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Diversity of quinoa genetic resources for sustainable production: A survey on nutritive characteristics as influenced by environmental conditions

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Environmental extremes and climatic variability have enhanced the changes in numerous plant stressors. Researchers have been working to improve "major" crops for several decades to make them more adaptable and tolerant to environmental stresses. However, neglected and underutilized crop species that have the potential to ensure food and nutritional security for the ever-growing global population have received little or no research attention. Quinoa is one of these crops. It is a pseudocereal, considered a rich and balanced food resource due to its protein content and protein quality, high mineral content, and health benefits. This review provides currently available information on the genetic resources of quinoa and their quality in terms of variability of economically important traits such as yield, and the content of bioactive compounds, such as protein and amino acid composition. The influence of variety and environmental conditions on selected traits is also discussed. The various types of nutrients present in the different varieties form the basis and are key for future breeding efforts and for efficient, healthy, and sustainable food production.

KEYWORDS

amino acids, genetic resources, nutritive value, protein, quinoa, environmental conditions

Introduction

Most staple foods comprise grain crops; therefore, feeding the ever-increasing global population means increasing the production of these crops (Bvenura and Kambizi, 2022). But it is well known that climate change is rapidly degrading the conditions of crop production. Salinization and aridity are forecasted to increase in most parts of the world (Choukr-Allah et al., 2016). Moreover, globally, the food crisis is mainly triggered by shocks such as drought and escalated by trade restrictions leading to price rises as an impact of the Covid-19 pandemic and as a consequence of the current war in Ukraine (Rahut et al., 2022).

As a consequence of this reality, new stress-tolerant or new alternative crops or species must be identified and used for future food security (Choukr-Allah et al., 2016). The present situation is that common wheat, rice, and maize as major crops seem to be near 80% of their potential. This shows the potential of many small-scale and marginal crops and wild plants that can be used as high-quality food sources. Since many of these species are well adapted to extreme environments, their role in the current scenario of climate change has become extremely important (Chrungoo and Chettry, 2021).

These crops have the potential to complement the major cereals and play a greater role in a safe household diet. A better understanding of these crops that feed the world and their potential role in nutrition will help secure their future and ensure food and nutrition security. *Chenopodium quinoa* Willd. was selected as one of the crops that will contribute to food security in the twentifirst century, because of its high resilience to extreme environmental conditions and its qualities as a functional food (Bvenura and Kambizi, 2022; Singh et al., 2022) and a potentially strategic crop that plays a vital role in food security and sovereignty (Rojas et al., 2015). In addition, quinoa has gained importance in international consumer markets in the last decade, which provides economic opportunities for Andean producers (Anaya et al., 2022). On the other hand, quinoa could be used for crop diversification in Europe and other parts of the world, outside of its genetic origin, as an alternative for marginal agricultural land (Jacobsen, 2017).

In the present work, we attempt to summarize the available information about quinoa genetic resources for the whole world by highlighting the situation in the Czech Republic. We also explore the results of current research focused on nutraceutical properties, including carbohydrates, lipids, proteins, amino acids, vitamins, and minerals. This overview provides an insight into the enormous variability of morpho-phenological traits and nutritive components which are possessed by quinoa germplasm cultivated in different global conditions and shows us how important it is to conserve and protect this richness.

Conservation of global quinoa genetic resources and history of research on quinoa in the Czech Republic

Quinoa plant genetic resources are essential for food and nutrition security and sovereignty of peoples, and they make a significant contribution to meeting the basic needs of humanity. They are part of ancestral and cultural heritage, especially for the countries of the Andean region. Their conservation and sustainable use are therefore the responsibility of society as a whole (Rojas et al., 2015). Quinoa is one of the underutilized crops with public breeding or evaluation programmes in South American countries such as Peru, Ecuador, and Bolivia (Galluzzi and Noriega, 2014). Quinoa seeds of different accessions are currently being conserved in several gene banks around the world (*ex situ* conservation). However, conservation of agrobiodiversity means conservation of the associated culture, that of indigenous farmers living in the Andean region (Bazile et al., 2016a; Jacobsen, 2017). Thus, although the importance of gene banks for biodiversity conservation is well known, the success of future conservation and breeding programmes depends on the transfer of knowledge and associated practices that can help to adapt quinoa to new regions (Ruiz et al., 2014).

Quinoa germplasm and its wild relatives are estimated at 16,422 accessions worldwide; it is held in 59 institutions (universities, gene banks, research, and agricultural institutions) in 30 countries around the world. 88% of accessions are conserved within the Andean region. The largest collections of quinoa and its wild relatives are held by institutions in Bolivia and Peru, with more than 6,000 accessions (Rojas et al., 2015). Compared to published data from many years ago about quinoa accessions conserved in gene banks (Jacobsen and Mujica, 2002), the collection, characterization, and evaluation of quinoa genetic resources have greatly improved in recent years.

According to available data, the genetic resources of quinoa conserved in collections outside the Andean region comprise a total of 2,137 accessions (Table 1). In the database, the biological status of 1,329 accessions is indicated as traditional cultivar/landrace, 552 accessions are listed as wild, while 1,007 accessions are shown as advanced/improved cultivar, and 100 accessions as others (Genesys, 2022). The provenance of accessions is mostly Peru, followed by the USA and Bolivia. In 1,329 accessions the type of germplasm storage is not identified, 543 genetic resources are kept in as long-term seed collection, 193 are conserved in seed collection, and 45 accessions in the short-term collection. In total, 478 accessions have safety duplication in Svalbard Global Seed Vault in Norway and 143 accessions in National Seed Storage Laboratory, USDA-ARS in the USA. Most of the accessions (1,306) are conserved in the International Center for Biosaline Agriculture in the United Arab Emirates. In Europe, the largest collection (528 accessions) is held by the Genebank of Leibniz Institute of Plant Genetics and Crop Plant Research in Germany (Eurisco, 2022).

In the Czech Republic, research on quinoa genetic resources began in 1999 with Dr. Anna Michalová, who obtained 22 quinoa genotypes from South America. Subsequently, a working collection of quinoa genotypes was established in the gene bank of the Crop Research Institute in Prague. The quinoa accessions were evaluated under field conditions for selected agro-morphological traits (days to flowering, days to harvest, 1,000-seed weight, etc.), and selected nutritional components in the seeds (crude protein content) were also analyzed in the laboratory. Evaluation of the quinoa working collection was stopped until 2016 when Dr. Dagmar Janovská and Dr. Petra Hlásná Cepková resumed work on quinoa

TABLE 1 Quinoa genetic resources in collections outside the South American region (Genesys, 2022).

Country	Holding Institute	Institute code	No. of accessions
United Arab Emirates	International Center for Biosaline Agriculture	ARE003	1,306
Germany	Genebank, Leibniz Institute of Plant Genetics and Crop Plant Research	DEU146	528
United States	North Central Regional Plant Introduction Station, USDA-ARS, NCRPIS	USA020	162
United Kingdom	Genetic Resources Unit, Institute of Biological, Environmental and Rural Sciences, Aberystwyth University	GBR016	23
Hungary	Centre for Plant Diversity	HUN003	19
Slovakia	NAFC-Research Institute of Plant Production	SVK001	14
Australia	Australian Grains Genebank, Agriculture Victoria	AUS165	13
Ethiopia	International Livestock Research Institute	ETH013	11
Slovenia	Crops and Seed Production Department, Agricultural Institute of Slovenia	SVN019	5
Australia	Australian Pastures Genebank	AUS167	4
Others			20
Total			**2,105**

genetic resources cultivated under the conditions of the Czech Republic. Currently, the working collection of quinoa includes 70 genotypes. They are being tested under field conditions using descriptors for quinoa and its wild relatives (Bioversity International et al., 2013) while analyses are being conducted in the laboratory to determine the nutritional quality of the seeds of each genotype. The promising material will be used for future breeding purposes.

Global production of quinoa

At present, quinoa is grown throughout North and South America, Europe, Asia, Africa, and Oceania (Hinojosa et al., 2021). Alongside South American countries, China, India, and some European countries cultivate quinoa (Bazile and Baudron, 2015; Mosyakin and Schwartau, 2015; Yang et al., 2019). However, the biggest world producers remain countries of the traditional region of quinoa cultivation: Peru, with the production of 100,115 t; Bolivia, with 70,170 t (Faostat, 2022); and Ecuador, with more than 4,500 t (Hinojosa et al., 2021), while the United States is the top importer (Bvenura and Kambizi, 2022). The global harvested area of quinoa almost doubled last decade from 95,979 ha in 2010 to 188,878 ha in 2020. Annual production in China was 20,000 t in 2018 and harvested area reached nearly 12,000 ha (Yang et al., 2019). Globally, the average yield slightly increased from 0.83 t.ha^{-1} in 2010 to 0.93 t.ha^{-1} in 2020 (Faostat, 2022). For example, in Ecuador, the obtained yield in the variety comprises 66% of the total quinoa area which is 1.30 t.ha^{-1} (Hinojosa et al., 2021).

In the last decade, quinoa has evolved from being a neglected traditional food to an important export crop, promoted as a "superfood" throughout the Western world (Bazile and Baudron, 2015; Nuñez De Arco, 2015). Rising demand among Western consumers has created new economic opportunities for quinoa farmers in Bolivia's southern Altiplano. The negative aspect of the high interest in quinoa and the extreme increase in demand for quinoa seeds is that it has caused a spectacular increase in market price (Tschopp et al., 2018). However, this quinoa boom has brought environmental disaster in the traditional regions of quinoa cultivation in Bolivia (Jacobsen, 2011). Similarly, in Peru, the area under quinoa cultivation has been expanded by 264% and its cultivation has spread to all regions of Peru (Bedoya-Perales et al., 2018) which had a strong negative impact on the environment – soil degradation, pest, and diseases occurrence; likewise on socio-economic links and relations in local communities (Jacobsen, 2011). In the context of the above-mentioned facts, countries of the Andean region have tried to make a great effort to establish a harmonious interaction between socio-economic and environmental demands (Bedoya-Perales et al., 2018) and apply strategies for saving quinoa diversity, established breeding and research priorities, built more transparent commercial chain policy, and ensure more efficient cooperation with local farmers and cooperatives to decrease the negative impact of quinoa growth expansion (Ruiz et al., 2014; Bazile and Baudron, 2015; Bazile et al., 2016a; Bedoya-Perales et al., 2018; Hinojosa et al., 2021).

Quinoa's adaptability to a diverse environment

In different countries around the world, farmers and researchers have been trying to find, test and introduce nutritionally valuable seed crops that would be suitable for diverse growing conditions, achieve satisfactory yields, and

TABLE 2 Different quinoa genotypes performance in different environments.

Plant Material	Growing condition	Locality, country	Agro-morphological evaluation	Biochemical markers	Seed yields	References
468 genotypes	Drip irrigation	Dubai, the United Arab Emirates	11 morphological traits	400 seed metabolites	n.d.	Tabatabaei et al. (2022)
two cultivar ICBA-Q5, Titicata	Field, supplemental irrigation	Rehamna region, Morocco	Physiological and morphological traits in plants, yield, and its components	n. d.	0.08–0.84 t.ha^{-1}	Taaime et al. (2022)
nine novel quinoa genotypes and 1 commercial cultivar Regalona Baer	Field with full and reduced irrigation	Atacama Desert	Physiological and morphological traits in plants, thermal infrared and hyperspectral imaging	n. d.	2.45–3.24 t.ha^{-1}	Dumschott et al. (2022)
15 quinoa varieties and five breeding lines	Eastern lowland region and Highland region, exp. fields	the Eastern lowland and northern highlands, Rwanda	Emergency, Days to flowering, Days to maturity, Plant height, Grain yield	n. d.	Min: 0.14 t.ha^{-1} QuF9P1-20 Max: 3.00 t.ha^{-1} NL-6	Habiyaremye et al. (2022)
30 quinoa accessions	Greenhouse	Tunja, Columbia	12 qualitative and 9 qualitative traits	n. d.	n.d.	Manjarres-Hernandez et al. (2021)
13 quinoa commercial or selected varieties	Field experiments	North-West European, Melle, Belgium	Seed characteristics	Chemical composition of seeds	Min: 0.47 t.ha^{-1} Atlas, Pasto Max: 3.42 t.ha^{-1} Vikinga, Titicaca	De Bock et al. (2021b)
Cultivars Regalona, Puno, titicaca, Vikinga, Q3, Q5	Field experiments under irrigation	Zamadueñas, Spain	Seed weight, area, viability, color, and germination rate, grain yield	Saponin content, protein content, AA profile, mineral content, FRAP assay, TPC, TFC	Min: 0.70 t.ha^{-1} Vikinga Max: 3.25 t.ha^{-1} Q3 cultivar	Granado-Rodriguez et al. (2021a)
Jessie, Marisma, Roja, Duquesa, Pasto	Field experiments under irrigation	Southwestern Spain	Above-ground biomass, HI, seed yield, 1000-SW, nutrient uptake	Moisture, fat, total dietary fiber, protein, carbohydrate, mineral, and ash contents	Min: 1.58 t.ha^{-1} Roja Max: 3.04 t.ha^{-1} Marisma	Matías et al. (2021)
Regalona, AG 2010, Cauhil, Morado	Field experiments under 5 irrigation treatments	Diguillín Province, Ñuble Region, Chile	Seed yield, seed yield efficiency	Total protein content, globulin and albumin yield, and technical efficiency	Min: 0.41 t.ha^{-1} Morado Max: 3.35 t.ha^{-1} Cahuil	Pinto et al. (2021)
KVL-SRA2, Chipaya, Q-37	Field experiment	Cairo, Egypt	Plant growth performance, leaf pigment	Protein, ash, fat, dietary fiber, total carbohydrate content, total saponin, and tannin content, TPC, TFC	Min: 1.20 t.ha^{-1} KVL-SRAZ Max: 2.40 t.ha^{-1} Q-37	El-Serafy et al. (2021)

(Continued)

TABLE 2 (Continued)

Plant Material	Growing condition	Locality, country	Agro-morphological evaluation	Biochemical markers	Seed yields	References
14 genotypes	Field experiments	Rabat, El Kbab, Meknes, Berrechid, Tinejdad	Germination rate, seed size and yield, plant height, stem diameter, dry matter, HI, 1000-SW, *Peronospora farinosa* sensitivity	n. d.	Min: 0.00 $t.ha^{-1}$ Amarilla de Marangani Max: 7.83 $t.ha^{-1}$ SW2	Thiam et al. (2021)
Q5 variety	Three levels of salinity, greenhause	Karakalpakstan, Uzbekistan	Plant height, shoot lengths, panicle weight, seed yield, 1,000-seed weight	Protein content, AA content, oil content, FA content, Element content	n.d.	Toderich et al. (2020)
six quinoa accessions	Field experiments	Northern Israel	Biomass and seed characterization	Chemical composition of seeds and biomass	Min: 1.54 $t.ha^{-1}$ accession 5 Max: 6.36 $t.ha^{-1}$ accession 4E	Asher et al. (2020)
six quinoa genotypes - Q18, Q21, Q22, Q29, AMES 13761, NSL 106398	Field experiments with three salinity treatments, drip irrigation	Dubai, United Arab Emirates	Various morphological traits of plants, seed yield, yield stability, HI	Protein content	Min: 1.27 $t.ha^{-1}$ Q21 genotype Max: 2.30 $t.ha^{-1}$ Q18 genotype	Hussain et al. (2020)
Q5 variety	The circular drainable lysimeters	Semi-arid area with a warm climate, Bahgar, Iran	Crop evapotranspiration, grain yield, biomass, water productivity	n. d.	n.d.	Ahmadi et al. (2019)
Different varieties	Field	24 provinces of China	Grain yield	Protein content	Min: 1.48 $t.ha^{-1}$ Longli Max: 5.27 $t.ha^{-1}$ Qingli-1	Yang et al. (2019)
Cultivar Regalona, Salcedo-INIA, Titicaca	Rainfed field experiments	El Pobo, Teruel, Spain; Arequipa, Peru; Río Hurtado, Chile	Grain yield, seed weight per plant, HI, plant height, Stem diameter, panicle length and diameter, plant weight, days to flowering, and maturity	Mineral composition, phytate content, protein content, AA content, FRAP assay, fiber, and saponin content	Min: 1.53 $t.ha^{-1}$ Titicaca Max: 5.17 $t.ha^{-1}$ Salcedo	Reguera et al. (2018)
Jessie, Titicaca, Puno, Zeno	Field experiments	Southwestern Germany	Soil mineral content, grain yield, 1000-SW,	Total protein, lipid content, FA and AA profile, saponin content	1.73–2.43 $t.ha^{-1}$	Prager et al. (2018)
Commercial genotype Regalona and one quinoa accessions	Three thermal treatments (increased night temperatures), exp. fields	Valvidia, Chile	Physiological and morphological traits of biomass, grain yields, chlorophyll content, water-soluble carbohydrates, grain protein content	n. d.	Min: 2.93 $t.ha^{-1}$ Accession Max: 6.00 $t.ha^{-1}$ Regalona	Lesjak and Calderini (2017)

(Continued)

TABLE 2 (Continued)

Plant Material	Growing condition	Locality, country	Agro-morphological evaluation	Biochemical markers	Seed yields	References
$F_{2:5}$ population	Field experiments	Coastal environment, Rabat, Morocco	16 qualitative and seven qualitative traits	n. d.	n. d.	Benlhabib et al. (2016)
10 landraces, eight varieties under development,three registered varieties	2–5 sites in nine countries	North Africa, the Near East, Asia	19 morphological and phenological traits	n.d.	Min: 0.20 t.ha^{-1} Sajama Iranshar Max: 2.05 t.ha^{-1} Titicaca	Bazile et al. (2016b)
10 quinoa cultivars	Field experiments under irrigation	Encalilla, North Western Argentina; Altiplano, Bolivia	Root, aerial, and seed biomass, plant height, grain yield	AA composition, total protein content	Min: 0.38 t.ha^{-1} Samaranti Max: 3.86 t.ha^{-1} Sayana	Gonzalez et al. (2012)
Titicaca	Field experiment under three salinity treatments and three irrigation regimes	Southern Italy	Seed yield, climatic conditions, soil water content, electrical conductivity	Saponin content, carbohydrate, protein, oil, ash, and dietary fiber content	Max: 2.3 t.ha^{-1} Min: 2.7 t.ha^{-1}	Pulvento et al. (2012)

HI, harvest index; TPC, total phenolic content; TFC, total flavonoid content; 1000-SW, weight of thousand seeds; n. d., not defined.

offer versatile applications in food production and consumption (Gardner et al., 2019; Toderich et al., 2020; Habiyaremye et al., 2022).

To fully exploit the potential of the crop for marginal environments, identification of new and high-yielding quinoa genotypes with good local adaptation and high nutritional quality are crucial, which requires intensified screening and adaptation research (Choukr-Allah et al., 2016).

Recently, the performance of different quinoa genotypes in different global environments with an emphasis on their adaptability and seed nutritional quality has been studied in many countries and regions (Table 2). The considerable variability in yield for different quinoa genotypes in the different environments was confirmed outside of the Andean region. The lower yields were observed at 0.08 t.ha^{-1} in Morocco (Taaime et al., 2022) and the highest at 7.86 t.ha^{-1} (Thiam et al., 2021) also in Morocco. The range of yield in experimental fields of the Czech Republic in 2018–2021 was estimated between 0.12 and 3.99 t.ha^{-1} (unpublished data). Observed yield levels in Northern Europe were 1–3 t.ha^{-1} (Pulvento et al., 2012; Jacobsen, 2017; Prager et al., 2018; De Bock et al., 2021b; Granado-Rodriguez et al., 2021b; Matías et al., 2021). However, quinoa yields over the years have remained unpredictable and very low, averaging between 1.2 and 1.4 t.ha^{-1} while the maximum attainable yield can be up to 8–10 t.ha^{-1} in Morocco. A range of factors was suggested as affecting production, such as the choice of cultivars, optimal sowing date, and nutrient management was suggested affecting the production (Choukr-Allah et al., 2016). In the same way, high salinity can reduce the yield significantly (Hussain et al., 2020). Grain yield was more influenced by the environment and the genotype-environment interactions. The results of (Thiam et al., 2021) confirmed the significance and challenge of evaluating the varietal grain yield stability across contrasting environments.

The marginal effect of salt stress on nutritional composition was presented by (Choukr-Allah et al., 2016), whereas (Hussain et al., 2020) reported a significant impact of salt stress on grain protein contents dependent on genotype. However, the salinity common in these regions promotes growth but up to a certain threshold, beyond which growth and productivity start to be negatively affected (Choukr-Allah et al., 2016). In testing 20 quinoa genotypes in two different environments in Rwanda, it was confirmed that low water availability affected the growth and yield of quinoa and there is a need to identify the best genotypes adapted to specific agro-ecological zones and even growing seasons (Habiyaremye et al., 2022).

Rising temperatures are challenge for quinoa as well as for other crops. High temperatures during flowering and heat stress during the vegetative stage in certain quinoa varieties considerably lowered yield and changed protein and fiber content (Matías et al., 2021). In the growing conditions of Chile, the influence of increased night temperature on quinoa plants was evaluated (Lesjak and Calderini, 2017). Grain yields were reduced in the range of 12–31% by increased night temperatures. Similarly, the aboveground biomass was affected negatively in contrast with values for harvest index, individual grain weight, grain protein content, and water-soluble carbohydrates, which have changed only slightly.

In Chile, the local landrace genotype Cahuil had the best performance regarding seed yield under water stress (Pinto et al., 2021). Further, the genotype Titicaca (originating from the Andes) showed a good adaptation to the Mediterranean environment with tolerance to salinity and drought (Pulvento et al., 2012). On the other side, in some regions of southeast China, the combination of the high temperatures and heavy rainfalls had negative effects on the growth of quinoa. Fortunately, quinoa germplasm collected from Taiwan showed resistance to high temperatures and heavy rainfalls (Yang et al., 2019). In quinoa growing in the conditions of Morocco, optimal temperatures (10–25°C), high and well-distributed precipitation, and short photoperiods contributed to better growth and the highest yield (Taaime et al., 2022). The susceptibility of quinoa to temperatures above 32°C was confirmed due to the flower closing during the day and limited pollination caused a reduction of the yield by up to 86% (Tovar et al., 2020).

The high degree of variability in the performance of nutritional profiles of quinoa seeds under various salinity stress was assessed while the nutritional value of seeds remained unchanged, especially the high protein content, all essential amino acids, high mineral content, and flavonoids (Pulvento et al., 2012; Toderich et al., 2020). On the other hand, high temperatures increased protein and fiber content (Matías et al., 2021).

However, the establishment of this crop in many agronomical areas outside South America is still limited. It could be considered that the quinoa cultivar selection process remains unfinished for new cultivation areas, including those located in southern Europe which are characterized by having intense precipitations at early growth stages and high temperatures at later stages of crop development (Granado-Rodriguez et al., 2021b). There is still very limited information regarding the stability of seed nutritional characteristics under changing environments (Granado-Rodriguez et al., 2021b).

As with any other new crop, one of the key factors for the successful introduction and establishment of quinoa under new climatic conditions will be the identification of appropriate planting material. Therefore, it is important to study the adaptation and yield of several potential quinoa genotypes from different provenances to select the most promising ones suitable for the local agro-climatic conditions (Choukr-Allah et al., 2016). Not only should adaptation of quinoa be discussed, but also sustainable establishment in a new environment.

Nutritional characteristics of quinoa seeds and plants

Quinoa has outstanding nutritional value in all its edible parts – seeds and leaves, which were recognized even by ancient populations that considered quinoa a sacred food (Jacobsen et al., 2003). Quinoa seeds are a superior source of vitamins, minerals, dietary fiber, and lipids with the presence of health-beneficial polyunsaturated fatty acids (Repo-Carrasco et al., 2003). As reported by Schlick and Bubenheim (1996), quinoa is one of the single food sources that can supply all essential macro and micronutrients required for balanced human nutrition.

Carbohydrates, starch, and total dietary fiber

Quinoa seeds contained a relatively high amount of carbohydrates, with the content ranging from about 42% reported in the variety “Roja” up to 83% found in accessions cultivated in Peru (Encina-Zelada et al., 2017). As summarized in Table 3, there are significant differences in carbohydrate content in various genotypes. For example, Miranda et al. (2012) detected higher carbohydrate content in Chilean highland ecotypes as opposed to southern ecotypes. Pereira et al. (2019) reported slightly higher mean carbohydrate content in black and white varieties but lower in red varieties. In spite of that, many other variables modify total carbohydrate content, such as environmental conditions and sowing date. For example, in sea level genotypes and one cross genotype cultivated in Argentina, winter sowing at 18°C resulted in expanded seed weight, and therefore higher carbohydrate content in seeds (Curti et al., 2018). On the other hand, high carbohydrate content negatively affects total protein content (Craine and Murphy, 2020; De Bock et al., 2021a,b).

In terms of environmental influence, increased carbohydrate content was reported for lowland/coastal quinoa genotypes “Regalona Baer” and “Villarrica” in arid conditions with lower soil organic matter content and a mean temperature of approximately 18°C during the growing season (Miranda et al., 2013). Experiments conducted with genotypes cultivated in Spain resulted in decreased carbohydrate content in a growing season with a mean temperature of approximately 25°C, in contrast to a growing season with a mean temperature lowered by 5°C (Matías et al., 2021). This was also supported by Garcia-Parra et al. (2022), indicating the highest carbohydrate content (65.5%) in cultivars grown in a cold climate.

The most prevailing component of quinoa carbohydrates is starch, situated primarily in the perisperm, in contrast to the cereals (Burrieza et al., 2014). The minimal value for starch content was 44%, found in genotype “Cica” (Jimenez et al.,

TABLE 3 Variability of the carbohydrate content in quinoa seeds divided according to the genotype name and seed color.

	Sample Genotype	Seed color	Production area	Carbohydrate content	References
Genotype name	Highland ecotypes: Ancovinto, Cancosa Central ecotypes: Cahuil, Faro Southern ecotypes: Regalona, Villarrica	n. d.	Chile	Min: 56.54 [1] Villarrica Max: 68.12 [1] Ancovinto	Miranda et al. (2012)
	n = 78 accessions	n. d.	Bolivia Brazil Peru	Min: 43.64 [1] Max: 76.37 [1]	Ferreira et al. (2015)
	n = 77 accessions	Beige Black Orange Yellow	Peru	Min: 78.48 [1] Max: 82.89 [1]	Encina-Zelada et al. (2017)
	Real	n. d.	Colombia	68.30 [1]	Contreras-Jimenez et al. (2019)
	Cica Kamiri Inga Pirca		Argentina	Min: 72.81 [2] Inga Pirca Max: 74.74 [2] Kamiri	Contreras-Jimenez et al. (2019)
	F5:F6 advanced breeding lines Cherry Vanilla CO407 Dave Kaslaea	n. d.	USA	Min: 69.56 [2] Max: 74.00 [2]	Craine and Murphy (2020)
	Atlas Jessie Marisma Pasto Pot_4 Roja	n. d.	Spain	Min: 41.52 [3] Roja Max: 52.62 [3] Pasto	Gomez et al. (2021)
	Blanca real Nariño Pasankalla Soracá Puno Titicaca	n. d.	Colombia	Min: 56.00 [1] Puno Max: 70.66 [1] Pasankalla	Garcia-Parra et al. (2022)
	Iniap Tunkahuan	n. d.	Ecuador	60.37 [1]	Villacres et al. (2022)
Seed color	Commercial – unknown (*n* = 29) Blanca Kancolla Blanca Hualhuas Negra Collana Negra Pasankalla Pasankalla Roja Pasankalla Rosada de Huancayo Salcedo INIA	Black Red White	Peru Spain	Min: 75.3 [2] Red quinoa Max: 77.0 [2] White quinoa	Pereira et al. (2019)

[1] The results are expressed as %. [2] The results are expressed as g.100 g^{-1} of dry weight. [3] The results are expressed as g.100 g^{-1} of fresh weight. Max, maximum value; Min, minimum value; n. d., not defined.

2019) cultivated in Argentina, whereas the most abundant starch content of 72.5% was described by (De Bock et al., 2021b) in genotype "Titicaca" grown under North-West European field conditions. Nonetheless, the values for total carbohydrate content in this study varied between different years of field experiments. Similarly, (Grimberg et al., 2022) characterized the genotype "Titicaca" as one with the most prominent starch content. (Aluwi et al., 2017) evaluated maximal starch content in genotype "CO 407D" [64% in dry weight (dw)] and the lowest for "UDEC-1" (55%), both cultivated in the USA.

Quinoa starch is rich in polysaccharide amylopectin, which represents 54–85% of dw (Dong et al., 2021; Kheto et al., 2022). Amylose content is, on the other hand, relatively low. It ranges from approximately 6% in "Tianjing Tibet Quinoa" (Li and Zhu, 2017) up to 20% in the Argentinian variety "Jujuy" (Nascimento et al., 2014). Specific starch and amylopectin structure give quinoa starch various functional properties that can be used in a wide range of food products (Li et al., 2016; Aluwi et al., 2017; Li and Zhu, 2017). Nevertheless, climatic conditions during the growing season may alter final functionality, even though starch biosynthesis is determined primarily by genetics (Garcia-Parra et al., 2021, 2022). Additionally, seed color seems to correlate with starch physiochemical properties, as reported by Peng et al. (2022), in opposition to Li et al. (2016), describing no correlation between the seed color and starch characteristics.

Total dietary fiber (TDF) content in quinoa is also highly heterogenous, ranging from approximately 7% (De Bock et al., 2021a) up to 23% (Granado-Rodriguez et al., 2021b). The variation can be explained by the genotype effect (Curti et al., 2018), but also by growing conditions since fiber content can be enhanced under saline conditions (Pulvento et al., 2012) and high temperatures during the grain filling period (Matías et al., 2021). Negative correlations were found between TDF, carbohydrate, and fat content (Vidueiros et al., 2015). Overall, high amounts of TDF (over 18% TDF) were found in genotypes "Rainbow", "Faro", "Baer", "Colorado 407D" cultivated in Poland (Sobota et al., 2020), "Titicaca" grown in Italy (Pulvento et al., 2012), and "Roja" and "Duquesa" grown in Spain (Matías et al., 2021). Less prominent amounts (below 14% TDF) were presented in "Faro Red", "Puno" (Sobota et al., 2020), "Pasto" (Matías et al., 2021), white Bolivian and Peruvian quinoas (Pellegrini et al., 2018), "Cica", "Kamiri" and "Inga Pirca" (Jimenez et al., 2019).

Protein content and amino acid composition

Quinoa seeds are often considered high in protein; yet overall protein content is quite variable (Table 4) and sometimes comparable to or higher than in most cereals such as wheat (12%), oat (13%), rice (7%), and corn (6%) (USDA, 2020). Variations in protein content were significant in several genotypes cultivated in distinctive agro-ecological conditions. For example, the cultivar "Jessie" originating in France was cultivated in Belgium and reached almost 19% protein content (De Bock et al., 2021b), whereas the same genotype cultivated in Germany reached a protein content of approximately 12% (Prager et al., 2018). Nevertheless, "Jessie" cultivated for two years in southwest Spain showed a steady mean protein content of 16.7% (Matías et al., 2021).

The Danish-bred cultivar "Titicaca" was analyzed in at least 10 studies under distinctive environmental conditions. Despite that, this genotype reached analogous values (13–15%) in the cultivation conditions of Ethiopia (Agza et al., 2018), Morocco (Mhada et al., 2020), Belgium (De Bock et al., 2021b), USA (Aluwi et al., 2017), and Germany (Prager et al., 2018). Besides this, slightly higher protein content (above 15%) was observed under cultivation in Poland (Sobota et al., 2020) and Colombia (Garcia-Parra et al., 2022). In addition, Reguera et al. (2018) reported higher protein content for "Titicaca" cultivated in Chile compared to Spain, which follows the results of Granado-Rodriguez et al. (2021a), reaching comparable values in mean protein content averaged for three cultivation years.

Genotype "Regalona", originating in southern regions of Chile, was described in at least eight studies. The values for protein content were quite inconsistent. Miranda et al. (2012), Graf et al. (2016), and Granado-Rodriguez et al. (2021a) detected protein content reaching approximately 13–15% for "Regalona" cultivated in Chile and Spain, whereas other authors achieved higher values of approximately 17% under field experiments in Chile and Egypt (Lesjak and Calderini, 2017; Reguera et al., 2018; Saad-Allah and Youssef, 2018). Even higher values were achieved by Gargiulo et al. (2019) (18.30%); however, the authors did not define the cultivation location.

The protein content of the Danish cultivar "Puno" was described in at least seven studies. The majority of the results were quite consistent in diverse environments (USA, Germany, Poland, Belgium, Colombia), ranging between 13 and 15% (Aluwi et al., 2017; Sobota et al., 2020; De Bock et al., 2021b; Garcia-Parra et al., 2022). On the other hand, (Garcia-Parra et al., 2021) evaluated slightly reduced protein content, reaching almost 12% in "Puno" cultivated in Colombia.

Although the Peruvian genotype "Pasankalla" was tested in at least 4 studies, the referred values of protein content are quite distant. Apaza et al. (2015) and Gargiulo et al. (2019) discovered protein content of 18.73–20.60%, while Garcia-Parra et al. (2021) and Garcia-Parra et al. (2022) achieved lower values (14.5–15.5%, respectively) during experiments conducted in Colombia. Genotype "Cahuil" originating in central Chile was investigated in a total of three studies. Miranda et al. (2012) reported protein content of 11.13%, whereas Graf et al. (2016) presented a lower concentration of nearly 9%. Aluwi et al. (2017) recognized a much higher protein content of 14.4% under cultivation in the USA.

Nonetheless, there are many factors affecting the resulting protein content. Besides the influence of genotype, the importance of soil matric potential (SMP) and nitrogen fertilization was indicated (Wang et al., 2020). High SMP values (over −55 kPa) cause significant water stress and may also limit nitrogen uptake, which concurs with other studies (Sun et al., 2014; Walters et al., 2016). Therefore, to reach optimal protein content, irrigation is crucial for some genotypes cultivated in adverse soil-water conditions, although slight water stress

TABLE 4 Variability of protein content in quinoa seeds divided according to the genotype and seed color.

	Genotype name	Seed color	Production area	Protein content	Reference
Genotype	Highland ecotypes: Ancovinto, Cancosa Central ecotypes: Cahuil, Faro Southern ecotypes: Regalona, Villarrica	n. d.	Chile	Min: 11.13 [1] Cahuil Max: 16.18 [1] Villarrica	Miranda et al. (2012)
	Breeding line AG2010 B080 Regalona	n. d.	Chile	Min: 17.40 [2] Max: 18.90 [2]	Escuredo et al. (2014)
	Jujuy Salta	n. d.	Portugal	Min: 12.20 [5] Jujuy Max: 16.30 [5] Salta	Mota et al. (2016)
	$n = 12$ accessions	Cream Gray Orange Yellow	Peru	Min: 13.58 [1] Quillahuaman INIA, cream Max: 17.83 [1] Pasankalla, gray	Apaza et al. (2015)
	$n = 9$ commercial varieties Ancovinto Blanco Ancovinto Roja Cancosa Socaire Cáhuil Faro Regalona Villarrica	Black Red White	Bolivia Chile Ecuador USA	Min: 7.47 [2] Kalustyan's Black, Peru Max: 15.73 [2] Wegman's Red, Bolivia/Peru	Graf et al. (2016)
	$n = 28$ accessions	n. d.	USA	Min: 13.00 [1] CO 407D WMF Max: 15.8 [1] QuF9P39-64	Aluwi et al. (2017)
	$n = 77$ accessions	Beige Black Orange Yellow	Peru	Min: 8.33 [1] Max: 11.38 [1]	Encina-Zelada et al. (2017)
	Kvl-sra2 Kvl-sra3 Regalona Q37 Q52	n. d.	Egypt	Min: 12.03 [2] Kvl-sra3 Max: 19.03 [2] Kvl-sra2	Saad-Allah and Youssef (2018)
	Titicaca	n. d.	Ethiopia	13.57 [2]	Agza et al. (2018)
	Jessie Puno Titicaca Zeno	n. d.	Germany	Min: 16.10 [1] Zeno Max: ≈ 12 [1] Jessie	Prager et al. (2018)
	Regalona Salcedo-INIA Titicaca	n. d.	Chile Peru Spain	Min: ≈ 14 [1] Salcedo, Peru Max: ≈ 17 [1] Regalona, Chile	Reguera et al. (2018)
	Altiplano Pasankalla Regalona Titicaca	n. d.	n. d.	Min: 15.40 [1] Titicaca Max: 20.80 [1] Altiplano	Gargiulo et al. (2019)
	$n = 25$ accessions	n. d.	Poland	Min: 12.40 [2] Q629, USA Max: 15.98 [2] Faro, Argentina	Sobota et al. (2020)

(Continued)

TABLE 4 (Continued)

Genotype name	Seed color	Production area	Protein content	Reference
F5:F6 advanced breeding lines Cherry Vanilla CO407 Dave Kaslaea	n. d.	USA	Min: 10.04 [3] Max: 13.68 [3]	Craine and Murphy (2020)
Puno Titicaca	n. d.	Morocco	Min: 13.41 [3] Puno Max: 13.43 [3] Titicaca	Mhada et al. (2020)
Q5	n. d.	Uzbekistan	14.40 [3]	Toderich et al. (2020)
$n = 13$ accessions	Dark White	Belgium	Min: 12.10 [2,a] Oro de Valle Max: 18.80 [2,a] Jessie	De Bock et al. (2021b)
IC341709 IC329184 IC507733 IC107299 NIC22513 NIC22506	n. d.	India	Min: 14.10 [1] IC341709, IC507733 Max: 15.40 [1] IC329184, NIC22506	Ghumman et al. (2021)
Puno Q3 Q3 Regalona Titicaca Vikinga	n. d.	Spain	Min: 13.80 [1] Max: 19.10 [1]	Granado-Rodriguez et al. (2021a)
$n = 14$ accessions	Dark White	Spain	Min: ≈ 9 [1] A-SE-06, white Max: ≈ 16.50 [1] A-SE-15, dark	Granado-Rodriguez et al. (2021b)
Gannan Geermu Haili	n. d.	China	Min: 11.60 [1] Geermu Max: 12.60 [1] Haili	Jiang et al. (2021)
Duquesa Jessie Marisma Pasto Roja	n. d.	Spain	Min: 13.20 [1] Roja Max: 20.40 [1] Duquesa	Matías et al. (2021)
Atlas Jessie Marisma Pasto Pot_4 Roja	n. d.	Spain	Min: 15.59 [4] Pasto Max: 18.73 [4] Atlas	Gomez et al. (2021)
Blanca Real Nariño Pasankalla Soracá Puno Titicaca	n. d.	Colombia	Min: 12.36 [1] Soracá Max: 16.56 [1] Titicaca	Garcia-Parra et al. (2021)

(Continued)

TABLE 4 (Continued)

	Genotype name	Seed color	Production area	Protein content	Reference
Seed color	Bolivian quinoa (BQ)	Black	Bolivia	Min: 11.62 ^{4} SQ, white	Pellegrini et al. (2018)
	Peruvian quinoa (PQ)	Red	Peru	Max: 13.66 ^{4} BQ, white	
	Spanish quinoa (SQ)	White	Spain		
	Commercial – unknown (n=29)	Black	Peru	Min: 14.4 ^{2} White quinoa	Pereira et al. (2019)
	Blanca Kancolla	Red	Spain	Max: 15.6 ^{2} Red quinoa	
	Blanca Hualhuas	White			
	Negra Collana				
	Negra Pasankalla				
	Pasankalla Roja				
	Pasankalla				
	Rosada de Huancayo				
	Salcedo INIA				
	n. d.	Black Yellow	Peru	Min: 16.20 ^{1} Black quinoa Max: 18.70 ^{1} Yellow quinoa	Sanchez-Resendiz et al. (2019)

^{1}The results are expressed as %. ^{2}The results are expressed as g.100 g^{-1} of dry weight. ^{3}The results are expressed as g.100 g^{-1} sample. ^{4}The results are expressed as g.100 g^{-1} of fresh weight. ^{5}The results are expressed as g.100 g^{-1} of the edible portion on a fresh weight basis. ^{a}The protein content per variety averaged over the different years of field trials. Max, maximum value; Min, minimum value; n. d., not defined.

may enhance protein content (Wang et al., 2020). The intense application of nitrogen from 80 to 240 kg/ha increased protein content by approximately 1.5%. The positive effect of nitrogen fertilization was also presented by Wu et al. (2016) and Jacobsen and Christiansen (2016).

In addition, protein content in quinoa rises under salinity treatment, which was reported for varieties "CO407D", "UDEC-1", "Baer", "QQ065" (Wu et al., 2016), and "NSL106398" (Hussain et al., 2020). In contrast, Ruiz et al. (2016) expressed a drop in protein content by 7–12% in coastal lowland Chilean landraces ("VI-1", "Villarrica") and genotype "R49" (salares ecotype). In terms of temperature influence, protein content under heat stress was outstanding in varieties "Pasto", "Marisma", "Jessie", "Roja", and "Duquesa" (Matías et al., 2021). Garcia-Parra et al. (2022) detected slightly higher mean protein values for cultivation in the cold climate of Colombia, compared to temperate and warm conditions; but, as reported by the authors, protein content was not rapidly affected by elevated temperatures. The exception in this paper was the cultivar "Pasankalla", showing a decline in protein content in hotter conditions.

Those results suggest the great potential of the selected quinoa genotypes for cultivation in adverse environments. A high correlation was detected between embryo weight ratio and protein content since proteins are mostly stored in the embryo (Gargiulo et al., 2019). Protein content negatively correlates with panicle height and panicle biomass, whereas positive correlations were determined for total phenolic content, antioxidant activity, and saponin content (Granado-Rodriguez et al., 2021b).

Probably even more important than overall protein content is the quality of protein, given by the composition of essential amino acids (EAA). Quinoa protein generally contains all EAAs and several authors throughout the literature have concluded that quinoa protein is complete due to the superior composition of amino acids (AA; Nowak et al., 2016; Maradini et al., 2017; Schmidt et al., 2021). Nonetheless, Craine and Murphy (2020) argue that many of those studies evaluated outdated daily requirements or considered AA requirement values only for adults, not for children, whose requirements for EAAs are greater. The authors further stated that the quinoa protein is only "nearly complete". Regarding this statement, Boye et al. (2012) labeled valine and lysine as limiting AA for children up to the age of 10 years. In comparison, Gonzalez et al. (2012) suggested lysine, tyrosine, and tryptophan as limiting AA for the age group of 2–5 years. Craine and Murphy (2020) identified low leucine content, which does not achieve the recommended daily requirements for infants and children, therefore considering it as limiting AA.

As expressed in Table 5, the content of each EAA shifted between authors. The most abundant EAA was leucine with the highest content in the variety "Atlas" (Gomez et al., 2021), whereas the least represented EAA was tryptophan, with the content reaching 0.58–1.9 in g.100 g^{-1} protein in genotypes "Chucapaca" and "Bastille", respectively (Escuredo et al., 2014; De Bock et al., 2021b). With regards to

TABLE 5 Minimum and maximum values of amino acid composition (g.100 g $^{-1}$ protein) in various quinoa genotypes and production areas.

	Miranda et al. (2012)	Gonzalez et al. (2012) [a]	Escuredo et al. (2014)[a]	Prager et al. (2018)	Wang et al. (2020)	De Bock et al. (2021b)[a]	Gomez et al. (2021)
N. of accessions	6	10	3	4	6	12	6
Production area	Chile	Bolivia NW Argentina (A) Encalilla, Argentina (E)	Chile	Germany	China	Belgium	Spain
Growing seasons	2011	2007–2009	2010–2011	2015–2016	n. d.	2017–2019	2017
Histidine	2.70 Ancovinto, Cahuil 3.50 Villarrica	1.36 Sajama (E) 3.79 CICA (A)	1.71 Regalona 2.17 AG2010	1.33 Zeno (2015) 2.48 Puno (2016)	3.16 QWQ 3.70 QBQ	2.50 Bastille 3.20 Zwarte	3.67 Atlas 8.31 Roja
Isoleucine	2.90 Cahuil 3.80 Ancovinto	1.65 Chucapaca (E) 3.40 CICA (A)	0.75 Regalona 0.82 AG2010, B080	2.00 Zeno (2015) 3.19 Puno (2016)	2.80 QWQ 3.58 QBQ	3.90 Zwarte 4.80 Rouge Marie	3.75 Pot_4 4.61 Roja
Leucine	6.40 Cahuil 7.20 Villarrica	3.75 Sajama (E) 7.46 Ratuqui (E)	2.27 B080 2.52 Regalona	3.67 Zeno (2015) 5.55 Puno (2016)	5.07 QGQ 6.5 QBQ	7.00 Pasto 7.60 Atlas, Jessie	4.55 Pot_4 5.67 Pasto
Lysine	4.10 Cancosa, Cahuil 4.80 Villarrica	2.44 Sajama (E) 6.72 CICA (A)	2.35 AG2010 2.42 B080	2.77 Zeno (2015) 4.99 Puno (2016)	5.07 QWQ 6.02 SWQ	4.60 Rouge Marie 5.90 Pasto	5.40 Atlas 13.55 Jessie
Methionine	1.40 Ancovinto 1.90 Villarrica	0.73 Sajama (E) 1.87 CICA (A)	0.31 AG2010 0.69 Regalona	1.10 Zeno (2015) 1.80 Jessie, Puno (2016)	1.67 [b] QGQ 2.09 [b] SGQ, QBQ	2.00 Atlas 2.60 Puno	1.37 Pasto 1.64 Atlas
Phenylalanine	3.90 Cancosa, Cahuil 4.50 Villarrica	2.26 Sajama (E) 4.55 CICA (A)	1.49 B080 1.54 AG2010	2.20 Zeno (2015) 3.55 Puno (2016)	2.62 [c] QGQ 3.70 [c] SWQ	3.60 Zwarte 4.50 Atlas	3.73 Atlas 4.81 Roja
Threonine	3.20 Cancosa 3.60 Faro	2.09 Sajama (E) 4.59 CICA (A)	5.53 B080 8.89 Regalona	2.13 Zeno (2015) 3.27 Puno (2015)	1.79 QGQ 2.15 SWQ	3.60 Atlas, Bastille, Rouge Marie 4.40 Zwarte	3.43 Atlas 7.82 Jessie
Tryptophan	n. d.	0.58 Chucapaca 1.05 Sajama	0.99 B080 1.07 Regalona	0.88 Zeno (2016) 1.11 Puno (2016)	n. d.	1.50 $n = 5$ accessions [b] 1.9 Bastille [b]	0.40 Pot_4 0.58 Atlas
Valilne	4.30 Regalona 4.90 Ancovinto	2.19 Chucapaca (E) 4.39 CICA (A)	1.83 AG2010 2.31 B080	3.80 Puno (2016) 5.67 Jessie (2016)	2.50 QWQ 3.58 QBQ	5.30 Bastille 6.40 Rouge Marie, Zwarte	3.76 Atlas 5.81 Roja

[a] Amino acid content per variety is averaged over the different years of field trials. [b] Values are expressed for Methionine + cysteine. [c] Values are expressed for Phenylalanine + tyrosine. n. d., not defined; NW, Northwestern; QBQ, Big black quinoa; QGQ, Sanjiang Gray, gray quinoa; QWQ, Qingli No.1, white quinoa; SGQ, Aihua No.1, gray quinoa; SWQ, Jiaqi Diamond No.1, white quinoa.

the previously mentioned limiting AAs, several genotypes accomplished the daily requirements for EAAs in infants and children (WHO/FAO/UNU, 2007). As such, sufficient lysine content (over 5.7 g.100 g^{-1} protein) was identified in genotypes "Jessie", "Pasto", and "CICA". Valine content (over 4.3 g.100 g^{-1} protein) was satisfactory in genotypes "Ancovito", "CICA", "Jessie", "Rouge Marie", "Zwarte", and "Roja". Suitable leucine content (over 6.6 g.100 g^{-1} protein) was found in genotypes "Villarrica", "Rataqui", "Atlas", and "Jessie". Tryptophan content (over 0.85 g.100 g^{-1} protein) was met in genotypes "Sajama", "B080", "Regalona", "Zeno", "Puno", and all genotypes analyzed by De Bock et al. (2021b) (Table 5).

Overall, the remarkable variations in EAA composition might be caused by genotype, environment, and their interactions. According to De Bock et al. (2021b), the content of EAAs varied between growing seasons, but not between varieties, in contrast to Prager et al. (2018), who noticed significant differences among cultivars and experimental years. In terms of cultivation area, Steffolani et al. (2016) pointed out that Bolivian varieties had higher essential AA content than Peruvian varieties. Gonzalez et al. (2012) indicated dissimilarities in AA content between two experimental sites with higher EAA content in the Bolivia/Argentina location, which authors then explain by adaptation of the genotypes to the conditions they were bred in. Reguera et al. (2018) noted that varieties grown in Chile did not exhibit inter-cultivar variations in AA content compared to the same varieties grown in Spain, except for cultivar "Titicaca" which had consistent AA content among varieties and locations. The highest EAA content in genotypes cultivated in the USA was recognized in samples from the Chimacum location, as opposed to Mount Vermont samples (Craine and Murphy, 2020).

Most of the EAAs were not negatively affected by salinity in "Q5", a new salt- and drought-tolerant line, except for tyrosine (Toderich et al., 2020). Aloisi et al. (2016) found variations in genotype response to saline conditions. EAAs remained constant or declined, except for increased methionine in genotype "R49", belonging to the group of salares ecotype; and leucine in genotype "Villarrica" (coastal-lowland ecotype). A strong decline in EAAs under salinity treatment was detected in genotype VI-1 (coastal-lowland ecotypes). Despite this, Ruiz et al. (2016) concluded better suitability of "VI-1" and "Villarrica" in saline environments in terms of growth, yield, phenolic content, and protein profiles compared to the "R49"; however, other nutritional characteristics were not studied in this paper. Therefore, the selection of saline-resistant genotypes and the analysis of nutritional modifications under stress are crucial.

An essential factor in protein quality evaluation is digestibility. The information about protein digestibility in available scientific literature is sparse and often outdated. For example, Ruales and Nair (1992) reported the true protein digestibility of raw and washed quinoa reaching almost 92%. In addition, the biological value of quinoa protein (above 80%) was considerably higher compared to common cereals or soybean. On the other hand, significantly lower protein biological values were reported by Paucar-Menacho et al. (2018). Recently, Shi et al. (2020) reported the *in vitro* protein digestibility (IVPD) in quinoa ranging from ~73 to 79% with *in vitro* protein digestibility corrected amino acid scores (IV-PDCAAS) of 48–57%. Authors reported lower values in cultivar "NQ94PT", compared to the commercial blend of cultivars "Kankolla" and "Blanca Juli". Further, Jimenez et al. (2019) reported quinoa IVPD of ~61–63% in varieties "Cica", "Kamiri", and "Inga Pirca" obtained from Argentina. In addition, Craine and Murphy (2020) evaluated the PDCAAS in varieties "Colorado D407" ranging from 0.74 to 0.90 and 0.78 to 0.95 for the 1–2 an10-year-old children, respectively.

Overall protein digestibility can be improved by various processing methods (Rizzello et al., 2016; Lorusso et al., 2017; Dong et al., 2021; He et al., 2022), as well as sprouting (Jimenez et al., 2019). On the other hand, digestibility is reduced by the presence of starch, fiber (Opazo-Navarrete et al., 2019), and various antinutritional compounds (Gilani et al., 2012).

Lipid content and composition

Lipid content is, among other factors, strongly affected by genotype (Curti et al., 2020; Garcia-Parra et al., 2022). Since the primary lipid storage is located in the embryo, embryo size may also correlate to overall seed lipid content (De Bock et al., 2021b). The highest lipid yield was described in the genotype "Yellow Marangí", cultivated in Peru, reaching almost 10% (Apaza et al., 2015), whereas the lowest lipid content reached nearly 3% in quinoa variety "QU5", cultivated in Belgium (De Bock et al., 2021a) and commercial variety "Gramolino" from Ecuador (Graf et al., 2016; Table 6). In addition, colored seed samples tend to exhibit higher lipid content than white seed samples (Pellegrini et al., 2018); yet Tang et al. (2015) and Shen et al. (2022) obtained the opposite findings. Overall oil content was negatively correlated to protein content (Matías et al., 2021).

In terms of oil production, quinoa performed well in a temperate climate since heat stress reduced average oil content by almost 30% (Garcia-Parra et al., 2022). Curti et al. (2018) found strong interactions between cultivar and sowing date, related to the various photo-thermal conditions during sowing. In a two-year experiment with cultivars "Titicaca" and "Jessie", stable results were achieved with a mean crude fat content of 7.5 and 7.3%, respectively (Prager et al., 2018). Unfortunately, there are only a small number of studies on quinoa oil production with regard to meteorological conditions during the growing season and the adaptive response of the genotype.

Quinoa lipid profile is composed predominantly of essential polyunsaturated ω-6 linoleic acid (C18:2), with a minimum of 43% in accession "CHEN 414" originating in dry valleys of North

TABLE 6 Variability of lipid content in quinoa seeds divided according to genotype name and seed color.

	Genotype name	Seed color	Production area	Lipid content	References
Genotype	Highland ecotypes: Ancovinto, Cancosa Central ecotypes: Cahuil, Faro Southern ecotypes: Regalona, Villarrica	n. d.	Chile	Min: 5.57 [1] Villarrica Max: 7.06 [1] Cahuil	Miranda et al. (2012)
	$n = 12$ accessions	Cream Gray Orange Yellow	Peru	Min: 4.88 [1] Illpa Inia, cream Max: 9.78 [1] Yellow Maranganí, orange	Apaza et al. (2015)
	$n = 9$ commercial varieties Ancovinto Blanco Ancovinto Roja Cancosa Socaire Cáhuil Faro Regalona Villarrica	Black Red White	Bolivia Chile Ecuador USA	Min: 2.93 [2] Gramolino, white, Ecuador Max: 5.62 [2] Ancovinto Roja, white, Chile	Graf et al. (2016)
	Ecologicos Quinoa Mum's Original Heirloom Organic Quinoa Quinta Quinoa-BC12a Inca Gold Quinoa Vitabio Royal Quinoa Quinta Quinoa-BC12 Quinta Quinoa-BM12 Quinta Quinoa-Ch12 Quinta Quinoa-CVC12 GoGo Quinoa Red Organic Quinoa Organic Garage Organic Red Quinoa	Golden Red White	Bolivia Canada Unknown	Min: 6.03 [1] Mum's Original Heirloom Organic Quinoa Max: 6.74 [1] GoGo Quinoa Red Organic Quinoa	Tang et al. (2016)
	$n = 28$ accessions	n. d.	USA	Min: 5.08 [1] Blanca Max: 7.5 [1] Red Head	Aluwi et al. (2017)
	$n = 77$ accessions	Beige Black Orange Yellow	Peru	Min: 5.35 [1] Max: 7.78 [1]	Encina-Zelada et al. (2017)
	Kvl-sra2 Kvl-sra3 Regalona Q37 Q52	n. d.	Egypt	Min: 6.20 [2] Q37 Max: 8.04 [2] Kvl-sra2	Saad-Allah and Youssef (2018)
	Jessie Puno Titicaca Zeno	n. d.	Germany	Min: 5.50 [1] Zeno Max: 7.50 [1] Titicaca	Prager et al. (2018)
	Titicaca	n. d.	Ethiopia	6.30 [2]	Agza et al. (2018)

(Continued)

TABLE 6 (Continued)

Genotype name	Seed color	Production area	Lipid content	References
Cica Kamiri Inga Pirca	n. d.	Argentina	Min: 6.53 [2] Kamiri Max: 7.48 [2] Cica	Jimenez et al. (2019)
Amarilla de Maranganí Blanca de Juli Roja Pasankalla Negra Collana	White Red Black	Peru	Min: 4.97 [1] Amarilla de Maranganí Max: 6.46 [1] Roja Pasankalla	Vera et al. (2019)
F5:F6 advanced breeding lines Cherry Vanilla CO407 Dave Kaslaea	n. d.	USA	Min: 4.56 [2] Max: 7.19 [2]	Craine and Murphy, 2020
n = 25 accessions	n. d.	Argentina Chile Denmark Poland USA	Min: 4.22 [2] Faro Red Max: 6.82 [2] Titicaca Red	Sobota et al. (2020)
n = 13 accessions	Dark White	Belgium	Min: 5.42 [2,a] Pasto Max: 8.54 [2,a] Summer Red, dark	De Bock et al. (2021b)
n = 7 commercial varieties	n. d.	Belgium Netherlands	Min: 2.74 [2] QU5 Max: 7.34 [2] n. d.	De Bock et al. (2021a)
IC341709 IC329184 IC507733 IC107299 NIC22513 NIC22506 IC415403	n. d.	India	Min: 7.50 [1] IC341709 Max: 8.70 [1] IC507733, IC107299	Ghumman et al. (2021)
Gannan Geermu Haili	n. d.	China	Min: 4.00 [1] Haili Max: 5.21 [1] Gannan, Geermu	Jiang et al. (2021)
Duquesa Jessie Marisma Pasto Roja	n. d.	Spain	Min: 5.90 [1] Duquesa Max: 6.60 [1] Marisma	Matías et al. (2021)
Atlas Jessie Marisma Pasto Pot_4 Roja	n. d.	Spain	Min: 3.90 [3] Pot_4 Max: 5.21 [3] Marisma	Gomez et al. (2021)
Blanca real Nari no Pasankalla Soracá Puno Titicaca	n. d.	Colombia	Min: 5.77 Pasankalla Max: 7.50 Soracá	Garcia-Parra et al. (2022)

(Continued)

TABLE 6 (Continued)

	Genotype name	Seed color	Production area	Lipid content	References
Seed color	n. d.	Black Red White	South America	Min: 6.57 ^{1} Black quinoa Max: 7.17 ^{1} Red quinoa	Tang et al. (2015)
	Bolivian quinoa (BQ) Peruvian quinoa (PQ) Spanish quinoa (SQ)	Black Red White	Bolivia Peru Spain	Min: 4.87 ^{3} BQ, white Max: 6.48 ^{3} BQ, red	Pellegrini et al. (2018)
	$n = 29$ commercial varieties Blanca Kancolla Blanca Hualhuas Negra Collana Negra Pasankalla Pasankalla Roja Pasankalla Rosada de Huancayo Salcedo INIA	Black Red White	Peru Spain	Min: 6.00 ^{2} White quinoa Max: 6.80 ^{2} Black quinoa	Pereira et al. (2019)
	n. d.	Black Red White	China Peru	Min: 5.68 ^{2} Black quinoa Max: 6.19 ^{2} White quinoa	Shen et al. (2022)
Production area	n. d.	n. d.	Argentina	6.31 ^{2}	Nascimento et al. (2014)
	n. d.	n. d.	Egypt	6.79 ^{1}	El-Sohaimy and Mehany (2015)
	n. d.	n. d.	China	Min: 5.61 ^{1} Max: 5.68 ^{1}	Wu et al. (2020)

^{1}The results are expressed as %. ^{2}The results are expressed as g.100 g^{-1} of dry weight. ^{3}The results are expressed as g.100 g^{-1} of fresh weight. ^{a}The lipid content per variety averaged over the different years of field trials. Max, maximum value; Min, minimum value; n. d., not defined.

Argentina (Vidueiros et al., 2015) and a maximum value of 63% in variety "Temuko" cultivated in the USA (Chen et al., 2019). Quinoa oil also contains a relatively high volume of monounsaturated oleic acid (C18:1), reaching minimum values of 16% in commercial variety "Quinta Quinoa-BC12" (Tang et al., 2016) and maximum values of 33% in accession "CHEN 465" originating in the transition zone of Northwest Argentina (Vidueiros et al., 2015). Saturated palmitic acid (C16:0) was presented in 3.4–13% in genotype "QuF9P39-73" (Chen et al., 2019) and white quinoa genotype (Tang et al., 2016; Shen et al., 2022), respectively. A negative correlation was found between palmitic acid (C16:0) and oleic acid (C18:1), as reported by (Chen et al., 2019).

Less abundant fatty acid in quinoa lipid profile is an essential ω-3 α-linolenic acid (C18:3), which reaches 4–8% (Tang et al., 2016; De Bock et al., 2021a,b; Shen et al., 2022); yet (Vera et al., 2019) found values reaching 11% in yellow quinoa cultivar. Vidueiros et al. (2015) determined the range for α-linolenic acid as 3.2–9.4% for accessions "CHEN 465" and "CHEN 60", respectively. Quinoa oil also has several minor fatty acids, such as myristic acid (C14:0), stearic acid (C18:0), behenic acid (C22:0), gadoleic acid (C20:1), arachidonic acid (C20:4), and erucic acid (C22:1); however, those are presented only in negligible amounts (below 2%; Tang et al., 2015; De Bock et al., 2021b; Shen et al., 2022).

Several authors noticed variations in fatty acid profiles between varieties (Tang et al., 2016; De Bock et al., 2021b; Shen et al., 2022), but Prager et al. (2018) did not report any significant alterations between varieties or years. Toderich et al. (2020) indicated changes in fatty acid composition in genotype "Q5" grown in saline soils. While the majority of fatty acids declined in medium salinity, the content of palmitoleic acid (C16:1) and arachidic acid (C20:0) was slightly raised. Besides that, the high mixed salinity of sodium chloride and sodium sulfate resulted in a significant increment of stearic acid (C:18:0). The authors also concluded that sulfate salinity affects the fatty acid composition more than sodium chloride type of salinity.

TABLE 7 Variability of lipid composition in quinoa seeds divided according to the genotype and seed color.

	Genotype name	Seed color	SFA (relative %)	MUFA (relative %)	PUFA (relative %)	ω-6/ω-3 (relative %)	References
Genotype	Ecologicos Quinoa Mum's Original Heirloom Organic Quinoa Quinta Quinoa-BC12a Inca Gold Quinoa Vitabio Royal Quinoa Quinta Quinoa-BC12 Quinta Quinoa-BM12 Quinta Quinoa-Ch12 Quinta Quinoa-CVC12 GoGo Red Organic Quinoa Organic Garage Red Quinoa	Golden Red White	Min: ≈ 10 Ecologicos Quinoa Max: ≈ 12 Quinta Quinoa-BC12	Min: ≈ 20 Quinta Quinoa-BC12 Max: ≈ 33 GoGo Quinoa Red Organic Quinoa	Min: ≈ 52 Organic Garage Red Quinoa Max: ≈ 63 Quinta Quinoa-BC12	Min: 5.30 Quinta Quinoa-BM12 Max: 10.60 Mum's Original Heirloom Organic Quinoa	Tang et al. (2016)
	$n = 28$ accessions	n. d.	Min: 3.30 CO 407 WMF Max: 9.10 QuF9P39-65	Min: 14.40 NL-7 Max: 28.30 UDEC2	Min: 36.70 NL-7 Max: 62.80 Temuko	n. d.	Chen et al. (2019)
	Amarilla de Maranganí Blanca de Juli Negra Collana Roja Pasankalla	Black Red White	n. d.	Min: ≈ 21 Amarilla de Maranganí Max: ≈ 34 Roja Pasankalla	Min: ≈ 55 Roja Pasankalla Max: ≈ 63 Amarilla de Maranganí	Min:4.68 Amarilla de Maranganí Max: 19.59 Negra Collana	Vera et al. (2019)
	$n = 13$ accessions	Dark White	Min: 10.20 Summer Red, dark Max: 13.40 Titicaca	Min: 18.10 Puno Max: 25.10 Vikinga	Min: 61.40 Vikinga Max: 70.60 Puno	Min: 6.70 Bastille Max: 12 Summer Red, dark	De Bock et al. (2021b)[a]
	Atlas Jessie Marisma Pasto Pot_4 Roja	n. d.	Min: 9.77 Jessie Max: 11.29 Pot_4	Min: 19.67 Marisma Max: 22.67 Roja	Min: 66.64 Pot_4 Max: 70.40 Jessie	Min: 7.03 Jessie Max: 8.92 Pasto	Gomez et al. (2021)
Seed color	n. d.	Black Red White	Min: 10.52 Black quinoa Max: 11.09 Red quinoa	Min: 29.88 Black quinoa Max: 33.29 Red quinoa	Min: 54.23 Red quinoa Max: 58.34 Black quinoa	Min: 5.62 White quinoa Max: 6.35 Red quinoa	Tang et al. (2015)
	Bolivian quinoa (BQ) Peruvian quinoa (PQ) Spanish quinoa (SQ)	Black Red White	Min: 10.66 BQ, black Max: 11.44 BQ, red	Min: 29.07 BQ, black Max: 33.28 BQ, red	Min: 55.28 BQ, red Max: 60.27 BQ, black	Min: 6.51 BQ, white Max: 11.42 PQ, white	Pellegrini et al. (2018)

(Continued)

TABLE 7 (Continued)

Genotype name	Seed color	SFA (relative %)	MUFA (relative %)	PUFA (relative %)	ω-6/ω-3 (relative %)	References
Unknown (n=29) Blanca Kancolla Blanca Hualhuas Pasankalla Roja Pasankalla Rosada de Huancayo Salcedo INIA Negra Collana Negra Pasankalla	Black Red White	Min: 27 Black, white quinoa Max: 29 Red quinoa	40 Black, red, white quinoa	Min: 31 Red quinoa Max: 33 Black, white quinoa	n. d.	Pereira et al. (2019)
n. d.	Black Red White	Min: 14.48 Black quinoa Max: 18.87 White quinoa	Min: 25.76 Red quinoa Max: 27.76 White quinoa	Min: 52.53 White quinoa Max: 56.87 Black quinoa	n. d.	Shen et al. (2022)

[a] Fatty acid composition per variety averaged over the different years of field trials. Max, maximum value; Min, minimum value; n. d., not defined. MUFA, mono-unsaturated fatty acids; PUFA, poly-unsaturated fatty acids; SFA, saturated fatty acids.

Elevated temperature, together with cultivar-specific response, resulted in lower content of some fatty acids, especially oleic acid (C18:1), stearic acid (C18:0), gadoleic acid (C20:1), and behenic acid (C22:0) (Matías et al., 2021). In contrast, the content of linoleic acid (C18:2) increased or remained unaffected in hot conditions in some cultivars (Curti et al., 2020; Matías et al., 2021). In terms of major fatty acid content, genotype "Jessie" with the shortest life cycle performed better in hot conditions compared to other genotypes. A very important role in quinoa oil quality is also played by optimal fertilization since correlations between some minerals and fatty acid content were observed by Matías et al. (2021).

Based on the available scientific literature, black genotypes tend to have higher polyunsaturated fatty acid (PUFA) content as opposed to red or white seed genotypes (Tang et al., 2015; Pellegrini et al., 2018; Pereira et al., 2019; Shen et al., 2022). Moreover, the highest monounsaturated fatty acid (MUFA) and saturated fatty acid (SFA) content were present in red genotypes (Tang et al., 2015; Pellegrini et al., 2018; Pereira et al., 2019; Vera et al., 2019), in contrast to Shen et al. (2022) who obtained opposed outcomes (Table 7). Nonetheless, as discussed in previous paragraphs, the content of fatty acids is strongly affected by genotype x environment interactions.

The overall nutritional quality of oils is characterized by the ω-6/ω-3 ratio, with an ideal composition of 1–4/1 in the human diet, as recommended by Simopoulos (2002). Nevertheless, the ω-6/ω-3 ratio of quinoa did not meet the required values since it ranged from 4.7% in variety "Amarilla de Maranganí" up to nearly 20% in variety "Negra Collana" produced in Peru (Vera et al., 2019; Table 7). Despite that, the fatty acid proportion and related nutritional quality are better than in amaranth with values reaching 33–69% (Tang et al., 2016; Paucar-Menacho et al., 2018).

Vitamin and minerals

Quinoa seeds generally contain a sufficient amount of minerals, such as Ca, Fe, Mg, Na, P, K, and Zn (Granado-Rodriguez et al., 2021a,b). As indicated by several authors, quinoa seeds have an even higher content of many minerals than common cereals (Martin et al., 2014; Nascimento et al., 2014; Mhada et al., 2020; Hussain et al., 2021). The content of minerals fluctuates due to genotype, soil type, year, and fertilization (Miranda et al., 2013; Prado et al., 2014; Pellegrini et al., 2018; Granado-Rodriguez et al., 2021a; Bock et al., 2022).

According to Granado-Rodriguez et al. (2021b), the content of P, Ca, and Fe remained unmodified between varieties, as opposed to K, Mg, and Na. Almost equivalent conclusions were defined by Matías et al. (2021), reporting significant fluctuations between cultivars in K and Mg contents, but also in P content, which conflicts with the previous study. Furthermore, Granado-Rodriguez et al. (2021a) stated that the content of Mg, Fe, and

Zn was not strongly modified by cultivar x year interactions. Reguera et al. (2018) noticed changes only in Zn between diverse locations, but not within cultivars, whereas De Bock et al. (2021b) recorded no variations in P and Ca content over the years but among the varieties. In addition, no difference between varieties was observed in P, Mg, and Fe concentrations; however, a higher accumulation of P was specific in dark-colored varieties. Higher content of P positively influenced the content of linoleic acid (C18:2) and negatively affected several MUFAs (Matías et al., 2021), which may explain, to some extent, why black seeded varieties contain higher PUFA content than red or white genotypes, as seen in Table 5. Strong correlations were also determined in P and protein content (Granado-Rodriguez et al., 2021b; Matias et al., 2022).

Significant contrasts in mineral concentration between cultivars were also analyzed between hot and cool years, which were probably caused due to little-understood heat-induced adaptation mechanisms and/or interactions among nutrients (Matías et al., 2021). Similar results were also confirmed by Tovar et al. (2020), who highlighted the relationship between heat exposure and specific stages of panicle development. Reguera et al. (2018) investigated aberrations in mineral content between varieties and the agro-ecological conditions they were grown in. According to their findings, the largest accumulation of Mg and Fe in seeds was characteristic of genotypes cultivated in Chile (Río Hurtado). Also, "Regalona" stored a larger amount of almost all analyzed minerals when cultivated in Chile, whereas "Salcedo-INIA" had a larger amount of Mg, Fe, Ca, and Zn when cultivated in Peru (Arequipa). In contrast to that, "Regalona", cultivated in Chile was characterized as the genotype with the lowest mineral content (Martin et al., 2014).

Genotypes "Pasto", "Dutchess", "Atlas", and "Summer Red" cultivated in Belgium had the highest amount of minerals, in contrast to the other studied genotypes in the experiment of De Bock et al. (2021b). Granado-Rodriguez et al. (2021b) also identified "Pasto", together with "Marisma", as genotypes with significantly higher mineral content. On the other hand, Matías et al. (2021) determined "Jessie" as the genotype with the highest mineral content. All genotypes in both studies were cultivated in Spain. In terms of adaptability to adverse conditions, Toderich et al. (2020) referred to the genotype "Q5" as suitable for saline environments since there was a remarkable increment of Fe, Zn, and Ca content under salinity. Mineral concentration varied under contrasting irrigation treatments, except for Mn concentration, which was not significantly different (Walters et al., 2016). The authors also estimated that heterogeneity in concentrations might occur due to the dilution effect.

Although there is not enough current data on overall vitamin content in quinoa, it was concluded in previous studies that quinoa has a satisfactory concentration of thiamine (B1), riboflavin (B2), niacin (B3), pyridoxine (B6), folic acid, and vitamins A, C, and E (Koziol, 1992; Ruales and Nair, 1992). Vitamin E is a general term for tocopherols (α-, β-, γ-, and δ-) and tocotrienols (α-, β-, γ-, and δ-), also named vitamin E homologs. According to Fischer et al. (2013), vitamin E content in quinoa seeds was ranging between 1.04–1.28 mg.100g^{-1}, and overall content was not altered by escalated moisture deficit in genotypes "Regalona", "B080", and "AG2010". Tang et al. (2016) found significant variations in overall vitamin E content and the composition of vitamin E homologs. The most abundant vitamin E homolog in quinoa was γ-tocopherol followed by α-tocopherol, and δ-tocopherol, which is in accordance with the results of Pereira et al. (2019) and Granda et al. (2018). No tocotrienols were detected in any of mentioned studies. Pereira et al. (2019) also determined higher content of γ- and β-tocopherols in the black genotype, but higher α-tocopherol content in the red genotype.

Miranda et al. (2013) uncovered significant alterations in vitamin B content caused by distinct environmental conditions in two studied localities with the highest concentration of B vitamins in the arid locality Vicuña in Chile. Granda et al. (2018) also observed diverse content of vitamin B. While the content of B2 and B6 was relatively similar among varieties, diverse values were determined for B1. The highest concentration of B1 was found in non-pigmented varieties "Tunkahuan" and "Titicaca". Increased content of B2 appeared in colored varieties and the highest content of B6 was identified in pigmented variety "Pasankalla". The vitamin C content also shows some changes between distinctive locations with the highest content (49.30 mg 100.g^{-1} dw) in genotype "Villarrica" cultivated in location Temuco with a cold temperate climate (Miranda et al., 2013).

Summary

This overview provides a summary focused on current research of different quinoa genetic resources in diverse growing conditions. Quinoa is considered a highly nutritive crop that is also resistant to drought and salt suitable for marginal regions. According to our findings, the different environmental condition can have a strong impact on the nutritive compounds of quinoa seeds. Further, the adaptation of quinoa to adverse conditions has limitations in the case of elevated temperatures, high salinity levels, or a combination of weather extremes – heavy rainfall followed by temperatures over 30°C – together with cultivar-response may negatively affect growth and productivity which can result in changed content of nutritive compounds. However, an insight into the enormous variability of nutritive components possessed by quinoa germplasm cultivated in the different conditions of the world shows us how important it is to conserve and protect this richness, and to select outstanding accessions suitable to different conditions. It gives us the potential and hope to develop new varieties of quinoa adapted to different environments and production systems.

Author contributions

DJ and PC: conceptualization. PC and LD: resources and writing–original draft preparation. DJ, MJ, PC, and IV: writing–review and editing. DJ: supervision. DJ, PC, IV: funding acquisition. All authors contributed to the article and approved the submitted version.

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Conflict of interest

The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

Publisher's note

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