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Incorporated Administrative Agency, Fisheries Research Agency

World's first draft sequencing of the *Porphyra yezoensis* genome

**Points:**

- The genomic sequence of *Porphyra yezoensis* was determined.
- The information is useful for identifying traditional cultivars and breeding new cultivars.

The Fisheries Research Agency, Hitachi Software Engineering Co., Ltd. and Japan Software Management Co., Ltd. have been jointly decoding the entire genomic sequence of *Porphyra yezoensis* and have successfully assembled the draft sequence for the first time in the world. The laver, *Porphyra yezoensis* is widely cultivated in Japan and the yield amounts to about 80 billion Japanese yen per year.

This time, the entire genetic information in the nuclear genome was outlined (draft of the genome information) for the first time. The sequence information in the mitochondrial and proplast genomes was also decoded, revealing the entire genetic information of the laver cell.

The genomic information will help identifying laver cultivars, which are impossible to distinguish each other from the external appearance of the products, and genetic identification of cultivars will protect “breeder’s rights” from infringement of laver cultivars. Molecular technologies for laver cultivar identification will be improved, and the information used for breeding new cultivars that can adapt to recent changes in coastal marine environments, such as higher water temperature.

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