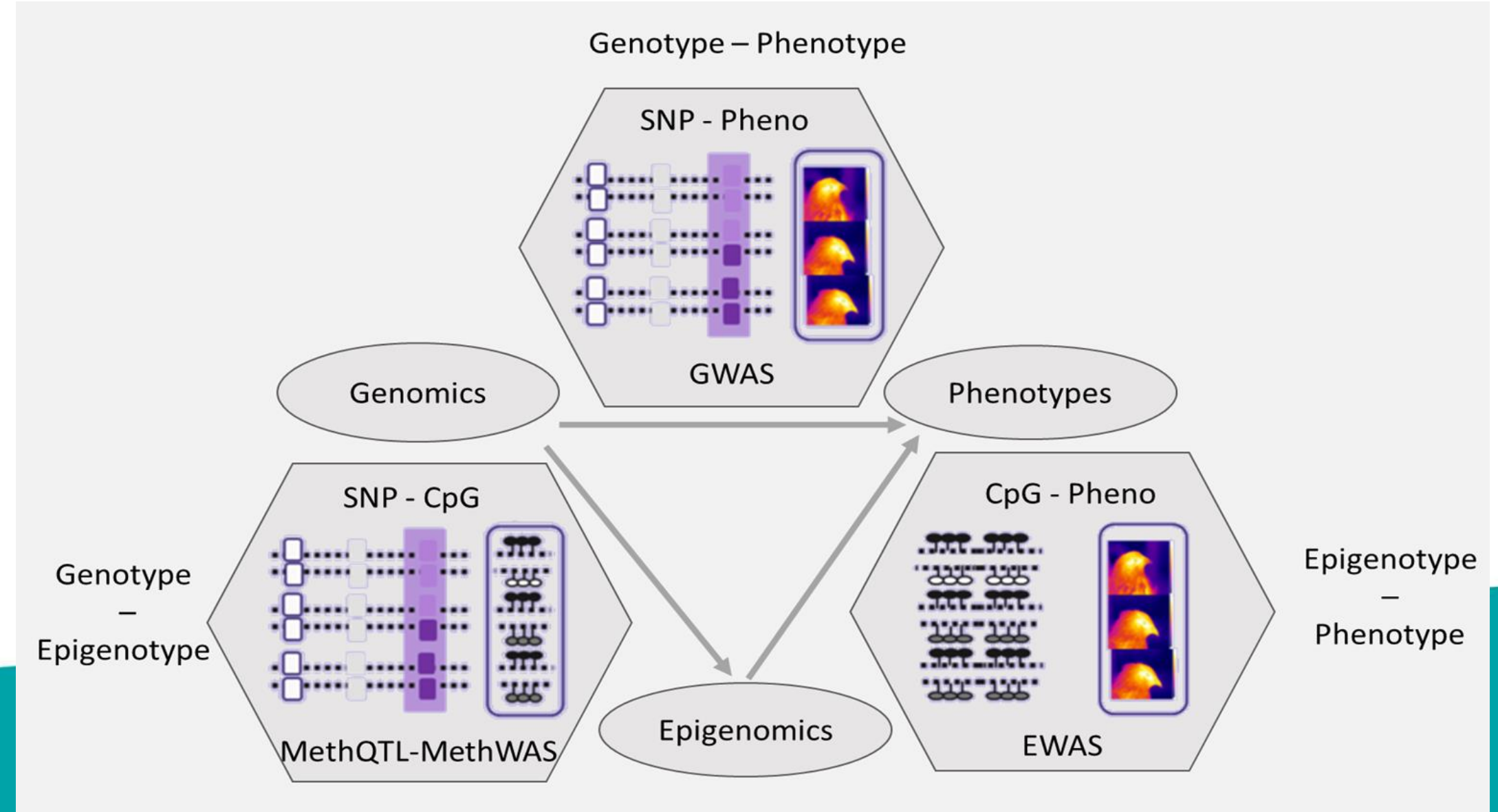
4 – Results: Influence of reproductive status



5 – Discussion and perspectives

Methylation patterns can be sensitive to environmental changes and can be transmitted to next generations. To evaluate the importance of non-genetic inheritance, one major difficulty lies in disentangling epigenetic effects from genetic effects.

We aim to answer this question by using **methylome** and **genome** data to better characterize **multigenerational inheritance** (RRBS data analysis to come) and analyze **transgenerational effects** (G2 data - May 2024).



Centre Toulouse Occitanie