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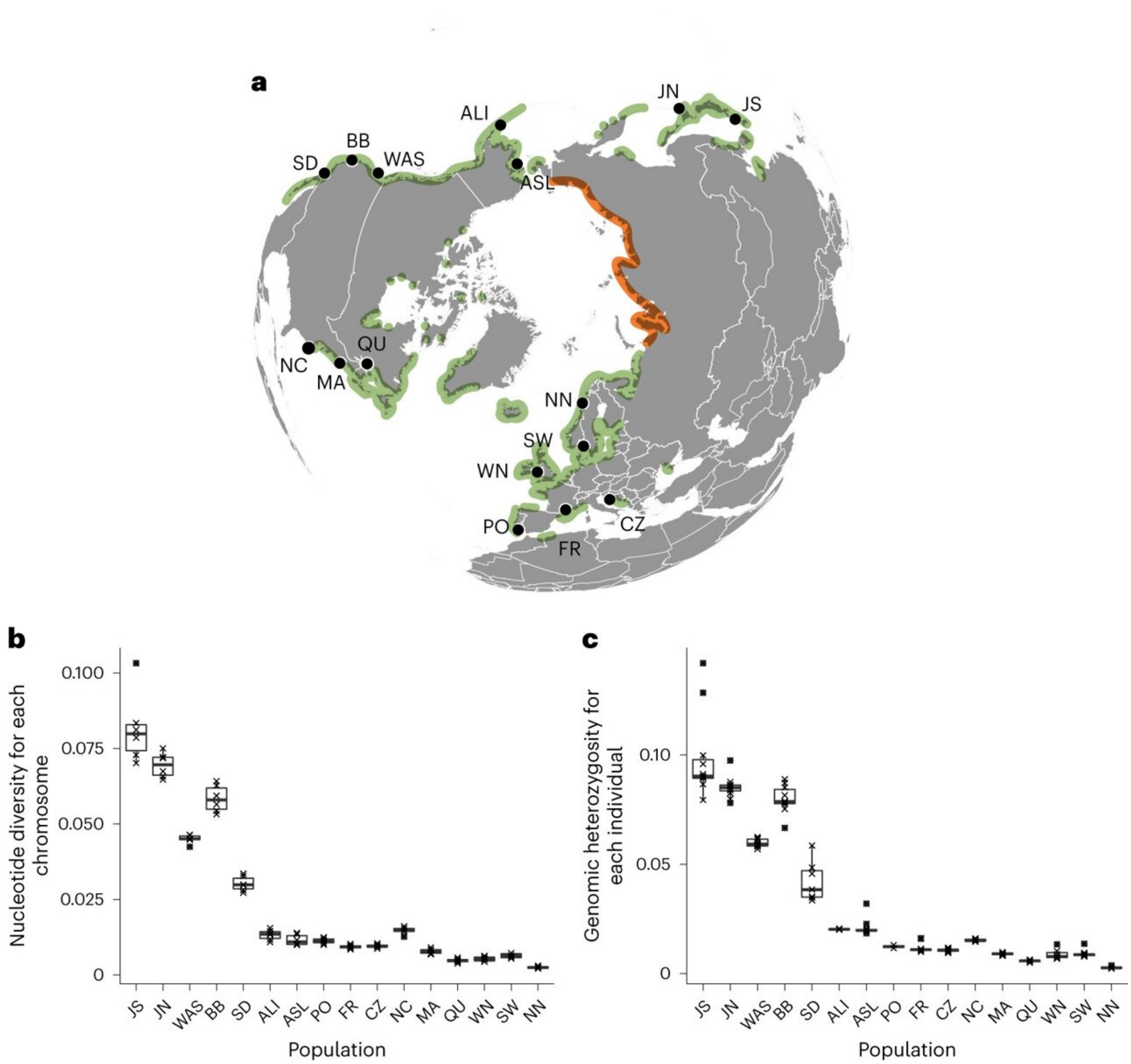
How eelgrass spread around the world

July 20 2023



Distribution and sampling sites for *Z. marina* and their widely varying genetic diversity. **a**, Green areas indicate the presence of *Z. marina*. Arctic Canada locations were added from ref. [76]. The orange line along the Siberian coastline represents the absence of *Z. marina* based on cursory surveys of Alismatales including *Z. marina* by Russian colleagues. The latter areas are characterized by gravel coasts, river outflows and turbid waters. Detailed location metadata can be found in Supplementary Table 1. **b**, Genetic diversity: box plots (median, 25/75% percentile, range whiskers within 1.5× of inter-quartile range, outliers >1.5× of inter-quartile range) of nucleotide diversity (π), calculated for each of the six chromosomes based on 44,865 SNPs (Supplementary Fig. 1). Each data point indicates one chromosome. **c**, Box plots of individual genome-wide heterozygosity H_{obs} based on 144,773 SNPs (data set ZM_neutral_SNPs; Supplementary Fig. 1), as (number of heterozygous sites)/(total number of sites with genotype calls). Each data point corresponds to an individual ($N = 2–14$ individuals, for exact values see Source Data Fig. 1). Statistical tests for differences in mean π or H_{obs} are given in Supplementary Table 4. WN, Wales-North; FR, Mediterranean France; CZ, Croatia. Credit: *Nature Plants* (2023). DOI: 10.1038/s41477-023-01464-3

Seagrasses evolved from freshwater plants and use sunlight and carbon dioxide (CO_2) for photosynthesis and are able to thrive in depths down to 50 meters. In contrast to algae, they possess roots and rhizomes that grow in sandy to muddy sediments. The grass-like, leaf-shoots produce flowers and complete their life cycle entirely underwater. Seeds are negatively buoyant but seed-bearing shoots can raft, thus greatly enhancing dispersal distances at oceanic scale.

As a foundational species, eelgrass provides critical shallow-water habitats for diverse biotas and also provides numerous ecosystem services including carbon uptake. Seagrasses have recently been recognized as one of the important nature-based contributions to store carbon in the ocean. The sediment below seagrass meadows can sequester between 30 and 50 times more carbon annually that the roots of forests on land. Unfortunately, the continuing loss of seagrass beds worldwide—including eelgrass—is of acute concern.

An international group of researchers coordinated by Professor Thorsten Reusch, Head of the Research Division Marine Ecology at GEOMAR Helmholtz Centre for Ocean Research Kiel, used complete nuclear and chloroplast genomes from 200 individuals and 16 locations to reconstruct and date the colonization history of the eelgrass Zostera marina from its origin in the Northwest Pacific Ocean to the Pacific, Atlantic and the Mediterranean.

The findings described in an article and a Research Briefing published in *Nature Plants* beg the question, "How well will eelgrass adapt to our new, rapidly changing climate?"

Using a phylogenomic approach the scientists were able to determine that eelgrass plants first crossed the Pacific from west to east in at least two colonization events, probably supported by the North Pacific Current. The scientists then applied two DNA "molecular clocks"—one based on the nuclear genome and one based on the chloroplast genome—to deduce the time when eelgrass populations diverged into new ones. The DNA mutation rate was calculated and calibrated against an ancient, whole genome duplication that occurred in eelgrass.

Both nuclear and chloroplast genomes revealed that eelgrass dispersed to the Atlantic through the Canadian Arctic about 243 thousand years ago. This arrival is far more recent than expected—thousands of years versus millions of years, as is the case with most Atlantic immigrant species during the Great Arctic Exchange some 3.5 million years ago.

Reusch explains, "We thus have to assume that there were no eelgrass-based ecosystems—hotspots of biodiversity and carbon storage—in the Atlantic before that time. Recency was also mirrored in an analysis of the associated faunal community, which features many fewer specialized animals in the Atlantic as compared to the Pacific eelgrass meadows. This suggests that there was less time for animal-plant co-evolution to occur."

Mediterranean populations were founded from the Atlantic about 44 thousand years ago and survived the Last Glacial Maximum. By contrast, today's populations found along the western and eastern Atlantic shores only (re)expanded from refugia after the Last Glacial Maximum, about 19 thousand years ago—and mainly from the American east coast with help from the Gulf Stream.

In addition, the researchers further confirmed the huge difference in genomic diversity between the Pacific and Atlantic, including latitudinal gradients of reduced genetic diversity in northern populations.

"Both Atlantic compared to Pacific populations, and northern versus southern ones are less diverse on a genetic level than their ancestors by a factor of 35 among the most and least diverse one," said postdoctoral scientist Dr. Lei Yu, first author of the publication, which was a chapter in his doctoral thesis. "This is due to bottlenecks arising from past ice ages, which raises concerns as to how well Atlantic eelgrass, will be able to adapt to climate change and other environmental stressors based on its genetic capacity."

"Warming oceans have already caused losses of seagrass meadows at the southern range limits, in particular North Carolina and southern Portugal. In addition, heat waves have also caused losses in shallow waters in some the northern parts of the distribution," noted Reusch. "This is not good news because seagrass meadows form diverse and productive ecosystems, and no other species is able to take on the role of eelgrass if meadows cannot persist under future conditions."

"One possibility for restoration might be to borrow some genetic diversity from Pacific eelgrass to fortify diversity in the Atlantic. Our next step is to interrogate the eelgrass pangenome. A new reference genome from Pacific eelgrass is currently under development and should tell us more about the adaptive ecotypic capacity across its global range of habitats," said Prof. Jeanine Olsen, emeritus professor from the University of Groningen who initiated the study and coordinated the work between the Joint Genome Institute (JGI) and the research team.

More information: Yu, L. etal, Ocean current patterns drive the worldwide colonization of eelgrass (Zostera marina), *Nature Plants* (2023). DOI: 10.1038/s41477-023-01464-3

Provided by Helmholtz Association of German Research Centres