

# Potential of Quinoa for Food and Nutritious Security Under Climate Change in the Era of Global Boiling

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Dr. Yukari Nagatoshi is the Project Leader of the “Resilient crops: Development of resilient crops and production technologies” project at JIRCAS, assuming the role in 2024. She completed her doctoral program at Yokohama National University in 2009. Following her graduation, she began her career as a postdoctoral fellow at the National Institute of Advanced Industrial Science and Technology (AIST) in the same year. In 2013, she transitioned to a postdoctoral position at JIRCAS. The following year, in 2014, she secured a tenure-track researcher position at JIRCAS. Her career continued to progress, and in 2019, she was promoted to the role of senior researcher at JIRCAS.

# Abstracts

Climate change has entered a new phase, often referred to as the era of global boiling, even as we rethink the conventional crop production system that is extremely dependent on a few crops from a food and nutrition security point of view. For a resilient food system, it is necessary not only to improve current major crops, but also to create new major crop candidates. It is from this perspective that we focus on quinoa (*Chenopodium quinoa*).

Quinoa, an annual pseudocereal, was first domesticated at least 7,500 years ago in the Andean region of South America. Quinoa seeds are extremely nutritious, containing a good balance of the five macronutrients (carbohydrates, proteins, fats, minerals, and vitamins) and dietary fiber. In addition, quinoa can be grown at low and high latitudes, from lowlands such as coastal areas to highlands as high as 4,000 meters, and in areas with temperatures ranging from below freezing to as high as 40°C. With its high nutritional value and diverse traits that allow it to adapt to different agroecosystems, quinoa is a promising candidate for a major crop for the next generation.

Quinoa was the staple food of the indigenous peoples of the Andes before Columbus, but its production and consumption were historically banned by the Spanish conquistadors in the 16th century because it was revered as a sacred "mother grain" used in indigenous ceremonies. As a result, quinoa was neglected for almost 500 years until the latter half of the 20th century, and the development of varieties and cultivation techniques lagged far behind. To expand the cultivation of quinoa as a major crop candidate worldwide, we are conducting research and development to accelerate quinoa breeding through cutting-edge plant science research. First, we created a representative quinoa inbred line and sequenced its genome for efficient genome breeding<sup>[1]</sup>. We have since developed almost 200 genotyped quinoa inbred lines, covering almost all quinoa-growing areas in South America, and performed their Genotyped-by-Sequencing (GBS) and phenotypic analyses to clarify the overall relationship between genotypes and phenotypes for salt tolerance and key growth traits<sup>[2]</sup>. In addition, we have developed a technology to elucidate quinoa gene function using a viral vector method that allows the analysis of endogenous gene function in quinoa<sup>[3]</sup>. We have recently sequenced the genomes of quinoa at the chromosomal level and are currently providing the most accurate reference genome information in the world<sup>[4]</sup>. Based on these findings, we are developing breeding materials and elucidating quinoa's stress tolerance mechanisms through breeding populations and genome-wide genotyping using next-generation sequencers<sup>[5]</sup>.

By recovering the lost 500 years of quinoa breeding in a short period of time through cutting-edge plant science research, we expect to contribute to the development of new crops that take full advantage of quinoa's diversity and potential. We hope that the genetic diversity of quinoa will contribute to future food and nutrition security as an important component of a robust food system under climate change in the era of global boiling.

[1] Yasui Y. *et al.*, *DNA Res.*, 23, 535-546 (2016).

[2] Mizuno N. *et al.*, *DNA Res.*, 27, dsaa022 (2020).

[3] Ogata T. *et al.*, *Front. Plant Sci.*, 12, 643499 (2021).

[4] Kobayashi Y. *et al.*, *Front. Plant Sci.*, 15, 1434388 (2024).

[5] Kobayashi Y. & Fujita Y., *Plant Biotech.*, *in press* (2024).