

Summary

Study on the artificial induction of zooid formation and the phylogenetic taxonomy in genus *Ulva* (Chlorophyceae) in Japan

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Synchronous gamete formation in *Ulva* was induced in excised disks maintained sterilized seawater. Gametes were released from mature disk tissue on the morning of the second or the third day after excision. Using this synchronous gamete formation, crossing tests were made to determine the relationships 1) between the identified *Ulva pertusa* which is most common species in Japan and the European *Ulva rigida* which is cosmopolitan species, and 2) between *Ulva pertusa* growing as an attached form on exposed rocks and the floating *Ulva* forming “green tide” inside calm bays.

U. pertusa crossed with *U. rigida* from the Netherlands but not with *U. rigida* from France. In the phylogenetic analysis of ITS1 sequences, *U. pertusa* and *U. rigida* from the Netherlands were clustered and *U. rigida* from France separated from them. *U. rigida* from France have microscopic protuberances in margin of the thallus different from *U. pertusa* and *U. rigida* from the Netherlands without the protuberances. From these results it was concluded that *U. pertusa* and *U. rigida* from the Netherlands belong to the same taxon and *U. rigida* from France is a different species from them. Phillips (1988) supposed that *U. rigida* from France is not original *U. rigida*. The present study supports her supposition. Because *U. rigida* from the Netherlands agree with description of *U. rigida*, I suppose that *U. rigida* from the Netherlands is original *U. rigida* and *U. pertusa* is a synonym of *U. rigida*.

The floating *Ulva* thalli were collected from five major green tide sites in Japan (Yokohama, Mikawa, Miyajima, Kochi and Hakata). Reproductive maturation was induced in *U. pertusa* and the floating thalli from each site. Mating between induced gametes was observed. It is therefore believed that the floating thalli from Yokohama, Mikawa and Miyajima were mainly *U. pertusa*, while those from Kochi and Hakata were of a different species (*Ulva* sp.1). Furthermore, the *Ulva* species found in Mikawa is also a species (*Ulva* sp.2) different from both *U. pertusa* and *Ulva* sp.1. These results were supported by the molecular analysis of ITS1 sequences.

The combination of crossing test and molecular analysis of DNA has been used for *Ulva* taxonomy for the first time in the present study. Two main taxonomic problems mentioned above have been solved by the combination study.