

PLANT GENOMES

Sea to summit

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Credit: Buiten-Beeld/Alamy Stock Photo

It is difficult to keep track of all sequenced plant genomes. New members are added seemingly every week to an exponentially growing list, from plants that are valued for economic, cultural or scientific reasons. Recently, international teams unveiled two new genomes: the common liverwort (*Marchantia polymorpha*) and the Andean quinoa (*Chenopodium quinoa*).

Rootless and non-vascularized liverworts are descendants of some of the earliest plants. An analysis of their genome sequence is akin to travelling half a billion years back in time to understand the crucial transition from algae to land plants, and the later evolution towards modern plants. Survival on land implied evolutionary innovations to avoid drying out and for

protection from direct solar radiation.

Marchantia's simpler genome is used today as a model for pathways that have become extremely complex in modern angiosperms.

On the other side of the plant spectrum, quinoa produces edible seeds that are gluten-free, nutritious and well-balanced, containing fibres, starch, proteins and minerals. This pseudo-cereal, originally domesticated by pre-Columbian cultures living on the high Andean plateaus, can tolerate a lot of environmental abuse, particularly concerning salinity, water availability and temperature, and can grow at altitudes of more than 4,000 metres. This is actually the third published genome of quinoa, expanding the window on genetic variability that could be used by potential breeders. This study focuses on nutrient synthesis pathways and mechanisms of salt tolerance, notably through transcriptome analysis of salt-sequestering epidermal bladder cells.

It is quite fascinating to think that in less than 20 years, we went from a colossal multi-year effort to sequence the first tiny model plant genome, to today's almost routine sequencing of a profusion of other plants, including humble ancestors and cultivars of exotic grains.

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