

# Genetic improvement in quinoa (*Chenopodium quinoa* Willd.)

Prajapati Hetalben B.<sup>1</sup>, Dr. K. N. Chaudhari<sup>1</sup>, Dr. R. K. Kalaria<sup>2</sup> and Dr. S. S. Patil<sup>1</sup>

<sup>1</sup>Department of Genetics and Plant Breeding, College of Agriculture, Navsari Agricultural University, Bharuch, Gujarat

<sup>2</sup>Bioinformatic section, ASPEE Shakilam Biotechnology Institute, Navsari Agricultural University, Surat Gujarat

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## Introduction

Quinoa (*Chenopodium quinoa* Willd.  $2n = 4x = 36$ ) is an annual herbaceous species belonging to family Amaranthaceae. It is a domesticated staple food in Andean South America. Quinoa plant is a C3 species with 90 percent self-pollinating (Gonzalez et al., 2011). It is also known as golden grain, superfood, gold of people, food for the future, golden grain, mother of all grains and qualified as a

functional food. It is naturally gluten-free and a rich source of dietary fibers and natural antioxidants such as vitamin E and minerals. It is a complete protein and offers all nine essential amino acids. Despite its good nutritional values, it also contains bitter tasting compounds called saponins in its seed coat that interfere with the biological utilization of nutrients (Koziol, 1992).

## Breeding Objectives

- |                      |                                   |                                    |
|----------------------|-----------------------------------|------------------------------------|
| 1. Yield improvement | 4. Resistance to biotic stresses  | 7. Adaptation to different regions |
| 2. Grain quality     | 5. Resistance to abiotic stresses | 8. Forage and animal feed          |
| 3. Early maturity    | 6. Agronomic characteristics      |                                    |

## Breeding Methods

### 1. Conventional methods

- |                    |                     |
|--------------------|---------------------|
| a. Introduction    | d. Bulk method      |
| b. Selection       | e. Backcross method |
| c. Pedigree method |                     |

### 2. Non-conventional methods

- |                       |
|-----------------------|
| a. Mutation breeding  |
| b. Molecular breeding |

## Case Study

Pawar et al. (2022) studied the association of yield and yield-contributing characters in thirty genotypes of Quinoa. The magnitude of the genotypic coefficient of variation was lower than the phenotypic coefficient of variation. High heritability (b.s.) with high genetic advance as percent mean was recorded for inflorescence per plant, branches per plant, inflorescence width, inflorescence length, and seed yield per plant indicating that these traits were predominantly governed by additive gene

action. Seed yield per plant positively correlated with plant height, branches per plant, inflorescence per plant, inflorescence length, inflorescence width, and seed volume weight per 10 ml. Path analysis showed direct selection based on character *i.e.* inflorescence width, plant height, seed volume weight per 10ml, inflorescence per plant, and days to 50 percent flowering can help to improve seed yield in quinoa.

**Pawar *et al.* (2023)** studied the thirty genotypes grouped into eleven clusters. They found the highest mean values of cluster IX for characters inflorescence length, inflorescence per plant, plant height, branches per plant, seed volume weight, seed yield, days to flowering and maturity. Cluster III showed the highest mean value for characters branches per plant, inflorescence per plant, inflorescence length, inflorescence width, and seed volume weight. The character days to maturity (28.97 %) showed maximum contribution towards the total divergence.

**Anchico-Jojoa *et al.* (2023)** studied the hybridization between progenies and agronomic characterization of the F2 generation in quinoa. Progenies with the presence of pigmentation in the inflorescence and axils (dominant) originated from Aurora (A88) and Piartal (P88) as a male-parents. Progenies with the absence of pigmentation (recessive) which were originated from BRS Syetetuba (BX4 and BX8) and were used as female parents. The genotype resulting from the cross P88 × BX4 showed the best agronomic characteristics, being considered promising to continue in the quinoa breeding program.

**Mastebroek *et al.* (2002)** studied the combining ability using half-diallel and six genetically diverse nearly homozygous breeding lines. They found highly significant differences in GCA effects between the lines for plant height at maturity, early flowering, early maturity, seed yield and thousand seed weight. Significant SCA effects were only found for plant height at maturity. These large GCA effects and low SCA effects suggest that

these traits were governed by additive genetic effects.

**Gomez-Pando *et al.* (2021)** selected the seeds of the variety ‘Amarilla Marangani’ which were irradiated with 150 and 250 Gy of gamma-rays and were evaluated in two experimental locations in Peru : coastland at La Molina and highland at Huancayo. Resistance to downy mildew and other agricultural traits in the M3 and M4 generations were studied. Six mutants with 30% leaf infection were obtained at the coastland site in the progeny of plants exposed to 150 Gy. Five additional mutants with 40% leaf infection were found in the progeny of plants exposed to 250 Gy. In the highland trial, only seven lines were identified with 30% severity (foliar area with symptoms) among the plants from the 150 Gy experiment. The parent materials showed 70–80% disease severity. They Identified 18 mutant lines with quantitative resistance to *Peronospora variabilis* and identified lines with tolerance to this pathogen.

**Derbali *et al.* (2023)** studied the physiological and biochemical traits that could be used as screening criteria for selecting salt-tolerant genotypes. They used four quinoa varieties (Tumeko, Red Faro, Kcoito and UDEC-5), which were cultivated using a hydroponic system and treated for 2 weeks with different NaCl concentrations (0, 100, 300, and 500 mM). Salt treatment decreased plant growth depending on NaCl concentrations, plant organs and varieties. Red Faro and UDEC-5 exhibited low levels of Na<sup>+</sup> accumulation. *Chenopodium quinoa* could be used as a potential alternative crop for salt-affected areas.

### Conclusion

- Quinoa has a high protein content with all nine essential amino acids and is a naturally gluten-free crop.
- Genetic improvement in quinoa for seed yield and quality might be possible through selection due to the presence of a wide range of variability.
- High heritability and genetic advancement indicate that traits are primarily governed by additive gene action, suggesting that selection for desired traits is more effective.

- A study of combining abilities was found to be helpful for the selection of desirable parents as well as cross-combination for designing future breeding programs.
- Gamma-ray irradiation of Quinoa seeds led to mutations resulting in mildew resistance and helpful for improving quinoa.

- Quinoa could be used as a potential alternative crop for salt-affected areas due to its varying salt tolerant among genotypes.

## References

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