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This research, conducted by a team stationed in China, focuses on seagrasses and its ability to adapt to the marine environment. This is because Seagrasses used to be terrestrial plants (monocotyledons), but they evolved and adapted to be able to live in marine environments. The study of these seagrasses showed that the emergence of seagrasses represents one of the most striking evolutionary transformations in the evolutionary history of angiosperms (Chen et al, 2022). Research done by other research showed that these seagrasses had lost many different genes that they used to share with terrestrial or floating aquatic plants, however this also leaded to the discovery of the gene that relates to salt tolerance which, which is present in these aquatic plants.

This study focuses on Mitochondria because they are unique organelles found in eukaryotic cells that have their own genetic system. They provide energy for all cellular life activities which is why they are known as the ‘powerhouse’ of the cell. The study of mitochondria focuses even more specifically on the functional genes found within mitochondria. The sequence of the mt genomes is very conservative, however the number, location, and order of the functional genes vary greatly among different species. The researchers are studying the adaptation ability of these seagrasses to enhance their understanding of the evolution of these plants' adaptative ability. The researchers believe that there has been no other study done like this before on seagrasses and have the intent to be able to better understand the seagrass genetics from these results. (Chen et al, 2022)

The research and experimentation were done on two specific seagrasses, both of which are endangered; Zostera japonica and Phyllospadix iwatensis. The results helped support genome size reduction, gene loss, and adaptive evolution in seagrass by providing new evolutionary evidence. The researchers found that a large number of sequences repeated in the seagrasses and the most abundant ones were 31-50 bp repeats. The results also provided new information that showed the loss of extensive ribosomal protein genes throughout evolution. That being said, there were actually two exceptions to that, and the genes are the rps7 gene and the rpl16 gene. Genes that were also found that help suggest their adaptive ability to the marine environment include atp8, nad3, ccmFn, and matR. It is thought that the genes nad3, nad6, and ATP8 play a role in the ability to adapt to the low amount of oxygen in the environment while the gene ccmFn is reported to increase transcription levels in embryos subjected to osmotic stress and salt. The MatR gene has been retained as a conserved ORF in the mtDNAs in just about all angiosperms. The researchers speculate that these two genes also play an important role in the ability of seagrasses to adapt to marine environments. (Chen et al, 2022)

Chen, J. et al. Comparative analysis of mitochondrial genomes reveals marine adaptation in seagrasses. *BMC Genomics* **23**, 800 (2022)