Trends in seaweed research

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Teaser: A letter on the evolution of trends in seaweed research with respect to the development of technology and generation of knowledge, as well as difficulties and future perspectives in seaweed research.

Marine macroalgae, better known as seaweeds, are classified according to their pigmentation into brown (Phaeophyta), red (Rhodophyta), and green (Chlorophyta) seaweeds. They are widely used as food, as ingredients in cosmetics and fertilizers, and in hydrocolloid production (e.g. agar and alginate). Seaweeds are of ecological importance because they assist in supplying oxygen to the sea and act as one of the primary producers in the marine food chain. Some seaweeds have the capacity to remove heavy metals from the water and can potentially be used in biomonitoring and in the bioremediation of such pollutants. Seaweeds also possess excellent survival strategies to withstand the many environmental stresses that they are exposed to. For all these reasons, together with their unique life-cycle and physiology, seaweeds are interesting study subjects. In this Letter, we would like to highlight the development of seaweed research and to emphasize the importance and difficulties in developing a useful genetic model.

A timeline highlighting important areas in seaweed research is shown in Table 1. Since the 1940s, when the potential of agar production from seaweeds was recognized, taxonomy, physiology and biochemistry have been the main research focus. Physiological aspects related to the production of hydrocolloids and pigments, and to mass cultivation of seaweeds, have been of particular interest. These areas of research laid the foundation of our understanding of seaweed biology. Despite the development and progress of functional genomics in terrestrial plants, seaweeds had received little attention worldwide and were not included in efforts to elucidate gene functions. It was not until the 1990s that studies on the molecular genetics of seaweeds were initiated. These studies were pioneered with the development of genetic transformation

techniques on seaweeds [1] and the characterization of genes involved in carbohydrate synthesis [2]. The adaptation of molecular techniques enabled a more reliable and systematic way of inferring evolutionary relationships among different strains or species.

Genetic research in seaweeds entered a new phase following the first use of the expressed sequence tag (EST) approach to study seaweed genomics [3] – a relatively inexpensive and quick approach for novel gene discoveries. However, the number of reported seaweed ESTs to date (of which >80% are from the red seaweeds *Porphyra* and *Gracilaria*) accounts for only 0.11% of all publicly available ESTs (Release 20/01/2006 http://www.ncbi.nlm.nih.gov/dbEST/). The EST collection of *Porphyra yezoensis* at Kazusa DNA Research Institute in Japan (http://www.kazusa.or.jp/en/plant/porphyra/EST/index.html) represents the most comprehensive, publicly available EST database for seaweed.

The EST approach has spurred the development of seaweed research at the molecular level, an emerging area being research on seaweed defence mechanisms against pathogens and environmental stresses, which is assisting in formulating strategies for crop protection and cultivation [4]. However, what is needed is a seaweed genetic model that is easy to culture in vitro, that is susceptible to genetic modification and testing, and that has a wide geographical distribution. Some researchers have proposed the red seaweed *Porphyra yezoensis* as a seaweed model [5], but the research group at the National Centre for Scientific Research (CNRS) in France recently named a brown seaweed, *Ectocarpus siliculosus*, as their candidate [6]. Because of the differences in

physiology and developmental biology among the red, brown and green seaweeds, a move to have a genetic model for each of these seaweed groups appears desirable. No matter which seaweed the research community decides on, it is likely to be some time before a consensus is reached regarding a seaweed genome sequencing project because the scenario of seaweed research and the choice of a model plant can be financially biased owing to climate and geographical differences and/or government policies among different countries.

Seaweed research has not been receiving appropriate attention and funding in the past, and the availability of seaweed genomic data is still scarce compared with that of terrestrial plants. Given that seaweeds share little similarity with other organisms, the limited amount of genomic data available makes the task of elucidating the function of unknown genes from seaweeds difficult. This is further complicated because nucleic acid extraction from seaweed can be species- or strain-specific owing to the nature of the cell wall and its extracellular matrix [7]. Although the ongoing advances in molecular and computational approaches in genomics should accelerate the progress of seaweed research, a platform for more-effective communication and information exchange among seaweed research scientists (e.g. http://www.seaweed.ie/) is useful for attracting funding support. However, much more is needed; in particular, collaborative and networking efforts to gather the financial resources and expertise available worldwide to study seaweed genomics. New approaches in understanding seaweed physiology, biochemistry and molecular biology should contribute to an improved market value of seaweed produce and new insights into human nutrition, and enable genetic engineering of favourable agronomic traits, such as disease resistance, through

genetic manipulation and transformation of seaweed genes in economically important crops.

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Table

Table 1. The timeline of seaweed research.

Years	Activity/research highlights	References
1940s	Discovery of hydrocolloids from seaweeds; seaweed biology; research on seaweed as food.	[8]
1952	First International Seaweed Symposium in Scotland.	
1960s – 1970s	Taxonomic classification; biogeography and ecophysiology of seaweeds.	[9]
1980s – early 1990s	Mutant studies; seaweed cultivation and biotechnology; properties of hydrocolloids and their applications in industries; drug discovery and bioactive compounds from seaweeds; classical genetics	[10,11]
Mid 1990s	Genetic transformation and tissue culture; molecular phylogenetics; small-scale gene cloning and characterisation.	[1,2,12]
1997	Introduction of EST approach in large-scale study on molecular genetics.	[3]
2000s –	Search of a model plant for large-scale genomic study; shift to multi-disciplinary research.	[5,6]