

GENOMICS

From sea to sea

The genome sequence of the marine flowering plant eelgrass (*Zostera marina*) sheds light on how marine algae evolved into land plants before moving back to the sea.

SUSAN L. WILLIAMS

Eelgrass (*Zostera marina*) is a member of a family of highly specialized, sexually reproducing, marine flowering plants known collectively as seagrasses. It is an unlikely model for plant evolution, but is a useful one because it has undergone major habitat shifts: it evolved from marine algae into a terrestrial flowering plant, then moved back to the sea again. In a paper online in *Nature*, Olsen *et al.*¹ describe the complete genome sequence of eelgrass. Their study marks the culmination of 8 years' work by 35 scientists from around the world, and should help plant biologists not only to dissect how eelgrass evolved, but also to gain a better understanding of flowering-plant evolution in general.

Seagrasses have been largely ignored by evolutionary biologists, perhaps because they are so often out of sight. But eelgrass can form vast green coastal-sea meadows that support many species (Fig. 1), including ecologically and economically valuable organisms such as halibut, clams and endangered sea otters. As such, it is a good model system in which to analyse how genetics plays into ecosystem functioning — an understanding of which is the linchpin for human efforts to conserve biological diversity in the face of a rapidly changing Earth. Moreover, eelgrass is as productive in terms of biomass as are maize (corn) and sugar cane, and its root mat stabilizes sediments and thus shorelines. Indigenous peoples from the US Pacific Northwest to Mexico have built cultures around eelgrass, and Europeans have used it to stuff furniture and to insulate homes, and have even grazed cattle on intertidal meadows².

Eelgrass is unusual from an evolutionary standpoint, too. The plant completed a remarkable feat when it readapted from a freshwater to a marine lifestyle and became able to compete with seaweeds. Its evolutionary path began with marine green algae, which evolved to cope with terrestrial habitats and to produce flowers and seeds. Then, angiosperms (the collective name for flowering plants)

entered fresh water — an evolutionary step that seems to have been made many times. From the freshwater angiosperm lineage, eelgrass, along with a few other seagrass species, diverged to return to the sea. But it seems that this step occurred just three times³, indicating the extreme nature of this habitat shift.

Despite the plant's evolutionary and ecological importance, genetic analysis of eelgrass did not begin until the 1990s (ref. 4), more recently than for other angiosperms such as wheat, peas and land-dwelling grasses. The early studies were fraught with setbacks, because it proved difficult to purify the DNA and protein variants found in different plants of the species. Furthermore, scientists have never successfully

artificially selected or genetically engineered eelgrass. Thus, the classic approach of crossing plants cannot be used to delve into seagrass genetics. Given this problematic history, Olsen and colleagues' sequence represents a major advance.

The complete genome sequence reveals that, in moving from calm lakes and ponds to the rough, salty ocean, eelgrass lost several key gene groups. It lost all of the genes involved in stomata (pores on plant leaves that regulate gas exchange and minimize water loss). These pores are not essential in seagrasses, because the plants are not prone to moisture loss, and they absorb dissolved gases directly through outer cell layers. The organism also lost genes that confer protection from ultraviolet light, as well as those involved in sensing far-red light — these wavelengths do not penetrate very far in coastal waters.

During the move to the sea, eelgrass regained genes encoding cell-wall compounds that were lost when marine algae transitioned to land. These genes have crucial roles in allowing osmotic adjustment to salt, and in promoting nutrient uptake and gas exchange in saltwater environments. Other evolutionary innovations include changes that enable pollen to stick to stigmas (the tips of female flower parts) in salt water, an expanded capacity to capture light and to photosynthesize in dim coastal seas, and a loss of genes encoding the proteins that synthesize and sense volatile terpenes, compounds that are common in aromatic herbs but that would not be effective in an aqueous environment in their putative role of deterring predators in the ocean.

The eelgrass genome is valuable for several reasons. For evolutionary biologists, it represents a missing piece in the puzzle of angiosperm evolution. It also provides a wealth of information that will improve our understanding of diverse biochemical pathways. For example, identification of the DNA sequences of genes that confer tolerance to salt water means that the plant could provide a model system in which to study how agricultural crops might adjust to increasingly saline soils.

Eelgrass is remarkably adaptable, growing under ice in the Arctic Ocean and surviving scorching heat in the Mexican state of Baja California. It also has the largest distribution of any plant in the temperate Northern Hemisphere. For marine ecologists, the genome is a powerful tool for uncovering the adaptations that allow the plant to thrive in a wide range of environmental conditions. This ability to adapt might be the



Figure 1 | Eelgrass ecosystems. The eelgrass *Zostera marina* is home to an abundance of wildlife, including sea anemones.

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key to surviving environmental changes such as ocean acidification, warming and freshening that are occurring under global climate change. It is already known that eelgrass populations that are more genetically diverse survive disturbances better, can be restored more rapidly, produce more biomass and support more animals than their less-diverse counterparts⁵. Now, the genome will help researchers to delve into exactly which genetic elements facilitate such high biomass production and resilience.

Olsen and colleagues' genome-sequencing feat may have come just in time. Seagrass ecosystems are being lost rapidly, with

seagrass fields disappearing at a global rate of about one American-football field every 30 minutes; some species and their associated animals are even threatened by extinction⁶. The disappearances are attributable to human disturbances such as building marinas, over-fertilizing coastal waters and aquaculture⁷. Seagrass restoration and conservation efforts are under way across the globe, and an understanding of the genes that adapt these fascinating species to marine life can only help these efforts. ■

Susan L. Williams is at the Bodega Marine Laboratory and Department of Evolution

and Ecology, University of California, Davis, Bodega Bay, California 94923, USA.
e-mail: slwilliams@ucdavis.edu

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