

Genetic and phenotypic variation of agronomic traits and salt tolerance among quinoa inbred lines

Chenopodium quinoa (quinoa) has been recognized as a key crop with great potential for improving global food security due to its outstanding nutritional properties and ability to tolerate abiotic stresses such as drought and high salinity. However, a genome complexity derived from allotetraploidy and a genetic heterogeneity resulting from partial outcrossing have hampered genetic analysis of quinoa over the years. We established a standard inbred quinoa accession Kd and were first in the world to provide the draft genome sequence (2016 Research Highlights: Draft genome sequence of an inbred line of *Chenopodium quinoa*, an allotetraploid pseudocereal crop with high nutritional properties and tolerance to abiotic stresses). Moreover, an understanding of the genotype-phenotype correlation between comprehensive inbred lines will bring about advances in molecular breeding and research due to the molecular elucidation and genetic improvement of quinoa.

To evaluate genetic diversity in quinoa, we genotyped 5,753 single nucleotide polymorphisms (SNPs) in 136 inbred lines using Genotyping-by-Sequencing (GBS) based on next-generation sequencing. Our quinoa inbred lines were classified into three genetic sub-populations, corresponding to northern highland, southern highland, and lowland sub-populations using STRUCTURE, a neighbor-joining phylogenetic and principal component analysis. We also assessed salt tolerance and important growth traits (1,000-grain weight, plant height, stem diameter, leaf dry weight, seed yield per plant, and days to flowering) and generated a heatmap that provides a succinct overview of the genotype-phenotype relationship between inbred quinoa lines. Most lowland and southern highland lines were able to germinate even under high salinity conditions. In addition, most lowland lines displayed larger plant sizes and late flowering phenotypes, indicating that lowland lines are more suitable for growth in a temperate climate than the other lines.

The heatmap of the phenotypic traits, combined with the phylogenetic tree, provides quick access to the genotype-phenotype state of each quinoa line. We will therefore be able to accelerate the development of climate-resilient quinoa through efficient molecular breeding and research.

(Y. Kobayashi, Y. Fujita, N. Mizuno [Grad. Sch. Agri., Kyoto Univ., present affiliation: NARO], M. Fujita [RIKEN CSRS], S. Fukuda [Fac. Agri., Tottori Univ., present affiliation: Ishihara Sangyo Kaisha, Ltd.], K. Tanaka, T. Tanaka, H. Mizukoshi [Actree Co. Ltd.], E. Nishihara [Fac. Agri., Tottori Univ.], Y. Yasui [Grad. Sch. Agri., Kyoto Univ.]

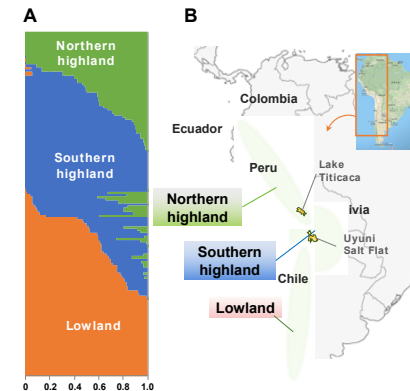


Fig. 1. Population structure of quinoa inbred lines based on SNP genotype data
(A) Each quinoa line's genome is represented by each bar on the y-axis, and the colors of the bar indicate the proportion of estimated membership in the three sub-populations. Lines having <80% of inferred ancestry from any one group are identified as an admixture.
(B) Distribution of quinoa grouped into northern and southern highland and lowland sub-population in South America

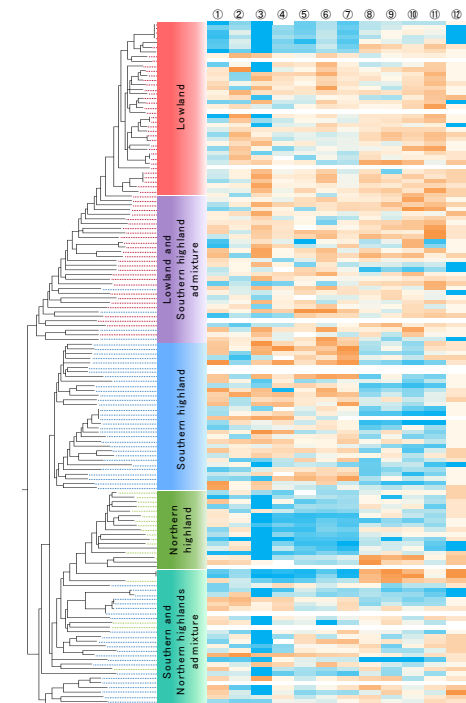


Fig. 2. Heatmap of the phenotypic traits combined with the phylogenetic tree of quinoa inbred lines

①-③: the average total hypocotyl and root length (mm) of seeds treated with 0, 300, and 600 mM of NaCl for 24 hours, 4 days, and 16 days, respectively; ④-⑦: thousand grain weight (g) during 2014-15 (Tsukuba), 2015-16 (Tsukuba), 2016 (Tsukuba), 2016-17 (Tottori); ⑧: plant height (cm); ⑨: stem diameter (mm); ⑩: leaf dry weight (g); ⑪: seed yield per plant (g); ⑫: days to flowering