Available online at www.agrifarming.org

DOI: http://dx.doi.org/10.18782/2582-7146.250

ISSN: 2582 – 7146

Current Research in Agriculture and Farming

Curr. Rese. Agri. Far. (2025) *6*(1), 14-25

Review Article

Peer-Reviewed, Refereed, Open Access Journal

The *Chenopodium quinoa* Crop Improvement: A Comprehensive Review Analysis

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Received: 19.12.2024 | Revised: 25.02.2025 | Accepted: 28.02.2025

ABSTRACT

Native to the Andes, quinoa (Chenopodium quinoa Willd.) is a very nutritious pseudocereal that is attracting attention from all over the world due to its remarkable nutritional profile, capacity to withstand extreme conditions, and potential to support food and nutritional security. With five main ecotypes—Altiplano, Valley, Saltflat, Sea-level, and Yunga—each suited to certain environmental circumstances, it is grown across a variety of agroecological zones. Quinoa has gynomonoecious flowers, with a wide range of morphological characteristics that serve as the foundation for the distinctness, uniformity, and stability (DUS) categorization. Quinoa has an allotetraploid genome (2n=4x=36), and breeding is difficult due to its intricate floral biology and inheritance pattern. However, trait mapping and diversity investigations have been sped up by developments in molecular genetics, including development of SSR and SNP markers. Breeding initiatives for quinoa are now being carried out mainly in South America, North America, Europe and up to some extent in Asia, marking a significant advancement in quinoa improvement programs worldwide. However, because of issues like its high saponin content, lack of locally adapted cultivars, and breeding challenges, quinoa is still underutilized in India. A well-coordinated national breeding program is necessary to achieve quinoa's full potential in India. Multi-location testing, targeted hybridization with male sterility and marker- assisted selection, strategic germplasm acquisition, and the development of reliable seed systems are all necessary for this. Such initiatives will open the door for nutritional improvement and sustainable quinoa farming in underserved Indian communities.

Keywords: *Chenopodium quinoa, genetic improvement, Low saponin.*

INTRODUCTION

Quinoa (*Chenopodium quinoa* Willd.) is a dicotyledonous annual plant from the Amaranthaceae family (previously Chenopodiaceae), which also includes other significant crops like spinach (*Spinacia oleracea* L.) and sugar beet (*Beta vulgaris* L.). Alongside its wild relatives (*Chenopodium carnosolum, C. petiolare, C. pallidicaule, C. hircinum, C. quinoa* subsp. *melanospermum, and C. ambrosioides incisum*), quinoa exhibits a wide range of diversity and applications (Fuentes et al., 2009a, b).

Cite this article: Mehta, L., Srivastava, D., & Thiyagarajan, K. (2025). The *Chenopodium quinoa* Crop Improvement: A Comprehensive Review Analysis, *Curr. Rese. Agri. Far. 6*(1), 14-25. doi: http://dx.doi.org/10.18782/2582-7146.250

Farmers in the Andean highlands (Altiplano) of Colombia, Ecuador, Peru, Bolivia, Chile, and Argentina have long cultivated and utilized these species (Mujica & Jacobsen, 2006).

Quinoa stands out for its excellent balance of nutrients, containing 4–9% oil, 16% protein (notable for its optimal essential amino acid profile), and 64% carbohydrates (Bhargava et al., 2006; & Vega-Gálvez et al., 2010). With a 51–61% starch content, it can be processed like cereals for flour production (Mastebroek et al., 2000; Repo-Carrasco et al., 2003; Bhargava et al., 2006; & Stikic et al., 2012). It is also a rich source of vitamins, antioxidants (α- and γ-tocopherol), and minerals. Additionally, its lipid fraction contains 55–66% linoleate and linoleate (Repo- Carrasco et al., 2003; Vega-Gálvez et al., 2010; Fuentes & Bhargava 2011; & Stikic et al., 2012). Quinoa is naturally gluten-free, making it suitable for developing gluten-free foods for individuals with celiac disease (Jacobsen 2003). The growing recognition of its nutritional benefits has led to a significant rise in global demand for processed quinoa products (Mujica & Jacobsen 2006; & FAO, 2011).

Quinoa's ability to thrive in harsh environments and under low-input agricultural systems makes it an ideal crop for marginal lands (Ward, 2000; Jacobsen et al., 2003; Fuentes & Bhargava, 2011). Despite its potential to address global food security, quinoa remains under- researched and underutilized, classified as a neglected crop (Rojas et al., 2009). Only 101,500 hectares are cultivated annually, producing approximately 80,200 tons—a 70% increase over the past 12 years (FAO, 2011). While most production remains in South America, quinoa is grown in the USA (Colorado), Canada, and France, with experimental trials underway in China, Europe, India, and Africa (Jacobsen et al. 2013). Quinoa is known mainly for its good quality amino acids and mineral contents. Table 1 presents relative amino acid contents in quinoa and other staple food crops.

Historically, quinoa seeds were used to make flour, soup, cereal, and alcoholic beverages. The plant has also been used for animal feed (as green foliage), medicinal purposes (anti- inflammatory, analgesic, and disinfectant), and as an insect repellent (Vega-Gálvez et al., 2010). Additional applications include desaponified powder for animal nutrition and fresh leaves for human consumption. In 2013, the Food and Agriculture Organization (FAO) declared the International Year of Quinoa (IYQ, 2013) to honor Andean Indigenous peoples for preserving and promoting quinoa through traditional practices that harmonize with nature (FAO, 2012).

Given its exceptional nutritional properties, adaptability to diverse agroecological conditions, and potential role in combating hunger and malnutrition, quinoa is positioned to become a critical component of sustainable strategies for feeding the growing global population (Jacobsen et al., 2013).

Phenotypic Characterization of *Chenopodium quinoa*

Quinoa (Chenopodium quinoa) is predominantly self-pollinating (autogamous), with natural hybridization rates ranging from 10–17%, depending on the overlap of flowering with the activity of pollen vectors (Mastebroek et al., 2002; & Spehar & Santos, 2005). The plant is gynomonoecious, meaning it produces both female and hermaphroditic flowers on the same plant. These small flowers (3–4 mm) come in three types: hermaphrodite, chlamydeous female, and achlamydeous female, forming a panicle-type inflorescence measuring 15–70 cm, often highly branched. There are certain characters used for defining the distinctness, uniformity and stability (DUS) in quinoa. These are presented in the table 2.

It is important to note that due to the flowers' size and arrangement, manual emasculation for hybridization is quite challenging (Ward, 2000). Male sterility, present in some cultivars (partially or entirely), has been a valuable tool for hybrid breeding (Ward, 1998; & Bhargava et al., 2006).

Genotypic Characterization of *Chenopodium quinoa*

Cytological studies reveal that quinoa is an allotetraploid species (2n = 4x = 36; x = 9) exhibiting predominantly diploid chromosomal segregation, although occasional tetrasomic inheritance has been observed (Palomino et al., 2008; & Ward, 2000). Rare instances of combined disomic and tetrasomic segregation may result from genetic exchange between homeologous chromosomes, complicating genome mapping and analysis (Maughan et al., 2004; & Fuentes & Bhargava, 2011). Morphologically, quinoa belongs to the Chenopodium subsection Cellulata (alveolate-fruited) alongside other related species, including C. berlandieri complex, C. hircinum, and C. philippianum (Aellen & Just, 1929; Wilson, 1980; & Jellen et al., 2011).

Quinoa is thought to have originated from diploid species like C. pallidicaule, C. petiolare, and C. carnosolum, as well as tetraploid weedy species such as C. hircinum and C. quinoa var. melanospermum (Mujica & Jacobsen, 2006). Another theory suggests that quinoa descended from a North American ancestor, similar to C. berlandieri var. zschackei, which may have been transported to South America through human migration or bird dispersal, where it was later domesticated (Wilson, 1990). Molecular and cytogenetic studies, including analyses of 45S NOR and 5S rRNA genes, support the close relationship between quinoa and C. berlandieri var. zschackei, suggesting shared diploid ancestry (Kolano et al., 2008; & Maughan et al., 2006).

Quinoa's genetic diversity is concentrated in five main ecotypes tied to sub-centers of diversity, with the Altiplano region near Lake Titicaca recognized as the primary genetic diversity center (Risi & Galwey, 1984). Earlier studies identified Bolivia's southern highlands as the center of quinoa diversity (Gandarillas, 1979; & Wilson, 1988a). However, molecular data pinpointed the central Andean highlands (Altiplano of Peru and Bolivia) as the diversity epicenter (Christensen et al., 2007). Germplasm from Ecuador and Argentina shows limited diversity, suggesting that Ecuadorian quinoa likely originated from the Altiplano, while Chilean highland and lowland zones might have influenced Argentinian quinoa (Christensen et al., 2007).

Chilean quinoa exhibits significant genetic variation due to frequent outcrossing with weedy relatives like C. album and C. hircinum, especially in coastal lowland fields (Fuentes et al., 2009a). This genetic promiscuity has posed challenges for developing inbred lines in Southern Chile (I. von Baer, personal communication). Overall, quinoa exists as two distinct germplasm pools: the Andean highland quinoa and the quinoa cultivated by the Mapuche people in the coastal lowlands of central and southern Chile. A potential third pool includes C. hircinum from lowland Argentina, possibly a remnant of ancient quinoa cultivation in the region (Wilson, 1990; & Jellen et al., 2011).

The quinoa ecotypes

Based on their ecological adaption zones, quinoa types can be divided into five main groupings (Table 3, Figure 1). Among these are the Valley Quinoas, which may be found in rainfed regions like Huaraz, Valle del Mantaro, Ayacucho, and Abancay in Peru, as well as in inter-Andean valleys with irrigation, such as Urubamba in Peru and Cochabamba in Bolivia. In locations with more precipitation, such as northern Peru, Ecuador, and southern Colombia, a tall, branching ecotype developed into the Nariño variety, which is currently grown in Peru. These types can reach heights of up to three meters in irrigated areas. The highland regions surrounding Lake Titicaca and the Suni agroecological zone, which is 3,900 meters above sea level, are home to Altiplano Quinoas, which flourish in frigid climates with little precipitation. This group includes lakefront varieties such as Kcancolla, Blanca de Juli, and Tahuaco, as well as Cheweca, Ccoitu, Wariponcho, Chullpi, and Witulla, which are distinguished by their colorful panicles and resilience to cold. For early growth, saltflat quinoas, which are suited to the xerophytic environments of Bolivia's salt flats (salares), depend on moisture held in

planting holes. Although shorter fallow periods have recently resulted in decreased soil fertility, these types are part of a special production strategy where the soil is left fallow for 4–8 years after harvest. Sea-Level Quinoas are suited to humid climates and consistent temperatures and are found in coastal regions of Chile south of 30°S, including Concepción and Valdivia. Usually, they have darker, smaller grains. Last but not least, Yunga Quinoas, which are native to Bolivia's Yunga agroecological zone at elevations of 1,500–2,000 meters above sea level, flourish in hot, humid subtropical climates. When fully grown, these types are distinguished by their orange perigonium and stems. Yunga cultivars have demonstrated good development at higher elevations, such as 3,300 meters above sea level in K'ayra, Cusco, and have a long vegetative period of more than 200 days, despite the limited harvesting attempts.

Germplasm Collections and Research Programs

Globally, there are 16,263 ex situ Chenopodium accessions, primarily conserved in the Andean region, particularly in Bolivia and Peru (FAO, 2010). The Bolivian National Collection, housed at the Fundación para la Promoción e Investigación de Productos Andinos (PROINPA) and now managed by the Instituto Nacional de Innovación Agropecuaria y Forestal (INIAF), holds the largest ex situ seed bank with 4,312 quinoa accessions. These accessions have been extensively characterized for traits such as growth habit, panicle structure, grain size, physiological maturity, and nutritional and industrial value, with molecular tools being developed in collaboration with Brigham Young University (Jellen, 2013, personal communication).

In South America, other significant seed collections are maintained by the Universidad Nacional del Altiplano (UNAP, Peru), the National Institute of Agricultural Research (INIA, Peru), the Research Center for Andean Studies (CICA, Peru), and the National Seed Bank of Chile, overseen by INIA-Intihuasi in Vicuña. Outside the region, comprehensive ex situ collections exist at institutions like the Royal Botanical Gardens Kew (UK), USDA-ARS (USA), the National Bureau of Plant Genetic Resources (India), and IPK-Gatersleben (Germany) (Fuentes et al., 2009b). Notably, only the USDA-ARS and the Royal Botanical Gardens Kew hold wild Chenopodiaceae species, with the USDA-ARS managing 357 accessions of Chenopodium and related genera (Brenner, 1998, personal communication).

Research on quinoa genetics and breeding has been relatively limited, necessitating further investment in its genetic improvement (Jacobsen et al., 2003; Danial et al., 2007; & Rojas et al., 2009). Andean countries began quinoa breeding programs in the 1960s (McElhinny et al., 2007), followed by efforts in the 1980s in the USA and Europe to adapt the crop to new climates and agronomic conditions. In Europe, breeding initiatives started in the UK and Denmark, focusing on diverse genotypes. Although uniform lines were developed, no varieties were officially registered. Breeding efforts in the Netherlands began in 1986 using accessions from seed banks, botanical gardens, and universities, resulting in uniform lines suited for Western European climates (Mastebroek et al., 2002). Four Dutch and two Danish quinoa varieties are now registered (Jacobsen & Bendevis, 2013).

A significant program, the Project for Durable Resistance in the Andean Zone (PREDUZA), launched in the late 1990s, aims to enhance quinoa's resistance to biotic and abiotic stresses. Breeding efforts in Bolivia, supported by the McKnight Foundation and conducted by PROINPA, as well as national programs in Ecuador, Peru, and Bolivia, have faced inconsistent funding (McElhinny et al., 2007). In Asia, India’s National Botanical Research Institute initiated a breeding program to adapt quinoa to local conditions (Bhargava et al., 2006). Chilean private initiatives have developed cultivars and advanced lines using coastal and lowland genotypes. Similarly, research in the desert and highland regions has assessed the genetic diversity of quinoa lines from Salares (Fuentes et al., 2009b; & Fuentes

& Bhargava, 2011). Brazil has developed pioneering saponin-free quinoa varieties adapted to acidic soils of the savannah, marking a turning point in agricultural diversification (Spehar & Rocha, 2010). These global developments have been presented in chronological order in table 4.

Molecular Genetic Resources

The first molecular studies on quinoa utilized allozyme markers to assess genetic variability in domesticated and wild species, such as C. hircinum and wild quinoa ajara (Wilson, 1988a, b). These studies identified two main genetic groups: a coastal type from southwestern Chile and an Andean type from northwestern Argentina to southern Colombia, emphasizing the co- evolution of domesticated and wild populations (Wilson, 1988b). Protein-based approaches have also been employed to characterize quinoa seed storage proteins for cultivar identification and breeding to improve protein quality and quantity (Fairbanks et al., 1990).

DNA-based markers were first introduced in quinoa using random amplified polymorphic DNA (RAPD) (Fairbanks et al., 1993), enabling genetic variation analysis among Chenopodium species and hybrid identification for linkage map development (Maughan et al., 2004; & Jarvis et al., 2008). Simple sequence repeat (SSR) markers have been widely applied due to their co-dominant nature and ability to detect polymorphism (Mason et al., 2005). Tri- nucleotide motifs with at least 20 base pair repeats were found to be particularly effective for developing polymorphic microsatellite markers (Fuentes et al., 2012).

These SSR markers have potential applications in genetic studies of related species like C. pallidicaule (cañihua), C. berlandieri (huazontle), and C. giganteum (khan chi). In addition, single nucleotide polymorphism (SNP) markers have been developed from tissue-specific libraries to identify genes homologous to those in other plants (Coles et al., 2005). A large- scale SNP marker set was created to facilitate genetic studies and functional assays, revealing high mutation rates for transitions (A/G or C/T) compared to transversions (Maughan et al., 2012). However, these markers have limited application in phylogenetic studies due to their inability to distinguish closely related species.

The first genetic linkage map for quinoa was published in 2004 (Maughan et al.), with an updated version in 2008 (Jarvis et al.,), incorporating diverse molecular resources such as SSR, RAPD, and amplified fragment length polymorphism markers. More recently, SNP-based linkage maps have been developed, covering greater genetic distances and identifying undetected areas of the quinoa genome (Maughan et al., 2012).

To further explore the quinoa genome, bacterial artificial chromosome (BAC) libraries were established, revealing a di-haploid genome size of 967 Mbp (2C = 2.01 pg) (Stevens et al., 2006). These libraries demonstrated utility in identifying genes related to seed storage proteins, providing insights into genetic variation between highland and lowland genotypes.

Advancements in next-generation sequencing have revolutionized quinoa genomics, making it cost-effective to generate molecular markers for understudied species. Efforts have been made to annotate expressed sequence tags (ESTs) related to saponin biosynthesis, leading to the identification of candidate genes involved in this economically significant trait (Reynolds, 2009). Additionally, 291 new SSR markers have been identified, and transcriptional variation between sweet and bitter quinoa varieties has been analyzed using microarrays, uncovering genes related to saponin biosynthesis.

The critical Research Gaps in *Chenopodium quinoa* improvement in Indian context

There are a number of significant research gaps that prevent Chenopodium quinoa from being widely used and optimized in the Indian environment. Its gynomonoecious flower structure presents a major crossover issue, making conventional breeding techniques for creating new, improved varieties more challenging. Additionally, saponin-free accessions that are suited to the agroclimatic

conditions of India are conspicuously lacking. Quinoa's bitter taste and anti- nutritional qualities must be eliminated by further processing (such as washing or dehulling) due to the presence of saponins, which raises production costs and deters local processors and customers. These problems are exacerbated by the lack of coordinated breeding and research programs across different institutions, which disperses efforts and prevents the systematic development and distribution of quinoa cultivars that are high-yielding, saponin-free, and locally adapted. As a result, the crop's potential to improve nutritional security in India is limited.

A strong, cooperative national breeding program and strategic germplasm acquisition are the two main strategies required to close the important research gaps in Chenopodium quinoa development in the Indian setting. First and foremost, it is essential to import low-saponin accessions from overseas. This not only gets the desired "sweet" trait quickly, avoiding the need for drawn-out de novo breeding, but it also greatly increases the genetic diversity available to breeders, enabling them to choose lines with better yield, stress tolerance, and adaptability following extensive quarantine, characterization, and multi-location adaptation trials throughout India. Second, a nationwide cooperative breeding program that brings together State Agricultural Universities and ICAR institutions is essential for methodically creating quinoa varieties that are stress-tolerant, low-saponin, and high-yielding.

By fusing local adaptations with imported lines, this program must actively participate in hybridization, producing various populations. It must, however, use specific breeding methods to get around the inherent challenge presented by gynomonoecious flowers. These methods include creating and using male sterile lines, improving manual emasculation and pollination procedures, and—most importantly—using marker-assisted selection to quickly and effectively identify low-saponin content and other desirable traits. In order to guarantee that improved varieties are successfully distributed to farmers, such a program would concurrently concentrate on thorough multi-location evaluation, capacity building for specialized breeders, and the development of a seed system and supportive legislation.

Table 1: Essential amino acid (g /100g protein) profile of quinoa and other grains

Amino Acids	Quinoa	Maize	Rice	Wheat
Isoleucine	4.9	4	4.1	4.2
Leucine	6.6	12.5	8.2	6.8
Lysine	6	2.9	3.8	2.6
Methionine	5.3	4	3.6	3.7
Phenylalanine	6.9	8.6	10.5	8.2
Threonine	3.7	3.8	3.8	2.8
Tryptophan	0.9	0.7	1.1	1.2
Valine	4.5	5	6.1	4.4

Table 2: Important features used for DUS characterization of quinoa

S. No.	Characteristics	Scale	S.No.	Characteristics	Scale
1	Grain: saponin content	absent or low medium	12	Inflorescence: colour	White
		High			Green
2	VG Foliage: colour	Light green			Yellow
		Medium green			Orange
		Dark green			Pink
		Red			Purple

		Purple	13	Time of maturity	early
3	Foliage: glaucosity	Absent or weak			Medium
		Medium strong			Late
4	Leaf: size	Small	14	Plant: height	Short
		Medium large			Medium
5	Leaf: dentation	absent or weak			Tall
		Medium strong	15	Panicle: colour	Light Yellow
6	Leaf: angle of base	Acute			Brown
		Obtuse truncate			Black
7	Time of flowering	Early	16	Panicle: density	Sparse
		Medium			Medium
		Late			Dense
8	Stem: colour	White	17	Panicle: width	Narrow
		Green			Medium
		Yellow			Broad
		Purple	18	Seed: colour	whitish
9	VG Stem: stripes	Absent			yellow
		Present			red
10	Stem: colour of stripes	Green			light brown
		Yellow			grey
		Purple			black
		Red	19	Seed: colour without tegument	white
		pink			yellow
11	Stem: pigmentation at leaf axil	Absent			red
		very weak			grey
		Weak	20	1000 seed weight	very low
		medium strong			low
					medium
					high
					very high

Table 3: Characteristics of the different quinoa ecotypes

Quinoa Ecotype	Geographic Region	Characteristics	Rainfall (mm)	Min Temp
Valley Quinoas	Inter-Andean valleys (e.g., Urubamba, Peru; Cochabamba, Bolivia) and rainfed areas (e.g., Huaraz, Valle del Mantaro, Ayacucho, Abancay, Peru)	Can grow up to 3 meters tall in irrigated regions, In regions with higher precipitation (northern Peru, Ecuador, southern Colombia), evolved into Nariño variety, with sweet, white grains	700–1500	3°C
Altiplano Quinoas	Highland areas around Lake Titicaca, Suni agroecological zone (3,900 m.a.s.l.)	Thrive in low precipitation and cold temperatures; Includes Kcancolla, Blanca de Juli, Tahuaco (from lakeside regions); Also includes Cheweca, Ccoitu, Wariponcho, Chullpi, and Witulla with colored panicles and cold resistance	400–800	0°C
Saltflat Quinoas	Southern Bolivia, salt flats (salares)	Adapted to xerophytic conditions; Depend on moisture retained in planting holes for early development; Unique production system with 4–8 years of soil fallow, though shorter fallow periods have reduced soil fertility	250–400	-1°C
Sea-Level Quinoas	Coastal areas south of 30°S (e.g., Concepción and Valdivia, Chile)	Adapted to humid conditions and stable temperatures; Typically feature smaller, dark- colored grains	800–1500	5°C
Yunga Quinoas	Yunga agroecological zone, Bolivia (altitudes 1,500–2,000 m.a.s.l.)	Adapt to subtropical climates with high rainfall and heat; Notable for orange stems and perigonium at maturity; Showed satisfactory growth at higher altitudes (e.g., 3,300 m.a.s.l. in K'ayra, Cusco) with long vegetative period (over 200 days)	0–2000	11°C

Table 4: Table presenting the Key developments in the global expansion of quinoa by country and region over time

Region	Country	Milestone / Development	Period
South America	Peru	Largest global producer; cultivation area grew from 42,077 ha (2012) to 47,543 ha (2013).	2012–2013
South America	Bolivia	Production nearly doubled; cultivated area tripled.	1992–2010
North America	United States	Cultivation began in early 2000s; large-scale production in Colorado & Utah by 2014.	2000s–2014
North America	Canada	Trials initiated in early 2010s; successful production in Saskatchewan & Alberta by 2015.	2010s–2015
Europe	France	Small-scale cultivation initiated after trials in early 2010s.	2010s–2015
Europe	United Kingdom	Trials around 2010 led to small-scale cultivation by 2015.	2010–2015
Europe	Italy	Successful trials and small-scale production by 2015.	2010s–2015
Africa	Egypt	National campaign launched to promote quinoa as alternative to wheat and rice.	2018
Africa	South Africa	Trials in early 2010s; successful production by 2015.	2010s–2015
Asia	China	Initiated trials; small-scale production achieved by 2015.	2010s–2015
Asia	India	Successful cultivation in Rajasthan and Gujarat post early 2010s trials.	2010s–2015
Oceania	Australia	Trials began in early 2010s; small-scale production achieved by 2015.	2010s–2015
Global Trends	Global (75 countries)	Expansion from 8 countries (1980) to 75 countries (2014).	1980–2014
Global Trends	Peru, Bolivia, Ecuador	Combined production increased by 72%.	2000–2014

Figure 1: Andean region and geographic areas with ar-chaeological finds of *C.quinoa*. 1a NWA (Argentina); 1b Cuyo (Argentina); 2a Northern Altiplano (Bolivia); 2b Central Altiplano (Bolivia); 2c Southern Altiplano (Bo-livia); 3a North (Chile); 3b Coastal Centre and the Andes (Chile); 4 Peru; Source: FAO

CONCLUSION

Filling important research gaps is essential to quinoa's full potential in India. India can quickly diversify its genetic base and introduce important features by importing low-saponin germplasm. At the same time, it is critical to develop a strong, nationwide cooperative breeding program that actively uses cutting-edge strategies like marker-assisted selection and ways to get around the complexity of gynomonoecious flowers. The development of high-yielding, saponin-free, and locally adapted quinoa cultivars will be accelerated by this integrated approach, which combines international resources with focused home research. To improve farmer livelihoods, increase nutritional security, and solidify quinoa as a valuable commodity in India's agricultural landscape, such coordinated efforts are essential.

Acknowledgement

The authors would like to express their gratitude to researchers and scientists of Jaipur National University, Jaipur and other institutions for providing the direct and indirect support in framing the review article.

Funding: NIL.

Conflict of Interest:

There is no such evidence of conflict of interest.

Author Contribution:

All authors have participated in critically revising of the entire manuscript and approval of the final manuscript.

REFERENCES

Aellen, P., & Just, T. (1929). Key and synopsis of the American species of the genus *Chenopodium* L. *American Midland Naturalist, 30*, 47–67.

Bhargava, A., Shukla, S., & Ohri, D. (2006). *Chenopodium quinoa*: An Indian perspective. *Industrial Crops and Products, 23*, 73–87.

Christensen, S. A., Pratt, D. B., Pratt, C., Nelson, P. T., Stevens, M. R., Jellen, E. N., Coleman, C. E., Fairbanks, D. J., Bonifacio, A., & Maughan, P. J. (2007). Assessment of genetic diversity in the USDA and CIP-FAO international nursery collections of quinoa (*Chenopodium quinoa* Willd.) using microsatellite markers. *Plant Genetic Resources, 5*, 82–95.

Coles, N. D., Coleman, C. E., Christensen, S. A., Jellen, E. N., Stevens, M. R., Bonifacio, A., Rojas-Beltran, J. A., Fairbanks, D. J., & Maughan, P. J. (2005). Development and use of an expressed sequence tag library in quinoa (*Chenopodium quinoa* Willd.) for the discovery of single nucleotide polymorphisms. *Plant Science, 168*, 439–447.

Danial, D., Parlevliet, J., Almekinders, C., & Thiele, G. (2007). Farmers' participation and breeding for durable disease resistance in the Andean region. *Euphytica, 153*, 385–396.

Fairbanks, D. J., Burgener, K. W., Robison, L. R., Andersen, W. R., & Ballon, E. (1990). Electrophoretic characterization of quinoa seed proteins. *Plant Breeding, 104*, 190–195.

Fairbanks, D., Waldrigues, A., Ruas, C. F., Maughan, P. J., Robison, L. R., Andersen, W. R., Riede, C. R., Pauley, C. S., Caetano, L. G., Arantes, O. M., Fungaro, M. H. P., Vidotto, M. C., & Jankevicius, S. E. (1993). Efficient characterization of biological diversity using field DNA extraction and random amplified polymorphic DNA markers. *Revista Brasileira de Genética, 16*, 11–22.

Food and Agriculture Organization. (2010–2012). *FAO reports*. http://www.fao.org

Fuentes, F., Martínez, E., Hinrichsen, P., Jellen, E., & Maughan, P. (2009a). Assessment of genetic diversity patterns in Chilean quinoa (*Chenopodium quinoa* Willd.) germplasm using multiplex fluorescent microsatellite markers. *Conservation Genetics, 10*, 369–377.

Fuentes, F., Maughan, P., & Jellen, E. (2009b). Diversidad genética y recursos genéticos para el mejoramiento de la Quinua (*Chenopodium quinoa* Willd). *Revista Geográfica de Valparaíso, 42*, 20–33. http://www.rgv.ucv.cl/Articulo%2042-3.pdf

Fuentes, F., & Bhargava, A. (2011). Morphological analysis of quinoa germplasm grown under lowland desert conditions. *Journal of Agronomy and Crop Science, 197*, 124–134.

Fuentes, F., Bazile, D., Bhargava, A., & Martínez, E. A. (2012). Implications of farmers' seed exchanges for on-farm conservation of quinoa, as revealed by its genetic diversity in

Chile. *The Journal of Agricultural Science, 150*(6), 702–716.

Gandarillas, H. (1979). Genetica y origen. In M. E. Tapia (Ed.), *Quinoa y Kaniwa* (pp. 45–64). Instituto Interamericano de Ciencias Agricolas.

Jacobsen, S. E. (2003). The worldwide potential for quinoa (*Chenopodium quinoa* Willd.). *Food Reviews International, 19*, 167–177.

Jacobsen, S. E., Bendevis, M. A., Jorgensen, I., & Stolen, O. (1994). Cultivation of quinoa (*Chenopodium quinoa*) under temperate climatic conditions in Denmark. *Journal of Agricultural Science, 122*, 47–52.

Jacobsen, S. E., Sørensen, M., Pedersen, S. M., & Weiner, J. (2013). Feeding the world: Genetically modified crops versus agricultural biodiversity. *Agronomy for Sustainable Development, 33*, 651–662. https://doi.org/10.1007/s13593-013-0138-9

Jarvis, D. E., Kopp, O. R., Jellen, E. N., Mallory, M. A., Pattee, J., Bonifacio, A., Coleman, C. E., Stevens, M. R., Fairbanks, D. J., & Maughan, P. J. (2008). Simple sequence repeat marker development and genetic mapping in quinoa (*Chenopodium quinoa* Willd.). *Journal of Genetics, 87*, 39–51.

Jellen, E. N., Kolano, B. A., Sederberg, M. C., Bonifacio, A., & Maughan, P. J. (2011). *Chenopodium*. In C. Kole (Ed.), *Wild crop relatives: Genomic and breeding resources* (pp. 35–61). Springer.

Koziol, M. J. (1992). Chemical composition and nutritional evaluation of quinoa (*Chenopodium quinoa* Willd.). *Journal of Food Composition and Analysis, 5*, 35–68.

Kolano, B., Plucienniczak, A., Kwasniewski, M., & Maluszynska, J. (2008). Chromosomal localization of a novel repetitive sequence in the *Chenopodium quinoa* genome. *Journal of Applied Genetics, 49*(4), 313–320.

Koziol, M. J. (1991). Afrosimetric estimation of threshold saponin concentration for bitterness in quinoa (*Chenopodium quinoa* Willd). *Journal of the Science of Food and Agriculture, 54*(2), 211–219. https://doi.org/10.1002/jsfa.2740540206

Mason, S., Stevens, M., Jellen, E., Bonifácio, A., Fairbanks, D., Coleman, C., McCarty, R., Rasmussen, A., & Maughan, P. (2005). Development and use of microsatellite markers for germplasm characterization in quinoa (*Chenopodium quinoa* Willdenow). *Crop Science, 45*, 1618–1630.

Mastebroek, H., Limburg, H., Gilles, T., & Marvin, H. (2000). Occurrence of sapogenins in leaves and seeds of quinoa (*Chenopodium quinoa* Willd.). *Journal of the Science of Food and Agriculture, 80*, 152–156.

Mastebroek, H., van Loo, E., & Dolstra, O. (2002). Combining ability for seed yield traits of *Chenopodium quinoa* breeding lines. *Euphytica, 125*, 427–432.

Maughan, P. J., Bonifacio, A., Jellen, E., Stevens, M., Coleman, C., Ricks, M., Mason, S., Jarvis, D., Gardunia, B., & Fairbanks, D. (2004). A genetic linkage map of quinoa (*Chenopodium quinoa*) based on AFLP, RAPD and SSR markers. *Theoretical and Applied Genetics, 109*, 1188–1189.

Maughan, P. J., Kolano, B. A., Maluszynska, J., Coles, N. D., Bonifacio, A., Rojas, J., Coleman, C. E., Stevens, M. R., Fairbanks, D. J., Perkinson, S. E., & Jellen, E. N. (2006). Molecular and cytological characterization of ribosomal RNA genes in *Chenopodium quinoa* and *Chenopodium berlandieri*. *Genome, 49*, 825–839.

Maughan, P. J., Smith, S. M., Rojas-Beltran, J. A., Elzinga, D., Raney, J. A., Jellen, E.

N., Bonifacio, A., Udall, J. A., & Fairbanks, D. J. (2012). Single nucleotide polymorphism identification, characterization, and linkage mapping in quinoa. *The Plant Genome, 5*, 114–125.

McElhinny, E., Peralta, E., Mazón, N., Danial, D. L., Thiele, G., & Lindhout, P. (2007). Aspects of participatory plant breeding for quinoa in marginal areas of Ecuador. *Euphytica, 153*, 373–384.

Mujica, A., & Jacobsen, S. E. (2006). La quinua (*Chenopodium quinoa* Willd.) y sus parientes silvestres. In *Botánica Económica de los Andes Centrales* (pp. 449–457). Universidad Mayor de San Andrés.

Palomino, G., Hernandez, L. T., & Torres, E. D. (2008). Nuclear genome size and chromosome analysis in *Chenopodium quinoa* and *C. berlandieri* subsp. *nuttalliae*. *Euphytica, 164*, 221–230.

Repo-Carrasco, R., Espinoza, C., & Jacobsen, S. E. (2003). Nutritional value and use of the Andean crops quinoa (*Chenopodium quinoa*) and kañiwa (*Chenopodium pallidicaule*). *Food Reviews International, 19*, 179–189.

Reynolds, D. J. (2009). *Genetic dissection of triterpenoid saponin production in Chenopodium quinoa using microarray analysis* (Master's thesis). Brigham Young University, Utah, United States.

Risi, J., & Galwey, N. W. (1984). The *Chenopodium* grains of the Andes: Inca crops for modern agriculture. *Advances in Applied Biology, 10*, 166–169.

Rojas, W., Pinto, M., & Mamani, E. (2009). Logros e impactos del Subsistema Granos Altoandinos, periodo 2003–2008. In *Encuentro Nacional de Innovación Tecnológica, Agropecuaria y Forestal* (pp. 58–65). INIAF.

Spehar, C. R., & Rocha, J. E. D. (2010). Exploiting genotypic variability from low-altitude Brazilian savannah-adapted *Chenopodium quinoa*. *Euphytica, 175*, 13–21.

Spehar, C. R., & Santos, R. L. D. (2005). Agronomic performance of quinoa selected in the Brazilian savannah. *Pesquisa Agropecuária Brasileira, 40*(6), 609–612.

Stevens, M. R., Coleman, C. E., Parkinson, S. E., Maughan, P. J., Zhang, H. B., Balzotti, M. R., Kooyman, D. L., Arumuganathan, K., Bonifacio, A., Fairbanks, D. J., Jellen, E. N., & Stevens, J. J. (2006). Construction of a quinoa (*Chenopodium quinoa* Willd.) BAC library and its use in identifying genes encoding seed storage proteins. *Theoretical and Applied Genetics, 112*, 1593–1600.

Stikic, R., Glamoclija, D., Demin, M., Vucelic-Radovic, B., Jovanovic, Z., Milojkovic-Opsenica, D., Jacobsen, S. E., & Milovanovic, M. (2012). Agronomical and nutritional evaluation of quinoa seeds (*Chenopodium quinoa* Willd.) as an ingredient in bread formulations. *Journal of Cereal Science, 55*, 132–138.

Vega-Gálvez, A., Miranda, M., Vergara, J., Uribe, E., Puente, L., & Martínez, E. A. (2010). Nutrition facts and functional potential of quinoa (*Chenopodium quinoa* Willd.): An ancient Andean grain. *Journal of the Science of Food and Agriculture, 90*, 2541–2547.

Ward, S. M. (1998). A new source of restorable cytoplasmic male sterility. *Euphytica, 101*, 157–163.

Ward, S. M. (2000). Allotetraploid segregation for single-gene morphological characters in quinoa (*Chenopodium quinoa* Willd.). *Euphytica, 116*, 11–16.

Wilson, H. D. (1980). Artificial hybridization among species of *Chenopodium*. *Systematic Botany, 5*, 253–261.

Wilson, H. D. (1988a). Quinoa biosystematics I: Domesticated populations. *Economic Botany, 42*, 461–477.

Wilson, H. D. (1988b). Quinoa biosystematics II: Free living populations. *Economic Botany, 42*, 47–494.

Wilson, H. D. (1990). Quinoa and relatives (*Chenopodium* subsect. *Cellulata*). *Economic Botany, 44*, 92–110.