

FIRST GENETIC INVENTORY OF **Galápagos** **macroalgae** FROM **marine iguanas** FORAGING GROUNDS BASED ON DNA-BARCODING

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Background

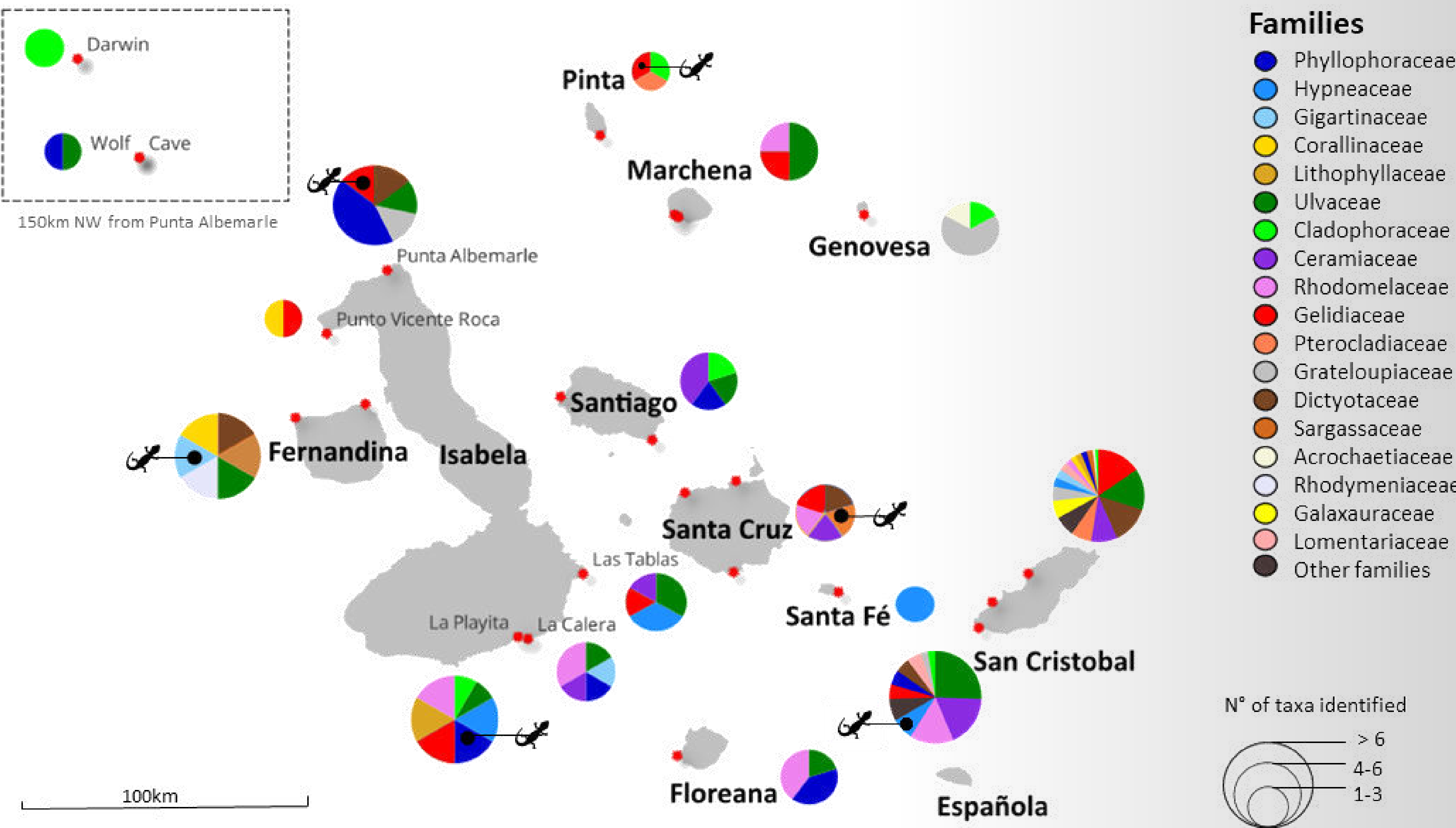
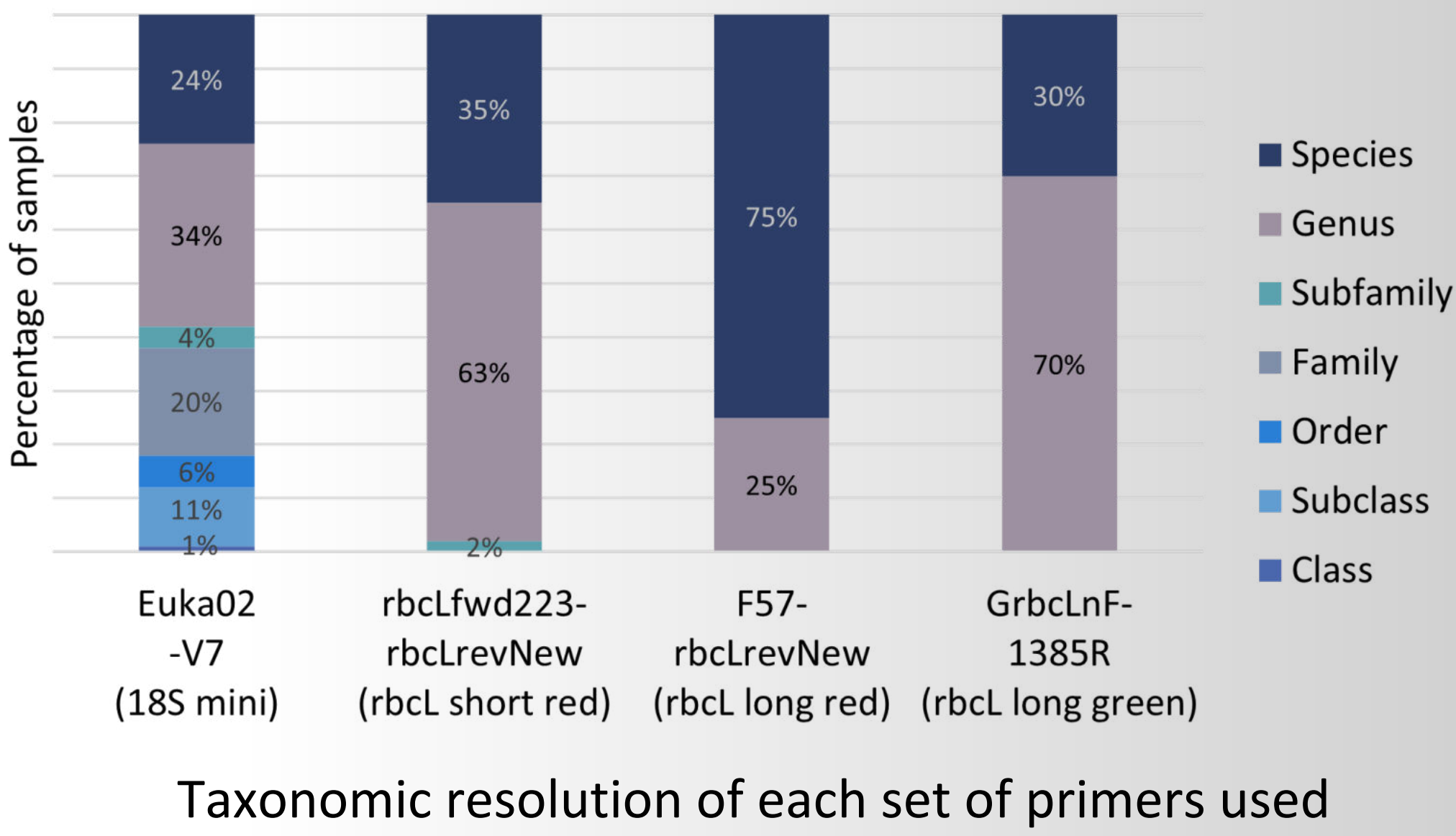
Marine macroalgae from the Galápagos have not been studied in detail and their taxonomic identification has mostly relied on morphology. So far around 300 species of macroalgae are listed for the Galápagos. However, molecular, i.e. DNA-based approaches to determine species richness and diversity are completely lacking.

In this study, we are exploring the diversity of macroalgae sampled in the coastal zone of foraging grounds of endemic marine iguanas, which feed almost exclusively on marine macroalgae. We use direct DNA barcoding of opportunistically collected algae samples along the archipelago.

This is part of an ongoing project to assess marine iguanas diet by genetically identify algae consumed through DNA-metabarcoding of their feces.

Results

We created a DNA barcode reference database with 250 macroalgae sequences (18S and rbcL) with a total of 177 specimens identified, including 135 red algae, 29 green algae, and 13 brown algae specimens. Among them, we found 18 **potentially new reports** of red macroalgae and 3 green algae not listed in the Galápagos before. Phylogenetic trees were created to verify the taxonomic identification with BLAST. In general, our sequences clustered together for the respective genus with high bootstrap support.



Map of the Galápagos archipelago showing sampling sites and the proportions of algae families identified for each island. The iguana symbol marks the algae taxa that was observed being eaten by marine iguanas.

Discussion

Although the taxa included in our database do not reflect algae distribution and diversity of each island, it is a preliminary assessment of macroalgae from the Galápagos with molecular methods.

Available molecular databases of algae are limited and many algae species reported in the Galápagos lack DNA referential sequences. This represented a challenge when assigning taxonomic identification to our sequences, but also strengths the importance of a first Galápagos macroalgae DNA database.

Our DNA-barcoding approach can be easily adapted for DNA-metabarcoding to identify algae species from samples that contain fragmented or degraded algal DNA such as environmental samples or feces.

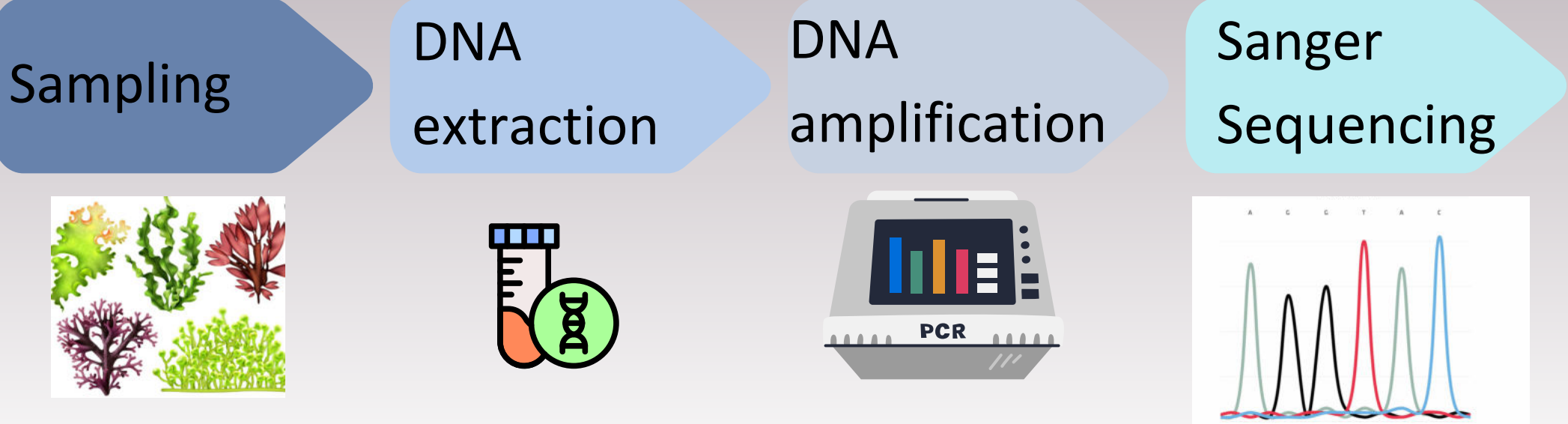
With this approach we can detect algae species from marine iguanas feces, to determine if the algae species identified here are also present or not in the marine iguanas diet.



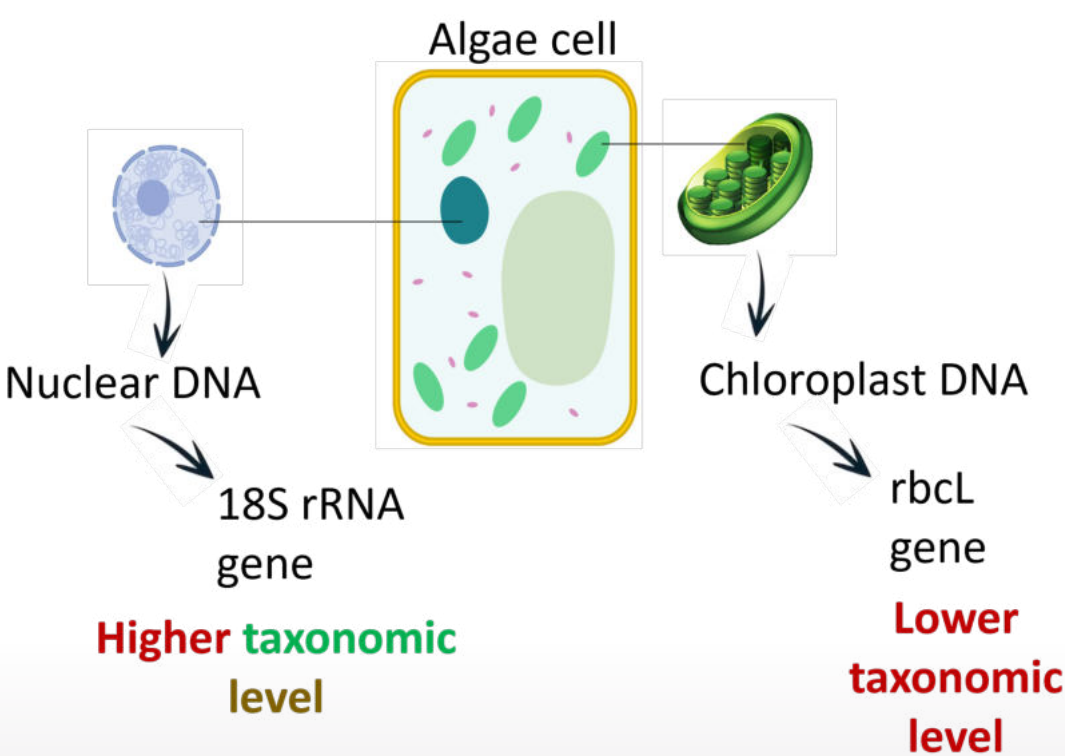
Objectives

- To provide a **first DNA-based genetic inventory** of macroalgae species for the Galápagos islands.
- An overview of macroalgae from the foraging grounds of marine iguanas

Methods



- Macroalgae samples were collected opportunistically in the intertidal and subtidal zones in different islands.
- Primers from the 18S ribosomal gene were modified for a higher taxonomic level identification of all algal groups.
- Rbcl primers were used for different algae. New primers for a short rbcL barcode were designed for higher specificity and resolution towards red algae (preferred by marine iguanas).



Target taxa	Barcode	DNA type	Lenght
Red, green, brown algae	rbcl long	chloroplast	approx. 1300 bp
Red, green, brown algae	18S mini	nuclear	130 bp
Red algae (Rhodophyta)	rbcl short	chloroplast	223 bp