Epigenetic modifications in the coral *Acropora cervicornis* after hurricane impacts in Culebra Island, Puerto Rico

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Background

DNA methylation is the process of adding a methyl group to the 5 carbon position of a cytosine ring (**Fig. 1**). This is an epigenetic modification that can be removed or inherited without any disruption of the original DNA sequence. Its role is yet under investigation but, it has been suggested to be essential for the regulation of development, gene suppression, genetic imprinting and overall acclimatization.
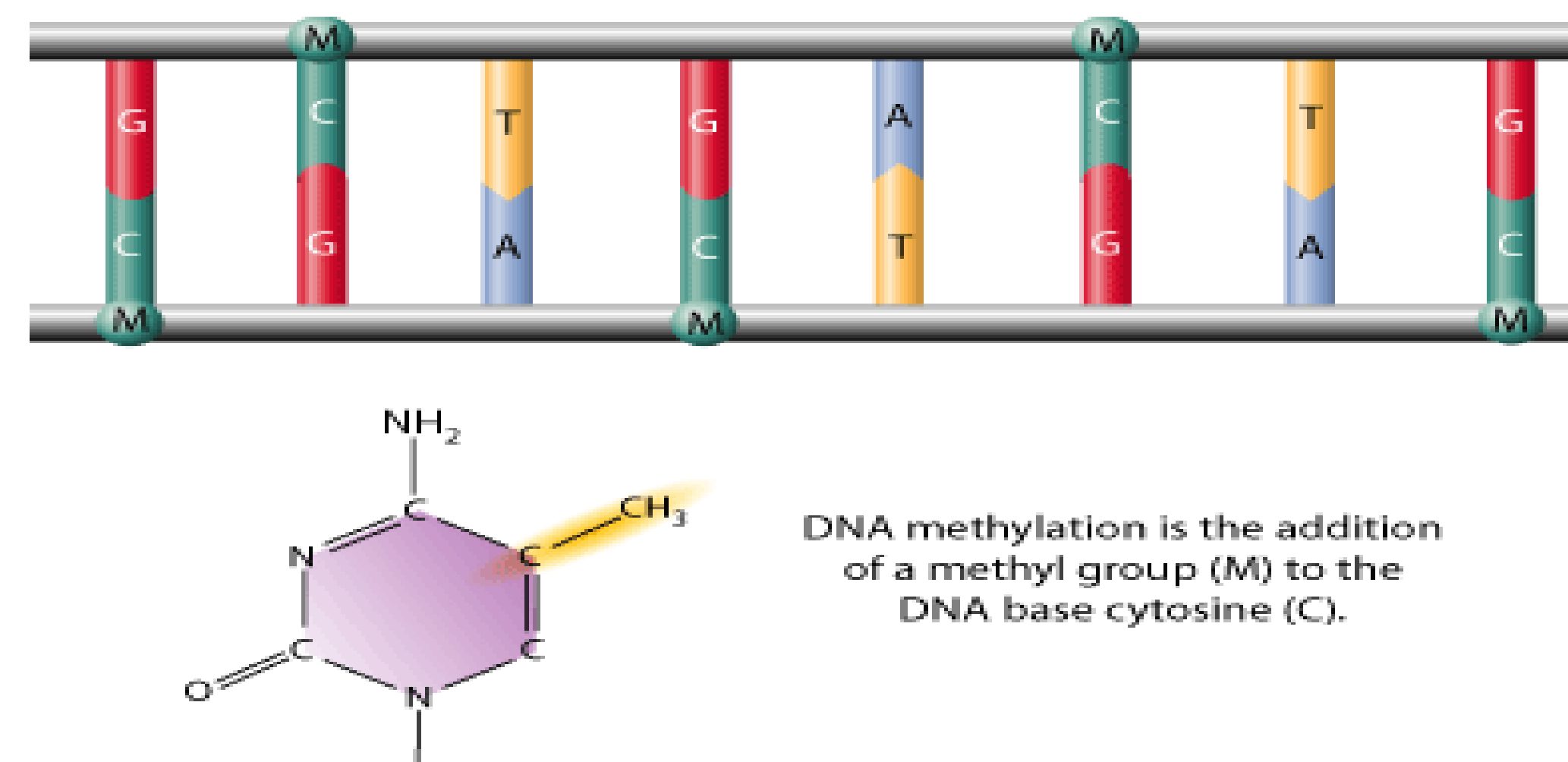

DNA methylation is the addition of a methyl group (M) to the DNA base cytosine (C).

Figure 1. Example of DNA methylation.

Goals

- Determine if DNA methylation differs spatially.

- Determine if standing genetic variation modulates DNA methylation levels.

- Explore the potential demographic cost of DNA methylation, and correlate DNA methylation levels with coral growth rate at different depths.

Methodology

- Samples from 27 *A. cervicornis* colonies (**Fig. 2**) were collected from three different reefs in Culebra, Puerto Rico (**Fig. 3**). All colonies were healthy at the moment of sampling.
- Two fragments were collected from each colony and subsequently outplanted at experimental locations (**Fig. 3**) and depths (5 and 15 m) for further growth rate assessment.
- The length of coral fragments was measured upon outplanting and after one month to determine growth rate.
- Coral tissue was extracted and its DNA isolated in the lab.
- DNA methylation quantification was performed using ELISA.
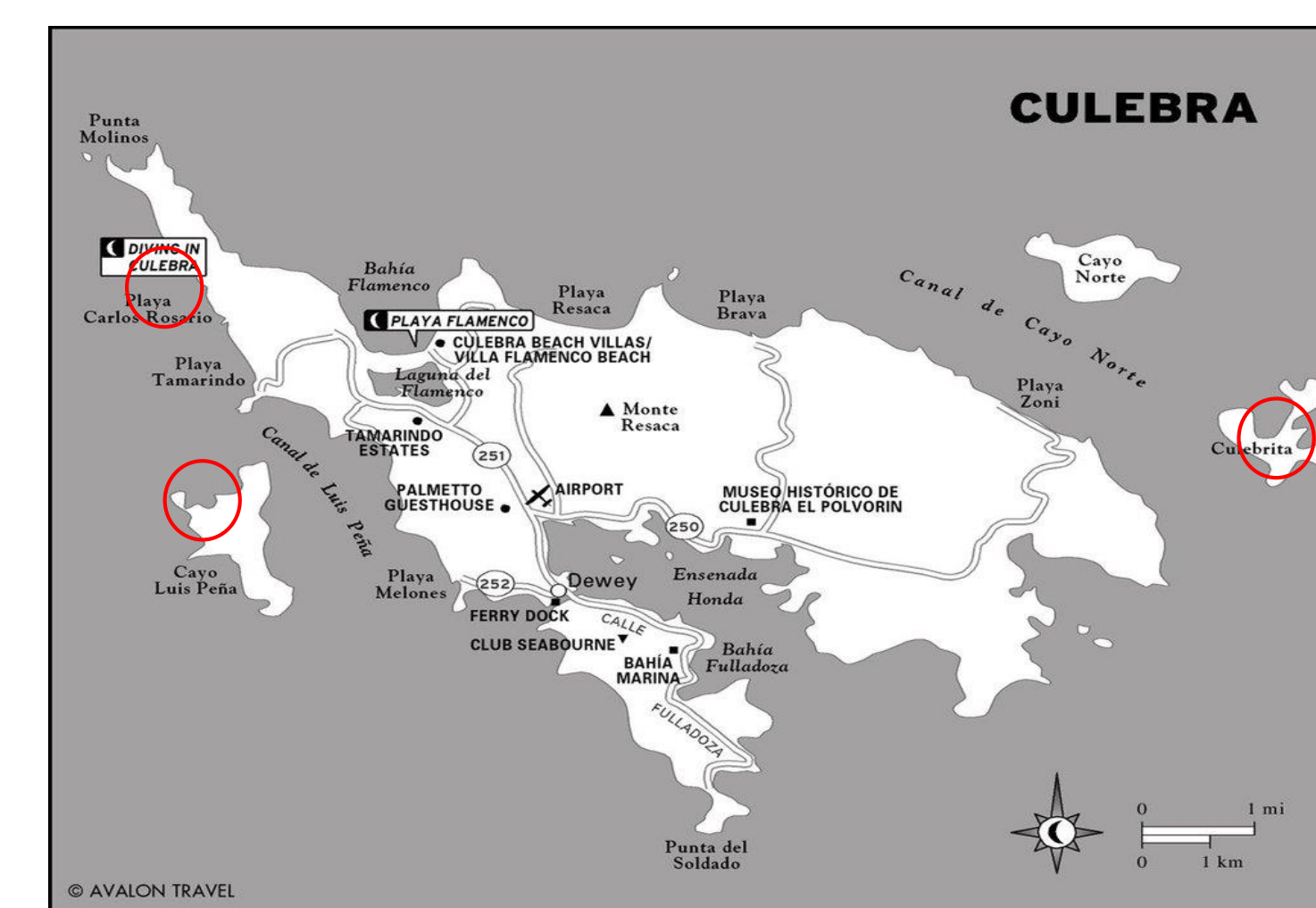

Figure 2. The stony coral *Acropora cervicornis*.

Figure 3. Locations of coral sample collection.

Results

- DNA methylation is greater in Carlos Rosario samples, but it does not differ statistically from the other two locations (**Fig. 4**).
- Two Way PERMANOVA tests indicate that growth rates are not affected by depth ($p=0.087$) nor by location ($p=0.316$, **Fig. 5**).
- A positive (weak) correlation was found between overall DNA methylation and growth rates (**Fig. 6**, R=0.065, $p=0.727$).
- Logistic regression analyses (**Fig. 7**) indicate that survival is not associated with DNA methylation levels ($p= 0.054$).
- Overall, most of the variation observed in DNA methylation is explained by genotype, rather than by coral geographic origin.
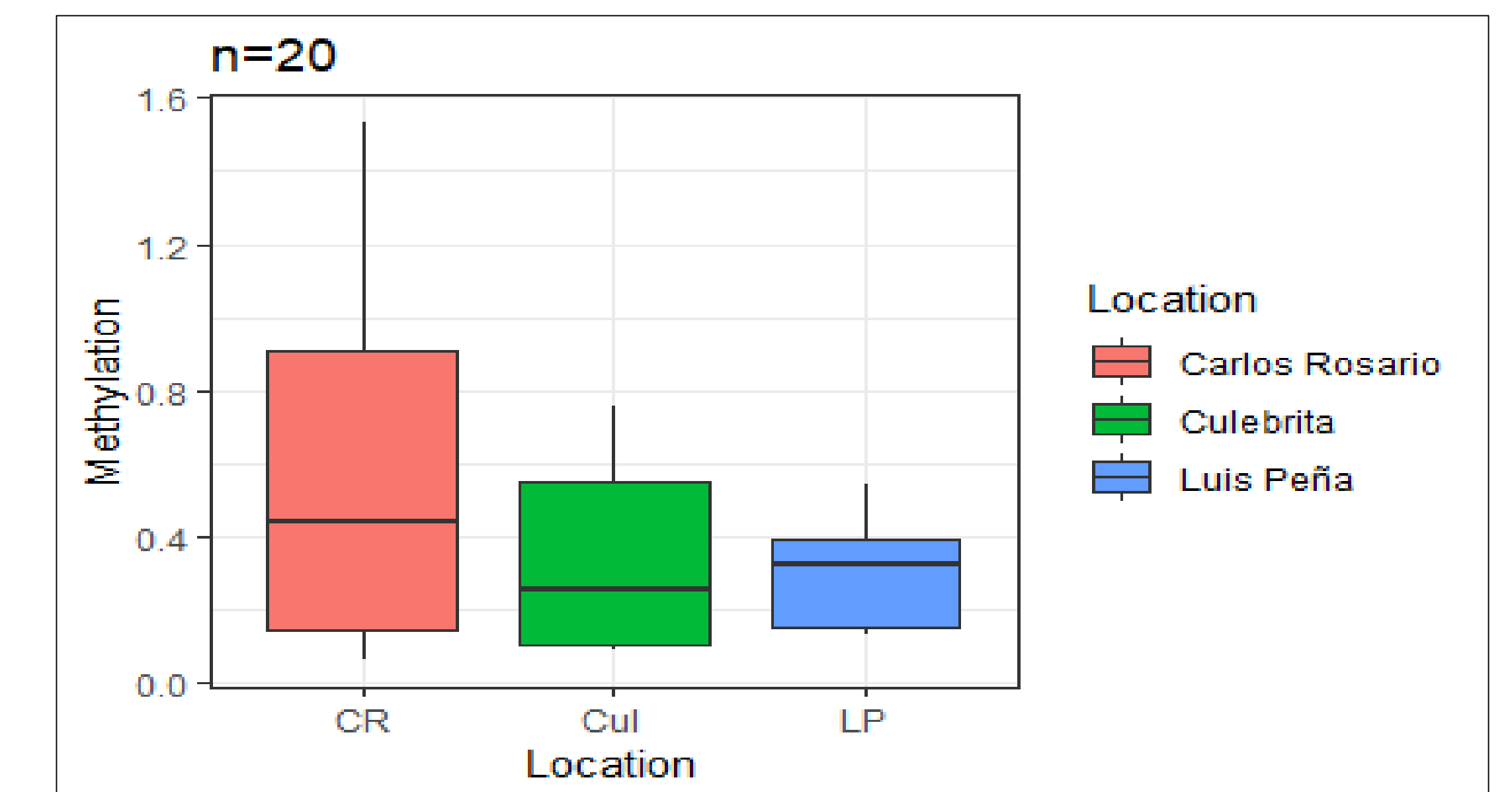

Figure 4. Total DNA methylation levels (%) in coral samples based on their geographic origin.
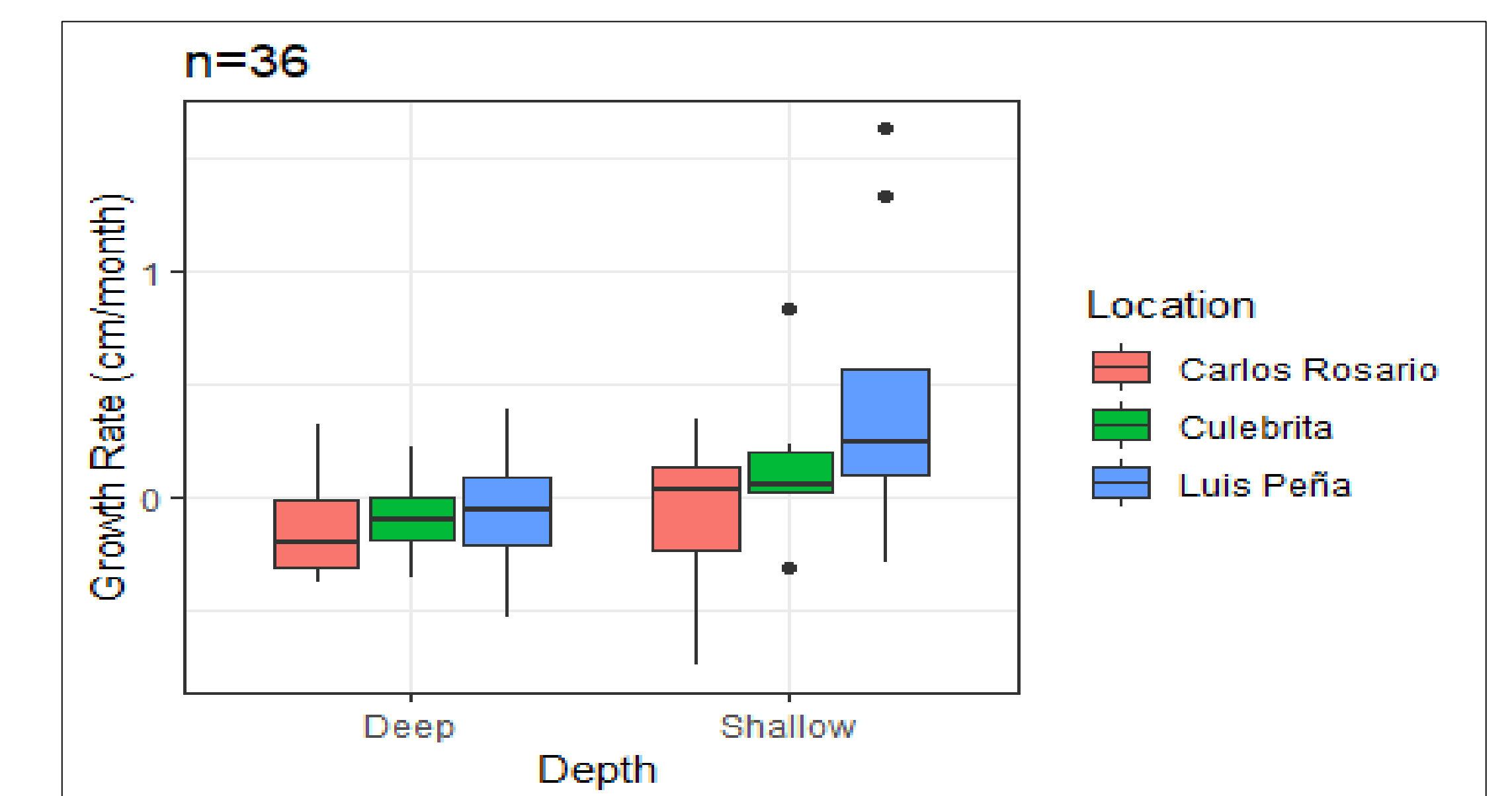

Figure 5. Coral growth rates at different depths based on their geographic origin.
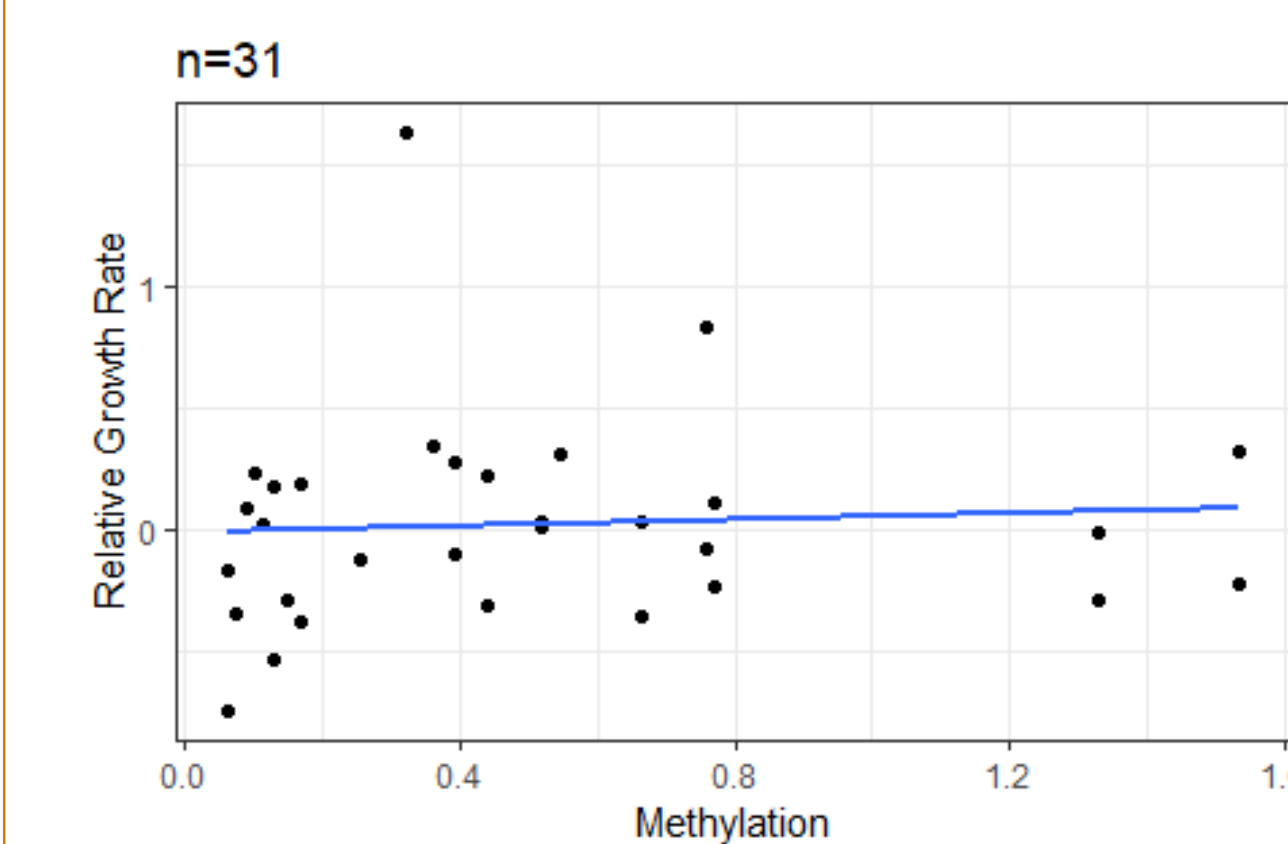

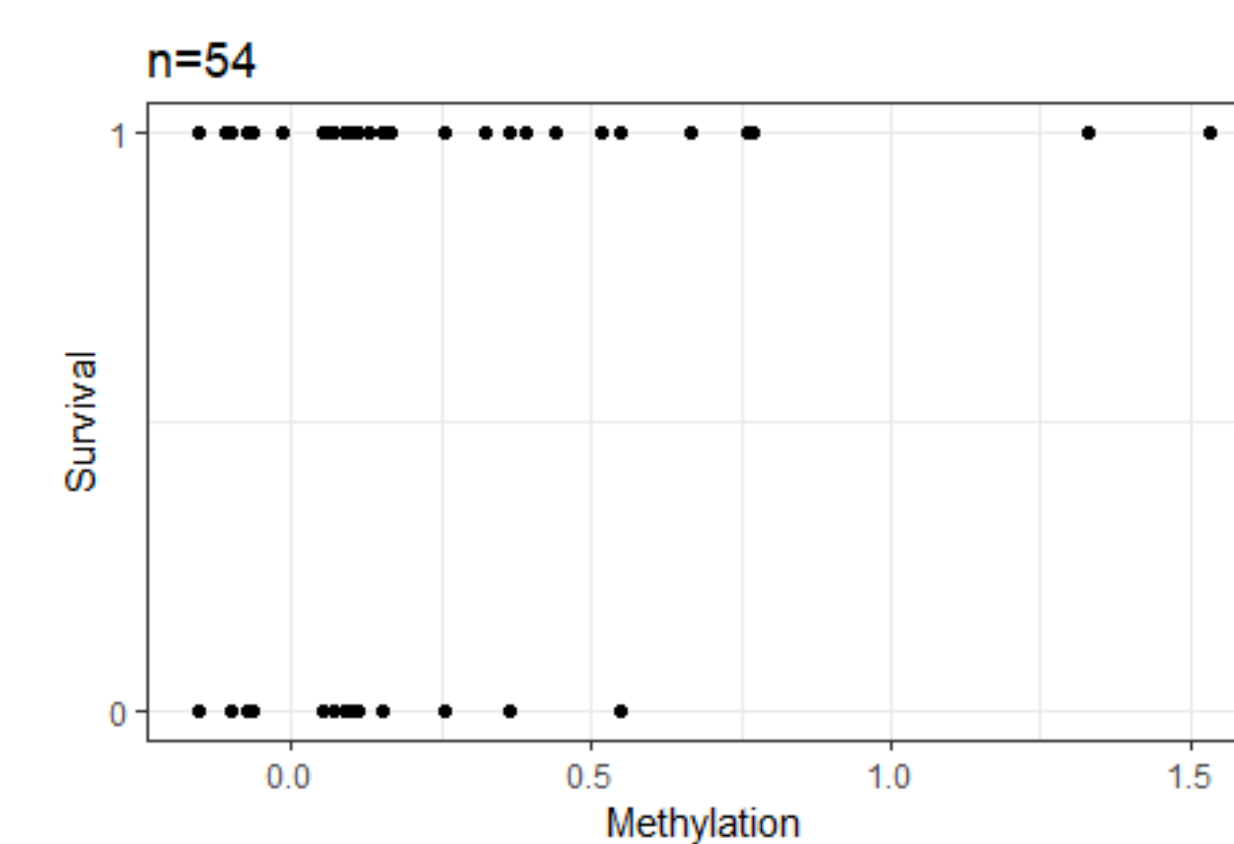**Figure 6.** Correlation analysis between coral DNA methylation and growth rate.

Figure 7. Relationship between coral DNA methylation level and survival.

Take-home message

DNA methylation is the most widely studied epigenetic mark in environmental epigenetic analyses. This study represents the initial phase of a longer project, aimed at determining the regulatory role of DNA methylation on coral growth and survival performance. The present results suggest that coral demographic performance is not influenced by their geographic origin nor modifications in DNA methylation in 1 month old outplants. However, the subtle tendencies observed lead us to expect that as the project moves forward the role of DNA methylation on demographics will become more evident.

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