

## How *Ulva* blooms: Unravelling the genetic architecture of green tides

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Every year, more and more ‘green tides’ occur. A green tide happens when a green seaweed, most often sea lettuce, *Ulva spp.*, blooms incredibly fast, and is beached afterwards. These tides can stretch areas bigger than Flanders, >20.000 km<sup>2</sup> (1) along the coast, and can last 3-4 months (1). *Ulva* blooms cause a big disruption to the local ecosystems, but also impact human activities like tourism and represent a big cost to clean up. And because *Ulva* occurs around the world, so do these tides. However, the mechanisms surrounding them are still somewhat a mystery. What causes these blooms? Is it genetics, is it due to the environment? Or, more likely, is it due to a combination of both? In short, my project aims to find out what the genetic component is of these blooms (2). *Ulva compressa*, a macroscopic green seaweed that occurs around the world, is the focus of this study. The first step is to understand the genetic diversity. This is where the pangenome of *Ulva compressa* comes in. Now, what is a pangenome exactly? And how do we use it?

A pangenome is, ideally, a complete collection of all genes within that species. More realistically, it is a big collection of several genomes from different populations, with different phenotypes (3). Why do we want, or need, a pangenome? We hypothesize that the intraspecific genetic variation (meaning, the variation within our species), is very high in *Ulva compressa*. In the few available genomes, there are large observable differences: In size alone, some individuals can have a genome that’s almost double the size of other individuals (4, 5). We need a pangenome to encapsulate all of this variation. Starting with a reference genome, other genetic material is carefully added, matched and compared to this reference. Here, we’ll be able to see which genes are universal in our species, and which genes are unique to some individuals. Unique genes and other genetic variation (insertions, deletions, single-nucleotide polymorphisms) in common genes will be studied to understand the phenotypic differences between strains.

The reference genome in our case will be two lab strains. We are currently improving the reference genomes using longer reads, which will give us a better resolution than the one currently published. When this genome is assembled, we will start adding our other strains. For this, we will sequence individuals from across the world: The Netherlands, France, Germany, Denmark, Ireland, China, Japan, Chile, and are still collecting more. This will give a clear overview of the genetic diversity found within *Ulva compressa*. Additionally, we are documenting different phenotypic traits such as growth rate, morphology and rhizoid formation to perform genome-wide association studies. This pangenome will be the basis for other, more detailed genetic analysis that will follow in the coming years of this project.

### References

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### Keywords

*Ulva Compressa*; Green Tides; Pangenome; Algal Blooms; Population Genomics