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REVIEW ARTICLE

Quinoa microbiota and its importance for sustainable crop production

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Abstract

Quinoa is a crop that can contribute to food security under current climate scenarios. The crop is noted for its unique nutritional properties and adaptability to stressful environmental conditions. Its introduction to new regions is focused on organic crop production technologies, which stimulates research using microbiological approaches. The microbiota of quinoa is not well understood; however, studies of microorganisms associated with quinoa indicate their diversity. Symbiotic microbiota can be useful for improving the adaptive potential of new varieties, reducing susceptibility to pests and diseases, and ensuring sustainable production. The possibilities of practical use of symbiotic relationships of the quinoa with many species of bacteria and fungi remain poorly studied.

Keywords: Quinoa, Microbiota, Rhizosphere, Environment, Agrocenosis

Introduction

Quinoa is a crop with a specific range and nature of microorganisms relationships. The wide representation of the Chenopodium genus in most zones (where quinoa is introduced) implies the formation of new algorithms for the species interactions with microorganisms, primarily in the rhizosphere. The results of this interaction (based on the economic characteristics of quinoa) can be characterized as neutral, beneficial or harmful. Some microorganisms species negatively affect plants through infection or competition. Other species, including PGPB bacteria and mycorrhizal fungi, stimulate plant growth, relieve stress, facilitate nutrient mobilization and increase yield. Microbial biodiversity affects the productivity and stability of quinoa agrocenoses, so its management is important for agricultural production and environment (Mącik et al., 2020).

Literature Review

Some aspects of the quinoa microbiota

Chenopodium quinoa Willd. (quinoa) is considered as a crop that can provide sustainable food supplies in near future (Jaikishun et al., 2019; Maliro, 2021). Crop has the potential to contribute to food security under current climate scenarios (Ruiz et al., 2014; Angeli et al., 2020). This characteristic is connected with outstanding nutritional properties of seeds (Guo et al., 2021; Pathan & Siddiqui, 2022) and its tolerance to environmental stressors (Choukr-Allah et al., 2016; Hinojosa et al., 2018; Nolen, 2023). High concentration of various vitamins and minerals in seeds as well as absence of gluten makes quinoa beneficial for people with lactose intolerance, anemia, and celiac disease (Navruz-Varl & Sanlier, 2016; Lutz et al., 2017). The crop is highly genetically diverse with a large number of varieties and genotypes, which has contributed to its expansion to 120 countries over the past decade (Alandia et al., 2020; Cepková et al., 2022). Quinoa is actively introduced on the European continent. In Ukraine, two varieties have been registered in recent years - Quartet and Komyza (originator: Sumy National Agrarian University). A feature of its distribution in most cases is the orientation to organic production technologies (Jacobsen & Christiansen., 2016; Trotsenko, 2023). This stimulated the expansion of crop research, including the use of microbiological approaches (Hussin et al., 2017; Paco-Pérez & Guzmán-Vega, 2019; Rafique et al., 2022; Zahoor et al., 2022).

The isolation of the basic species of quinoa from the natural environment and the subsequent stages of crop formation took place in the specific conditions of Andes. Thus, the natural microbiota communities and their evolution could be represented by the native (aboriginal) microflora, the species composition of which were determined by the tendency of quinoa to monoculture on soils that are not suitable for other crop growing. The natural microbiota of quinoa associated with the area formation (and current distribution) is poorly understood. However, the identification and study of microorganisms associated with quinoa indicates their extraordinary diversity (Ortuño et al., 2021). First of all, these are groups of bacteria used various substrates produced by the plant: *Azotobacter sp., Azospirillum sp., Klebsiella sp., Bacillus sp., Pseudomonas sp., Rhizobium sp* (Castillo et al., 2022; Testen et al., 2022; Nolen, 2023). The microorganisms were isolated from different organs of the quinoa plant: seeds, leaves, roots and rhizosphere. Bacteria were represented by the genera of *Bacillus, Agrobacterium, Rhizobium, Pseudomonas.* Micromycetes of *Trichoderma. harzianum, T. afroharzianum, T. pseudoharzianum* were found. Ecological groups of bacteria are represented by species of non-symbiotic nitrogen fixers, phosphorus solubilizers, phytohormones producers (Karimi et al., 2020; Mahdi et al., 2020; Maestro-Gaitán et al., 2023). According to many researchers, the existing symbiotic biota can be useful for improving the adaptive potential of new varieties, reducing their susceptibility to pests and diseases. (Ortuño et al., 2021).The use of microorganisms can be an ideal substitute for pesticides, which pollute the environment and reduce biodiversity.

Microbiota and quinoa tolerance to environmental stressors

Abiotic stresses affecting modern agrocenoses – drought, waterlogging, soil salinity, heavy metal pollution, low temperatures – are studied on quinoa genotypes, most of which are concentrated in Bolivia and Peru (Paco-Pérez et al., 2019; Ortuño et al., 2021). Quinoa is unique crop for its adaptability and resistance to extreme conditions (Hinojosa et al., 2018; Maliro et. al., 2021). Quinoa can tolerate drought, soil salinity and low temperatures (Adolf et al., 2013; Jacobsen & Christiansen, 2016). The rhizosphere microbiota and its influence on crop tolerance to environmental stressors is studied by many scientists (González-Teuber et al., 2018; Cai et al. 2021). Microorganisms can increase plant resistance to abiotic stresses such as drought, salinity, nutrient deficiencies. Currently, bacterial species have been identified among such genera as *Azospirillum, Pseudomonas, Klebsiella, Azotobacter, Alcaligenes, Enterobacter, Arthrobacter, Bacillus, Serratia, Paenibacillus,* which improve drought tolerance in various plants, by providing osmotic adjustment, antioxidant activity, regulating hormonal levels and increasing nutrient uptake. The use of bacterial inoculants of these species is an alternative strategy for maintaining food security under drought conditions (Kour et al., 2020; Mącik et al., 2020; Riaz et al., 2021).

The rhizosphere microbiota with different sensitivity to water stress was analyzed. Native quinoa rhizobacteria have been identified with promising potential for drought stress reducing: representatives of *Bacillaceae*, *Thermomicrobiales* and *Frankiales*. Species of *Bacillus, Pseudomonas*, and *Serratia* genera are able to promote quinoa growth under water stress. *Serratia* species can survive in a variety of environmental conditions and compete with other microorganisms for plant colonization. *Serratia plymuthica* is an antagonist of pathogens and improves water stress tolerance (Nordstedt & Jones, 2021). Genotype, moisture conditions and root exudates had the greatest impact on the structure of quinoa microbiota (De Vries et al., 2020).

The fungal-root associations of quinoa contribute to the plant ability to tolerate drought conditions as well. The rhizosphere of quinoa harbors a diverse group of endophytic fungi, including *Penicillium (Penicillium minioluteum), Phoma, and Fusarium.* Fungal colonization improves quinoa productivity and its ability to withstand prolonged periods of drought (González-Teuber et al., 2018). Studying the characteristics of endophytic fungi, as well as bacterial endophytes in crop seeds revealed that colonization by microbial symbionts reduces the adverse effects of abiotic stresses and promotes plants to tolerate stressful environmental changes. These microorganisms have great potential for the development of biotechnology adapted to quinoa (Chumpitaz-Segovia et al., 2020; Kelbessa et al., 2023).

A separate research approach is the study of halotolerant rhizobacteria as a factor in improving the quinoa resistance to salinity stress. Halotolerant bacteria (*Enterobacter sp. and Bacillus sp.*), mineral-stimulating plant growth, have been used to reduce the effects of salt stress, due to their ability to fix nitrogen, produce siderophores, solubilize phosphates, and produce phytohormones (Mahdi et al., 2020; Yanez-Yazlle et al., 2021).

Low temperature is a stress factor that adversely affects plant physiology and biochemistry and the activity of soil microbial communities. The adaptive properties of psychrotolerant bacterial species are of great interest from the biotechnological point of view for the production of microbial inoculants. Psychrotolerant species have been reported to be used as biofertilizers due to their ability to stimulate plant growth. Psychrotolerant strains of *Pseudomonas* genus) were isolated from the quinoa rhizosphere of the Andean plateau. These strains exhibit different capacities to stimulate plant growth at low temperatures, with *P. silensiensis* and *P. plecoglossicida* being the most active species (Chumpitaz-Segovia et al., 2020). This indicates the potential for strains to be used as inoculants to improve quinoa development in regions where low temperature is a limiting factor for agricultural production.

Microorganisms as a solubilizers

Minerals are important for plant growth and development. However, their solubility is rather low. Microorganisms make minerals available to plants through solubilization owing to organic acids secretion (Maharana & Dhal, 2022). Species of bacteria-solubilizers such as *Achromobacter, Bacillus, Corynebacterium, Erwinia, Flavobacterium, Micrococcus, Paenibacillus, Pseudomonas, Sarcina, Serratia, Xanthomonas* were isolated from the rhizosphere (Divjot et al., 2021). These bacteria produce as well secondary metabolites, phytohormones and siderophores, which increase plant productivity. The *Bacillus* genus is the best-studied group with mechanisms that make them suitable for developing viable and stable bioproducts. (Mahdi et al., 2020; Rafique et al., 2022; Maestro-Gaitán et al., 2023). Phosphate-solubilizing bacteria of *Bacillus megaterium* and *Pseudomonas fluorescens* produce phosphatases and organic acids that solubilize organic and inorganic phosphorus (Mahdi et al., 2020). Among endophytic natural bacterial strains isolated from quinoa and analyzed for their ability to solubilize phosphate, some were selected as the most effective ones: *Paenibacillus polymyxa, Bacillus. simplex, B. мegaterium.* The species of *Bacillus altitudinis., Pontibacter lucknowensis, Pseudomonas furukawaii* and *Pseudomonas flexibilis* showed strong ability to solubilize phosphate, zinc and manganese, improved quinoa growth properties and physiological characteristics (Rafique et al., 2022; Trotsenko et al., 2024). Such promising bioinoculants could address the problem of mineral deficiency in plants, especially quinoa. This study invites researchers to evaluate these selected strains to explore their genetic and molecular mechanisms of mineral solubilisation and plant growth promotion under nutrient deficiency conditions.

Microbial fertilisers are alternative to chemicals. They consist of effective microbial strains that are components of the rhizosphere. Biofertilisers promote the absorption of mineral elements, stimulate plant growth, improve crop quality and increase plant resistance to stressors. Biofertilisers are a key component of integrated management that ensures the sustainability of agroecosystems. (Mącik et al., 2020; Kour et al., 2020). In practical terms, this direction is considered as inoculation of seeds with industrial strains of microorganisms. It is noted that inoculation with bacteria of *Bacillus* and *Pseudomonas* genus *i*mproves the germination quinoa seeds, increases laboratory germination, improves germination of seeds with a reduced level of viability (Trotsenko, 2023). Soil microorganisms can adapt to plants and can potentially be used for crop production without negative environmental impact.

Conclusions

Quinoa is a promising crop based on organic crop production technologies, which in turn involves the active use of biological mechanisms to increase its productivity. The most relevant areas of biologisation are the use of symbiotic relationships to increase the level of adaptability, quantity and quality of the crop. Despite its long history, modern quinoa crop has virtually no technologies using biological products. The possibilities of practical use of the identified symbiotic relationships of quinoa with many species of bacteria and fungi remain poorly understood. Future research should focus on the genetic basis and mechanisms involved in the study of the relationship between quinoa resistance to abiotic stress and plant chemical composition. This additional information will allow breeders to develop new varieties that are widely adapted to different environmental conditions and, in turn, will contribute to the global spread of quinoa.

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