CHAPTER: 1.5

QUINOA GENETIC RESOURCES AND *EX SITU* CONSERVATION

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Abstract

Quinoa (*Chenopodium quinoa* Willd.) is a potentially strategic crop that plays a vital role in food security and sovereignty. It makes an important contribution to the staple needs of the population and is part of the ancestral and cultural heritage of Andean countries. Its wide varietal diversity constitutes an extraordinarily valuable gene pool: wide range of colours of plant, inflorescence and seed; varying crop cycle duration; high nutrient and agro-industrial value; and high saponin content of grains. Thanks to its extraordinary genetic diversity, the crop is very adaptable to different agro-ecological conditions (soils, rainfall, temperature and altitude) and is tolerant to frost, drought and salinity. Worldwide, 16 422 accessions of quinoa and its wild relatives (*C. quinoa, C. album, C. berlandieri, C. hircinum, C. petiolare, C. murale* and *Chenopodium* sp.) are conserved in 59 genebanks distributed in 30 countries. Genebanks in the Andean region conserve more than 88% of the crop's accessions. Despite this immense diversity, it is not currently used to the full. The grain and processed products available on market are derived from a small set of landraces, which means that the genetic potential is underutilized. In general, countries do not have clear policies on the *ex situ* conservation of quinoa germplasm collections. Within countries with the greatest diversity, genebanks are poorly linked; and between different countries, the links are even worse.

Each genebank operates according to the goals of the institution, often reflecting individual interests of researchers rather than a strategy planned to complement the national programme. This chapter

reviews collections of quinoa germplasm in different countries, particularly in the Andean region, the distribution of its genetic variability and a description of the infrastructure and facilities used for its conservation. Information is also provided on characterization and evaluation, procedures for regeneration and multiplication and the documentation systems adopted. Lastly, the links between *in situ* and *ex situ* conservation are discussed.

Introduction

Over the past four decades, the number of *ex situ* germplasm collections has notably increased as a result of the worldwide effort to conserve PGRFA (plant genetic resources for food and agriculture) resources. These collections are maintained under very different conditions, depending on national or international policies, institutional environment, available expertise, facilities and budgets, and on the level of national and international cooperation (Engels and Visser, 2003). According to the Second Report on the State of PGRFA (FAO, 2010), the total quantity of samples stored ex situ throughout the world has increased by approximately 20% (1.4 million) since 1996, amounting to 7.4 million accessions stored in 1 750 genebanks. This increase in the number of accessions and diversity means that the highest international conservation standards must be adopted to handle the collections.

Setting up a genebank is no guarantee that a country's plant genetic resources will be conserved, or that the collections will be handled in accordance with proper conservation standards. These issues were highlighted in the first and the second report on the state of world's PGRFA (FAO, 1996; FAO, 2010). Genebanks are essential for the food security and sovereignty of a nation. They are part of a country's ancestral and cultural heritage are the responsibility of government and of society as a whole. Conservation therefore requires institutional support – the sustained provision of financial resources and availability of specialized staff with the equipment necessary to maintain germplasm collections and carry out conservation activities.

According to Engels and Visser (2003), increasing attention is being devoted to the regeneration of germplasm from a collection, given the possibility of genetic erosion over time when a bank is not properly managed. The maintenance and regeneration of collections thus involve rising costs. The economic management of a genebank involves the allocation of budgets to specific operations on the basis of an internal consensus regarding the costs involved and the genebank strategy.

The management of genebanks has often developed without proper planning. Furthermore, local germplasm management conditions vary enormously, resulting in a range of different management approaches and experiences. This is the case despite international efforts to standardize the management of genebanks, particularly for seed collections (FAO/IPGRI, 1994; Engel and Visser, 2003; Rao *et al*., 2007; FAO, 2013).

Quinoa genebanks and collections in the world

Quinoa seed has been classified as behaving in an "orthodox" manner (Ellis *et al.*, 1988). In other words, its viability can be maintained in a predictable manner within a controlled range of environmental conditions by reducing the seed temperature and moisture content (Ellis and Roberts, 1980). Ex situ conservation of quinoa is carried out in genebanks that use these seed properties to achieve the maximum storage time with minimum physiological activity and minimum loss of viability. Genebanks represent an efficient solution with a low cost-benefit ratio for quinoa seed conservation. A large quantity of seed samples may be stored in a relatively small space (Leon-Lobos *et al.*, 2010). Genebank management includes a series of stages and procedures that require staff trained in seed processing and regular checking of seed viability (FAO, 2013).

The FAO Second Report on the State of the World's PGRFA states that at international level there are 16 263 accessions of the genus *Chenopodium* (FAO, 2010), including quinoa (*Chenopodium quinoa* Willd.), qañiwa, qañawa or qañawi (*C. pallidicaule Aellen*), paico orepazote (*C. ambrosoides* L.) and other wild relatives of quinoa.

On the basis of recently updated information on *ex situ* collections of quinoa and its wild relatives, carried out with the support of FAO, Bioversity International and experts working with quinoa collections, it is estimated that the number of accessions of *Chenopodium quinoa* (see chapter 1.1), *C. album,*

Figure 1. Countries that conserve quinoa germplasm collections

C. berlandieri, C. hircinum, C. petiolare, C. murale and *Chenopodium* sp. conserved worldwide is 16 422 (Annex 1).

Thirty countries throughout the world conserve quinoa and its wild relatives in 59 genebanks (Figure 1). These are: 10 countries in the Americas (Argentina, Bolivia, Brazil, Canada, Colombia, Chile, Ecuador, the United States of America, Peru and Uruguay), 11 in Europe (Germany, Austria, Slovakia, Spain, Hungary, the Czech Republic, Portugal, the United Kingdom, Sweden, Turkey and Romania), 5 in Africa (Ethiopia, Kenya, Lesotho, Zambia and South Africa) and 3 in Asia (India, Japan and Jordan) and Australia (Annex 1).

Among the Andean countries, Bolivia and Peru are those that retain the greatest diversity, followed by Ecuador, Argentina and Chile. Among the remaining 25 countries in the world, Germany has 987 accessions, India 294, the United States of America 229 and Japan 191 accessions of quinoa and its wild relatives (Figure 2 and Annex 1).

Genebanks have been implemented in the Andean region since the mid-twentieth century. Management and conservation are preside over by agricultural institutions and universities, for example in Argentina, Bolivia, Colombia, Chile, Ecuador and Peru. Of the 16 422 accessions conserved worldwide, 14 502 (88%) are conserved in genebanks within the Andean region.

In **Bolivia** six genebanks conserve 6 721 quinoa accessions (Figure 3 and Annex 1). They are located in the *Centro Toralapa* (Toralapa Centre) run by INIAF (*Instituto Nacional de Innovación Agropecuaria y Forestal* – National Institute of Agricultural and Forestry Innovation), in the *Estación Experimental Choquenaira* (Choquenaira Experimental Station) run by UMSA (*Universidad Mayor de San Andrés* – Major University of San Andrés), in the *Centro de Investigaciónen Biotecnología y Recursos Fitogenéticos* (Biotechnology and Plant Genetic Resource Research Centre) run by UTO (*Universidad Técnica de Oruro* – Oruro Technical University), in the *Unidad Académica Tiahuanacu* (Tiahuanacu Educational Unit) run by UCB (Universidad Católica Boliviana – Bolivian Catholic University), in the *Centro Experimental Kallutaca* (Kallutaca Experimental Centre) run by UPEA (Universidad Pública de El Alto – El Alto Public University), and in the *Centro de Investigación y Promoción Comunal* (Municipal Research and Promotion Centre – CIPROCOM). The quinoa germplasm with the highest number of accessions managed by INIAF with 3 178 accessions is the National Quinoa Germplasm Collection; it is followed by the UTO and UMSA collections which have, respectively, 1 780 and 1 370 accessions (FAO WIEWS, 2013).

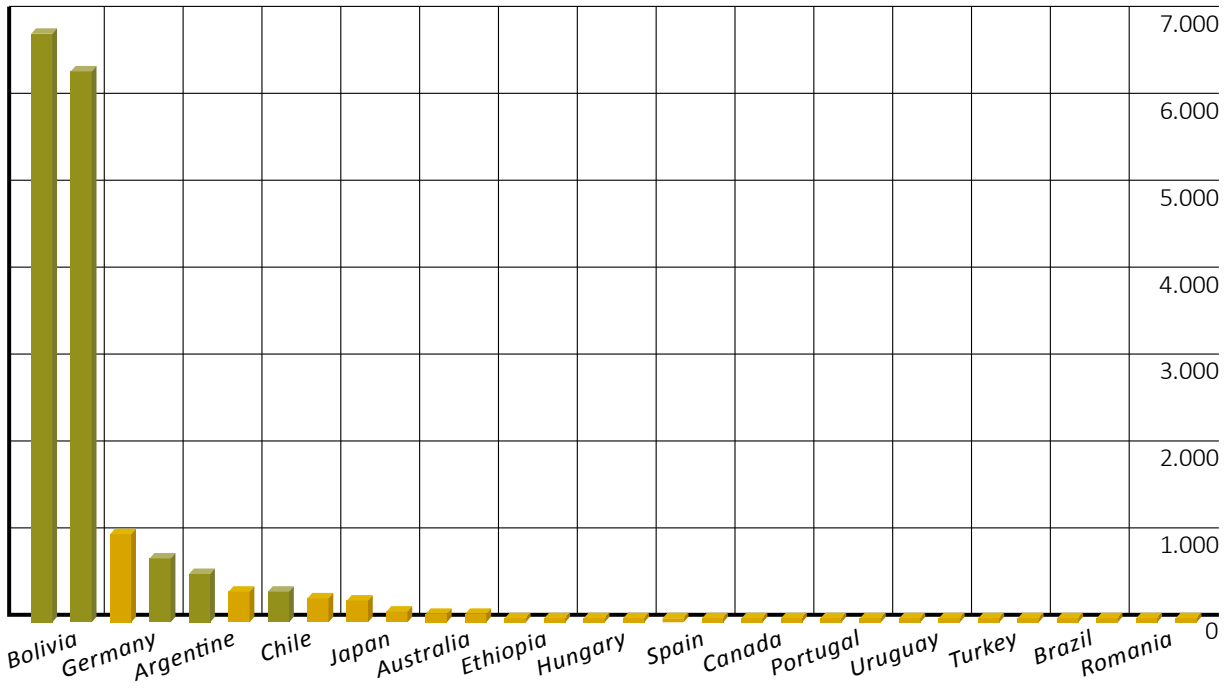

Figure 2. Number of quinoa accessions preserved throughout the world

In **Peru**, eight genebanks conserve 6 302 quinoa accessions (Annex 1). The genebanks are located in experimental stations run by INIA (*Instituto Nacional de Investigación Agropecuaria* - National Institute of Agricultural Research) in Illpa (Puno), Andenes (Cusco), Canaán (Ayacucho), Santa Ana (Huancayo) and Baños del Inca (Cajamarca), and in the *Universidad Agraria La Molina* (La Molina Agricultural University) of Lima, the *Universidad Nacional de San Antonio Abad* (San Antonio Abad National University) of Cusco and the *Universidad Nacional del Altiplano* (National University of the *Altiplano*) of Puno (Mujica, 1992; Bonifacio *et al*., 2004; Bravo and Catacora, 2010; Gómez and Eguiluz, 2011). The collections with the highest number of accessions are the *Universidad Nacional Agraria La Molina*, the *Universidad Nacional del Altiplano* and INIA in Puno with 2 089, 1 910 and 1 029 accessions, respectively (FAO WIEWS, 2013).

In **Argentina**, the national genebank conservation network holds a total of 492 quinoa accessions (Annex 1) conserved in the base genebank run by INTA (*Instituto Nacional de Investigaciones Agropecuaria* - National Institute of Agricultural Research) and partly duplicated in the active genebank of Northwest Argentina and the genebank of *Consulta* (Argentina MNII - *Mecanismo Nacional de Intercambio de Información* [National Information Exchange Mechanism], 2013; FAO WIEWS, 2013). This collection is the outcome of joint efforts by the Agricultural Faculty of UBA (*Universidad de Buenos Aires* - University of Buenos Aires) and INTA.

In **Ecuador**, 673 quinoa accessions are conserved by the National Department of Plant Genetic Resources and Biotechnology in the *Estación Experimental de Santa Catalina* (Santa Catalina experimental station) run by INIAP (*Instituto Nacional de Investigaciones Agropecuarias* - National Institute of Agricultural Research) (Ecuador MNII, 2013; FAO WIEWS, 2013; Peralta, 2006).

In **Colombia** the genebank run by the *Corporación Colombiana de Investigación Agropecuaria* (Colombian Agricultural Research Corporation) in Tibaitatá conserves 28 accessions (FAO WIEWS, 2013).

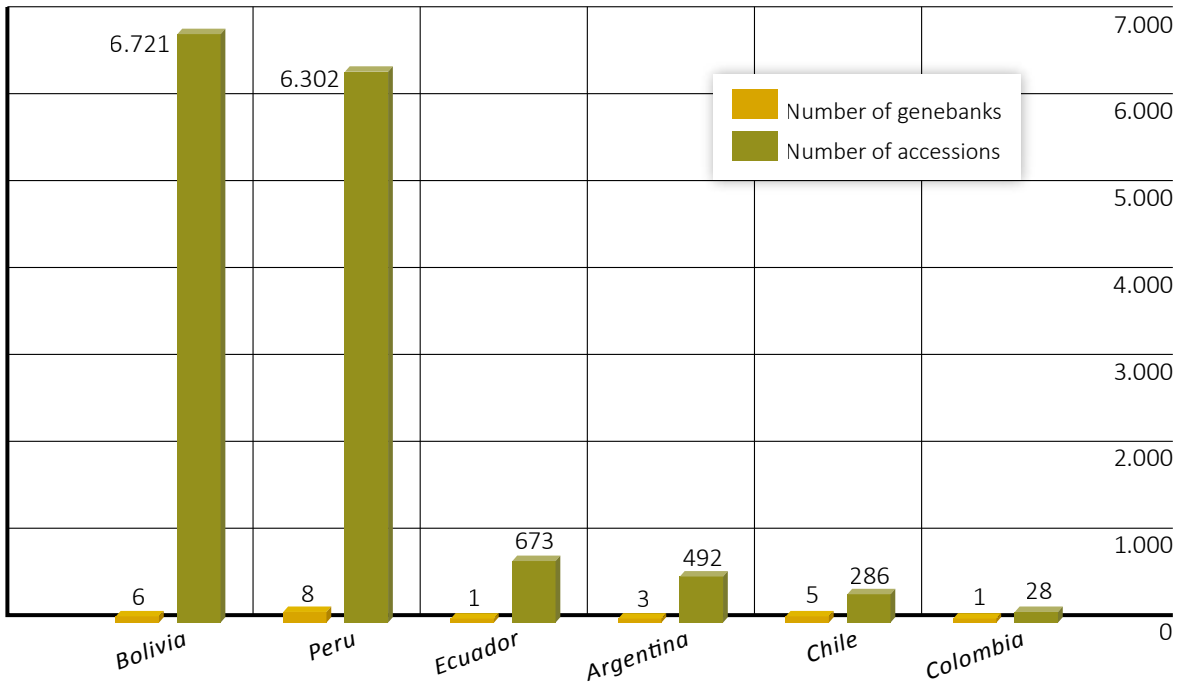

Figura 3. Number of accessions and genebanks conserving quinoa germplasm in countries of the Andean region

Of the 286 accessions conserved in **Chile** (Annex 1), 203 are stored in the base genebank of the *Centro Experimental Vicuña* - INIA (*Instituto de Investigaciones Agropecuarias* - Agricultural Research Institute), and the rest in the genebank of the Faculty of Agricultural Sciences of UACH (*Universidad Austral de Chile* - University of Southern Chile), in the active genebank of the *Centro Regional de Investigación Carillanca* (Carillanca Regional Research Centre) - INIA, in UNAP (*Universidad Arturo Prat* - Arturo Prat University), and in the Baer genebank (Barriga *et al*., 1994; Salazar *et al*., 2006; Madrid *et al*., 2011; Chile MNII, 2013; FAO WIEWS, 2013). Figure 4 indicates the geographical location of the 26 genebanks in South America that store quinoa. Twenty-four of these banks belong to countries in the Andean region.

Distribution of the geographical origin of quinoa collections conserved *ex situ*

It is essential to have access to proper information on quinoa distribution, because it is considered a potential and staple resource for national and global food security. By analysing the (available) passport information held by the banks, it is possible to establish an approximate representation of crop distribution and determine the areas of influence of each one, establishing where more in-depth action is required.

According to studies carried out with the **Bolivia** national collection (Rojas, 2002; Rojas *et al*., 2010), the geographical origin of the collection is distributed from 15°42'S (Omasuyos province, department of La Paz) to 21°57'S (M. Omiste province, department of Potosí), and from 64°19'W (Tomina province, department of Chuquisa to 69° 09' W (Manco Kapac province, department of La Paz). It is found at altitudes of and 2 400–4 200 m asl. (Figure 5).

The national quinoa collection in Bolivia houses a large number of accessions. A total of 3 178 are currently conserved, including cultivated and wild accessions collected between 1965 and 2008 in Altiplano communities and Inter-Andean valleys in the country in the departments of La Paz, Oruro, Potosí, Cochabamba, Chuquisaca and Tarija. The collection also includes germplasm from Peru, Ecuador, Colombia, Argentina, Chile, Mexico, the United States of America, Denmark, the Netherlands and the

Figure 4. Geographical location of the 26 genebanks in South America that store quinoa. Twenty-four of these banks belong to countries in the Andean region.

Figure 5. Distribution of quinoa germplasm conserved in INIAF, Bolivia

United Kingdom (Rojas *et al.*, 2010a; Rojas *et al.*, 2009).

Figure 5 shows that most accessions collected in Bolivia come from the Altiplano region, mainly in areas adjacent to the road that leads from Lake Titicaca, La Paz, Oruro, Challapata and Uyuni, in the case of the southern Altiplano, and also in the areas of Salinas de Garci Mendoza, Daniel Campos and Lipez. In the Inter-Andean valley region there is, on the other hand, a greater concentration of accessions from Cochabamba, Chuquisaca and Potosí than from Tarija.

In **Peru**, examination of the quinoa accessions stored in the seed collections of the *Universidad Nacional Agraria La Molina* and the *Universidad Nacional del Altiplano*, reveals that the distribution is mainly focused in the Inter-Andean valleys and mountains. Quinoa accessions have been collected from the Inter-Andean valleys at 2 200–3 500 m asl, mainly in the departments of Cajamarca, Ancash, Junín, Ayacucho, Huancavelica, Arequipa, Apurímac and Cusco. In the mountains, the accessions come from altitudes of 3 600–4 050 m asl, from the departments of Huancavelica, Arequipa, Apurímac, Cusco and Puno.

Of the 2 089 accessions held in the UNALM quinoa collection, 69.78% are from the department of Puno, 13.19% from the department of Cusco, 7.19% from the department of Apurímac and 6.28% from the department of Ancash. The four departments account for more than 96% of the total number of accessions stored in the university (Figure 6).

In **Chile**, quinoa accessions stored in the Intihuasi CRI (INIA Regional Centre) base genebank come from three main areas in the country (Figure 7). In the north, accessions are from the municipality of Colchane in the region of Tarapacá, and from the provinces of Elqui and Limarí in the region of Coquimbo. In the centre, accessions are mainly from the coast of the Libertador General Bernardo O'Higgins region. In the south, accessions are from the regions of Araucanía and Los Lagos (Madrid, 2011).

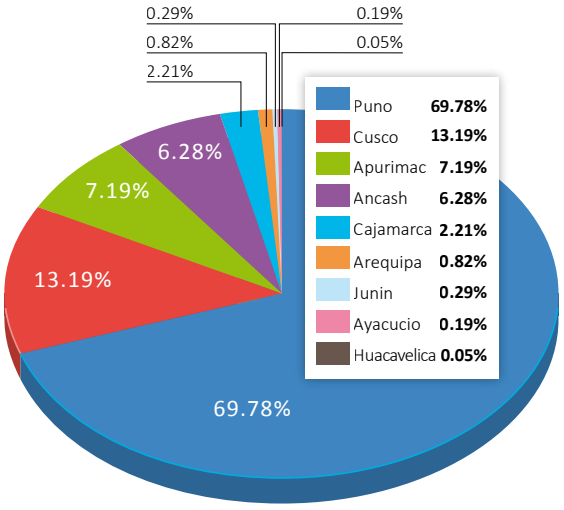

Figure 6. Distribution of quinoa germplasm stored in the *Universidad Nacional Agraria La Molina* of Peru by department.

Figure 7. Distribution of quinoa accessions stored in the Intihuasi base genebank run by INIA, Chile (according to Madrid, 2011)

Characteristics of conservation infrastructure

The storage room equipment is vital for preventing the rapid decline of quinoa seed viability and a reduction in germination percentage. The location and characteristics of the storage facilities where accessions are conserved in Bolivia, Peru and Chile are described below.

In **Bolivia** the national collection of Andean grains is located in the Toralapa experimental station run by INIAF (17°31'S, 65°41'W; 3 430 m asl), 73 km from the city of Cochabamba, on the old road to Santa Cruz.

This genebank has a storage room, a laboratory and a sample conditioning room. The storage room measures 72 m², its walls are made of brick and windowless, they are fully lined with expanded polystyrene and the floor is ceramic. The average temperature in the storage room is 15°C and the humidity is 40%. A dehumidifier system is used to remove moisture from the room.

The conditioning room measures 20 m². Here, seeds are prepared for laboratory analysis and their size is checked. In the adjacent laboratory, which measures 16 m², the biological quality of seeds is analysed (germination, plant health, moisture content etc.) before the accession is placed in storage.

Due to the climatic characteristics of the genebank location and the conditions of the storage room, it is only possible to carry out short- and medium-term conservation under natural conditions.

This type of storage has been used since the beginning of the Bolivian quinoa collection. Plastic storage containers, 0.4–2 mm thick, with a double lid and 1 000 g capacity, are used. These containers are able to withstand temperatures of 8–20°C and relative humidity of 15–60%. They are well designed for short- to medium-term storage (IPGRI, 1996). Under these conditions, accessions may be stored and conserved for approximately 20 years, depending on the genetic material (Figure 8).

In order to implement long-term quinoa conservation in Bolivia, research began in 2002 to test the use of silica gel and Borax for drying seeds, but the results failed to achieve the moisture levels as

Figure 8. Storage room and laboratory for the processing and germination of seeds in the Andean grains genebank run by INIAF in Bolivia

recommended in the Genebank Standards (FAO/IPGRI, 1994). This was mainly due to the nature of the small-scale prototypes that were built for this purpose (Rojas and Camargo, 2002).

In the subsequent year of research, it became possible to establish a protocol for implementation of long-term storage (Rojas and Camargo, 2003), in accordance with international standards (FAO/IPGRI, 1994), and long-term conservation began with 247 quinoa accessions comprising the "core collection" (Rojas, 2010).

This work represents the first experience of long-term conservation with Bolivian quinoa germplasm. The samples are 5 g per accession and the seed moisture content is 3–7%. These samples vacuum-packed and hermetically sealed in aluminium pouches and conserved at 20°C. After 5 years of storage (2008), the first monitoring operation was carried out on long-term stored seed. The results were encouraging, because the germination percentage remained stable at 90–98% (an improvement on initial germination percentages).

In **Peru** the main genebanks storing quinoa contain areas and/or rooms prepared for conservation but without cooling equipment. The areas are generally kept closed; temperature and humidity are low, as is typical of the climatic conditions in places located at > 3 000 m asl. This means that the genetic material can be conserved naturally for long periods.

In the *Universidad Nacional Agraria La Molina* (La Molina National Agricultural University), the genebank is situated in two locations: one in San Lorenzo in the department of Junín, at 3 200 m asl (under natural conditions typical of the locality); and the other on the La Molina campus, where two cold chambers are available with a capacity of 19 m³ with dehumidifiers and temperature gauges. In this case, the accessions are stored at temperatures of 4–5°C and 60–70% relative humidity.

The genebank of the *Universidad Nacional del Altiplano de Puno* (Puno Altiplano National University) is located in the Camacani Research and Production Centre in Platería – Puno (15°56'41"S, 69°51'30"W; 3 824 m asl). The genebank run by INIA (Puno) is located in the Illpa Experimental Station (15°40'55''S, 70°04'29''W; 3 815 m asl) (Bravo *et al*., 2010).

The Puno INIA genebank offers short- and medium-term storage for the quinoa collection at room temperature (Bravo *et al*., 2010). On the UNALM campus, on the other hand, storage is short term in both cool chambers and naturally cooled areas, because the collections are active and continually added to and assessed. Plastic or glass containers are used to store the seeds in both banks.

In **Chile**, the quinoa collections are stored in four banks. The base genebank of the Vicuña Experimental Centre (INIA) is located in the region of Coquimbo. This contains a 330-m² storage chamber under controlled conditions that operates at – 18°C and

20% balanced relative humidity, and uses sealed containers. It has the capacity to store 50 000 seed samples. The Carillanca CRI active genebank (INIA – *Instituto de Investigaciones Agropecuarias* [Agricultural Research Institute]) is located in Temuco (region of Araucanía). It contains a storage chamber that operates at -5°C and 40–45% relative humidity, and uses sealed containers (Salazar *et al*., 2006; León-Lobos *et al*., 2012; Madrid *et al*., 2011).

The *Universidad Arturo Prat* genebank is located in Iquique (region of Tarapacá), where the seeds are stored at 4°C. The Baer genebank is located in *Fundo 'El Hualle'* ('El Hualle' estate) (region of Araucanía). The seeds are stored in a dark environment and at room temperature and humidity; this form of storage does not allow the seeds to be kept in a good condition for subsequent germination (Salazar *et al*., 2006; Madrid *et al*., 2011).

Progress in the characterization and evaluation of quinoa

Characterization and evaluation are employed to describe the qualitative and quantitative characteristics of accessions. On the basis of these characteristics, it is possible to differentiate and discriminate between accessions, determine their potential utility, build core collections and identify duplicates in the collection. The characteristics, combined with passport data, constitute essential information for each accession. On this basis, it is possible to establish regional, national and international databases, networks and platforms to share the information.

In **Bolivia**, the national quinoa germplasm collection has been in existence for over 40 years. During this time, characterization and evaluation have focused, in particular, on agromorphological analysis. In 1985, the first catalogue of quinoa conserved in the genebank was published by the Patacamaya Experimental Station (Espindola and Saravia, 1985). The second edition, which was published in 2001 (Rojas *et al*., 2001), described the genetic variability of 2 701 quinoa accessions through 59 qualitative and quantitative variables. Although the information was recorded on the basis of a "Quinoa descriptors", published in 1981 by IBPGR (now Bioversity International). The catalogue reports information on many more variables which have been identified in various papers published since the 1980s.

A new "Quinoa descriptors" was subsequently proposed, validated by researchers from Ecuador, Peru and Bolivia (Rojas *et al*., 2003). The document was revised by more than 50 experts from 40 organizations in 10 countries, and served as a basis for publishing an updated list of "Descriptors for quinoa and wild relatives" (Bioversity International *et al*., 2013). It should be emphasized that the wild relatives of quinoa were included in this revised version.

In 2001, work started on evaluating the nutritional value and agro-industrial variables. Information was recorded on 555 quinoa accessions with the aim of increasing their use in the production of quinoa-based processed products. Work was also carried out on the molecular characterization of most quinoa accessions (Veramendi *et al*., 2013). The most notable results are set out below, grouped on the basis of certain parameters and according to the number of accessions evaluated (Bioversity International *et al*., 2013; Rojas and Pinto, 2013).

Agromorphological variables

The morphological and agricultural variability of quinoa germplasm observed phenotypically during the crop cycle was studied in Bolivia. The parameters of some variables of interest are given below (Rojas, 2003; Rojas *et al*., 2009; Rojas and Pinto, 2013; Bioversity International *et al*., 2013).

Growth habit. Although branching and growth habit are influenced by sowing density, four different growth habits could be identified in the quinoa collection (Figure 9).

The architecture of quinoa plants is very variable – at both varietal and intrapopulation level. This hinders the adaptation and/or design of harvest mechanization prototypes and makes other cultivation work very labour-intensive. For this reason, it is important to work and select varieties taking into account the growth habit. For example "habit 1" (corresponding to plants that do not develop branches) and "habit 2" (with branches to the bottom third) could be very well suited to mechanized harvesting. "Habit 3" generally corresponds to plants of the Inter-Andean valleys, whose plant architecture makes them a possible alternative for use as forage while their genes could contribute to crop expansion areas in valleys and places with higher rainfall (Rojas and Pinto, 2013).

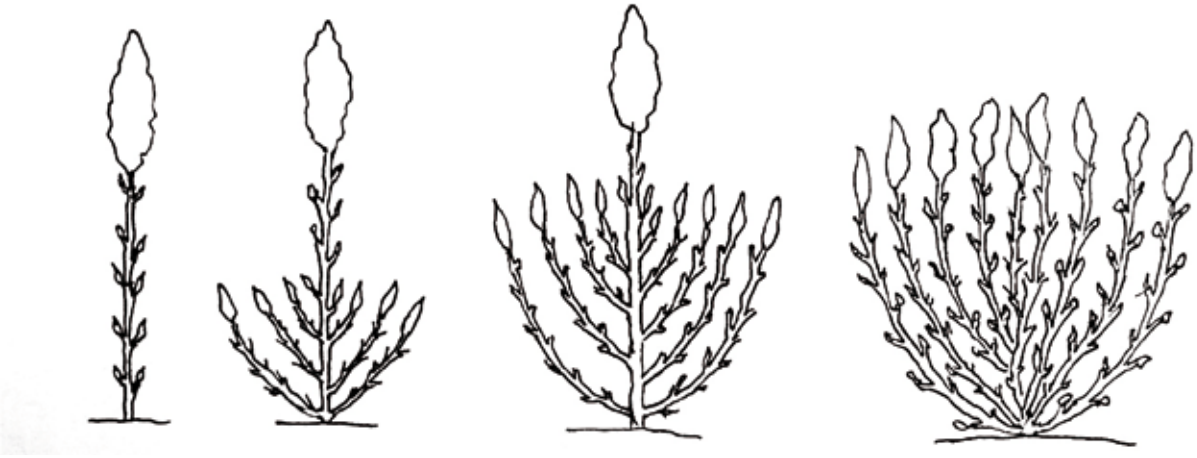

Figura 9. Quinoa growth habits: 1 Simple, 2 Branched to bottom third, 3 Branched to second third and 4 Branched with main panicle undefined (Rojas and Pinto, 2013; Bioversity International *et al*., 2013)

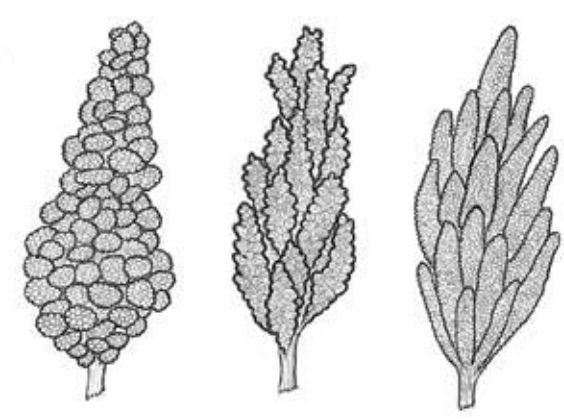

Figure 10. 1 Glomerulate, 2 Intermediate and 3 Amarantiform (Rojas and Pinto, 2013; Bioversity International et al., 2013)

Figure 11. Panicle shapes: amarantiform (left) and glomerulate (right)

Plant colour. Between the stages of "panicle emergence" and "start of flowering", four colours are expressed that are typical of the quinoa crop: green, purple, mixture and red. As the grain forms and physiological maturity is reached, the quinoa plants nevertheless display different colours and colour combinations: white, cream, yellow, orange, pink, red, purple, coffee, grey, black, mixtures and wild green.

Panicle shape and density. Three panicle shapes are observed: "amarantiform", when the glomerules are inserted directly in the secondary axis and have an elongated shape; "glomerulate", when the glomerules are inserted in the glomerulate axes and are globose in shape; and "intermediate", when the panicles express both amarantiform and glomerulate traits (Rojas and Pinto, 2013). The panicle may also be lax (loose) or compact – a characteristic determined by the length of the secondary axes and pedicels. It is compact when both are short (Figure 10).

Grain colour and shape. When quinoa grains reach physiological maturity, they display a wide range of colours, including: white, cream, yellow, orange, pink, red, purple, light coffee, dark coffee, greenish coffee and black. A total of 66 grain colours have been characterized in the Bolivian national quinoa collection (Cayoja, 1996).

There are four quinoa grain shapes (Figure 12). The cylindrical and lenticular shapes (determined by the appearance of the endosperm) of these grains

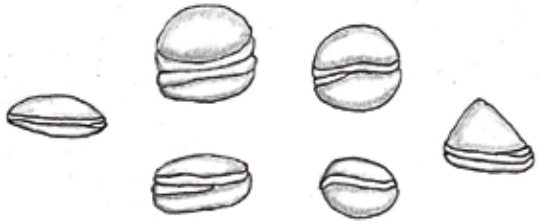

Figure 12. Quinoa grain shapes (from left to right) : 1 lenticular, 2 cylindrical, 3 ellipsoid and 4 conical (Rojas and Pinto, 2013; Bioversity International *et al*., 2013)

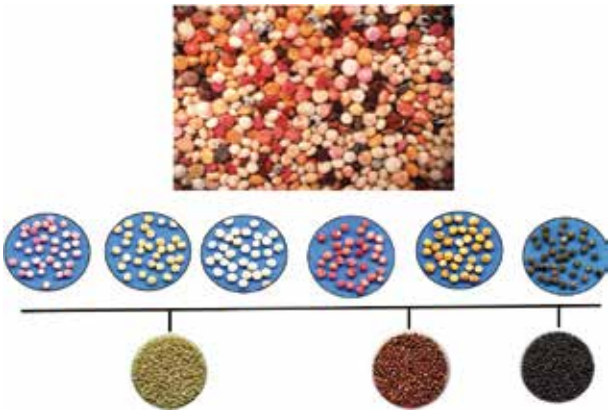

Figure 13. Diversity of quinoa grain shapes, sizes and colours compared with the three commercial colours

means that they can be satisfactorily used to make products that, due to their amylose and amylopectin content, can easily be used to produce custards, puddings and instant sauces. Similarly, depending on the starch grain size, they can also be used for the production of popped or puffed grains (Rojas and Pinto, 2013).

Figure 13 shows a wide diversity of quinoa grain shapes, sizes and colours. When the product is purchased in markets and fairs, however, consumers differentiate between three colours: white quinoa, coffee-coloured quinoa (known on the international market as "red quinoa") and black quinoa.

Quinoa grains are characterized by a particular feature: after desaponification, they assume three commercial colours. Mixtures of quinoa varieties are consumed and there is indirect underutilization of the crop's genetic potential. Quinoa consumption in both Andean countries and export countries corresponds to the raw material; farmers and companies normally mix a set of varieties in order to satisfy market demand in terms of volume.

Grain diameter. Grain diameter ranges from 1.36 to 2.66 mm; there is sufficient variability to imply it could be exploited through genetic improvement (Rojas, 2003). Small-grained quinoa varieties come mainly from the northern Altiplano and the Inter-Andean valleys, the large-grained accessions mainly originate in the Intersalare areas of Uyuni and Coipasa, corresponding to the southern Altiplano in Bolivia.

According to IBNORCA (2007), the quinoa grain may be classified into four categories according to its diameter: "extra large" (> 2.20 mm); "large" (1.75–2.20 mm); "medium" (1.35–1.75 mm); and "small" (< 1.35 mm). The "extra large" category includes 'Quinoa Real', whose main characteristic is the large size of its grains, making it very desirable on the international market. 'Quinoa Real' originates in Bolivia.

Its quality and reputation are exclusively due to the geographical environment in which it is produced, including the natural and human factors typical of the southern Altiplano (Rojas and Pinto, 2013).

Crop cycle. Some accessions reach physiological maturity within 119 days, while others take up to 220 days to mature (Table 1). This characteristic depends on the genotype. Quinoas of the Inter-Andean valleys are later than those of the Altiplano. The wide range of variation in the crop cycle is encouraging in terms of adapting the crop to variable weather conditions and climate change.

Grain yield per plant. Yields as high as 250 g per plant have been recorded. This variable also depends on the genotype and variables believed to contribute to yield, such as stem diameter, plant height, panicle length and diameter, and grain diameter.

Variables of nutritional and agro-industrial value

A summary of statistical parameters estimated for each characteristic of the nutritional and agro-industrial value of quinoa is given in Table 2. These are expressed on a dry basis (Rojas and Pinto, 2006; Rojas *et al*., 2007; Rojas and Pinto, 2008). The ac-

Table 1. Statistical parameters of central trend and dispersion for quantitative characteristics of Bolivian quinoa germplasm

Component	Minimum	Maximum	Mean	SD
Flower bud (days)	38	95	51.72	5.66
50% flowering (days)	60	145	93,5	12.04
Physiological maturity (days)	119	209	176.89	19.79
Harvest index	0.06	0.87	0.4	0.12
Stem diameter (mm)	10.16	26.26	17.12	2.66
Panicle length (cm)	15.4	62.8	37.41	8.09
Panicle diameter (cm)	2.86	19.42	6.85	1.66
Plant height (cm)	54	174.2	110,84	17.51
Grain diameter (mm)	1.36	2.66	1.96	0.23
100-g weight (g)	0.12	0.6	0.27	0.08
Saponin content (cc)	0	10.88	3.16	3.02

SD = Standard deviation; Source: Rojas (2003)

cessions show wide variability for most characteristics studied, which is a sign of the genetic potential of the quinoa germplasm.

The amount of protein ranges from 10.21% to 18.39% (Table 2). These values are wider than the range of 11.6–14.96% reported by Morón (1999), quoted by Jacobsen and Sherwood (2002). Although the quantity of protein is a basic aspect, the quality is specific and depends on the essential amino acid content. The quality of quinoa protein is higher than that of protein in cereals.

Figure 14 shows the distribution of protein content variation frequencies in part of the Bolivian quinoa collection. It can be seen that in most quinoa accessions, the protein content ranges from 12% to 16.9%, while in a small group of accessions (42), the content fluctuates between 17% and 18.9%. This latter group constitutes an important source of genes for promoting the development of products with high protein content.

In these accessions, the fat content ranges from 2.05% to 10.88% and averages 6.39% (Table 2). The upper range of these results is higher than the range of 1.8–9.3% described by βo (1991) and Morón (1999), quoted by Jacobsen and Sherwood (2002), who reported that the fat content of quinoa

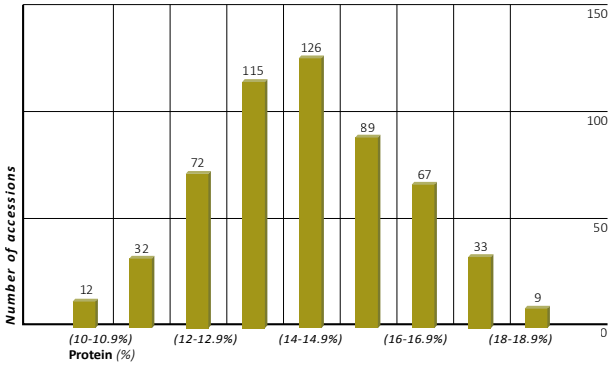

Figure 14. Variation in the protein content of 555 quinoa accessions

is high value due to the high percentage of unsaturated fatty acids. It is hoped that these quinoa values will be useful for obtaining fine vegetable oils for culinary and cosmetic use.

Genetic variation in starch granule size ranges from 1 to 28 µ. This variable makes it possible to provide agro-industrial guidelines for producing different mixtures with cereals and legumes in order to establish the functional character of quinoa. The starch granule needs to be small to facilitate the texturizing process. When the starch granule is small, it is easier to insufflate, as the spaces between the

Table 2. Characteristics of nutritional and agro-industrial value and simple statistics for Bolivian quinoa **germplasm** (n = 555 accessions)

Component	Minimum	Maximum	Mean	SD
Protein (%)	10.21	18.39	14.33	1.69
Fat (%)	2.05	10.88	6.46	1.05
Fibre (%)	3.46	9.68	7.01	1.19
Ash (%)	2.12	5.21	3.63	0.50
Carbohydrates (%)	52.31	72.98	58.96	3.40
Energy (kcal/100 g)	312.92	401.27	353.36	13.11
Starch grain (µ)*	1	28	4.47	3.25
Invert sugar (%)*	10	35	16.89	3.69
Fused water (%)*	16	66	28.92	7.34

Standard deviation; analysis performed by LAYSAA (Laboratorio de Análisis y Servicios de Asesoramiento en Alimentos Test Laboratory and Food Advisory Services), Cochabamba, Bolivia; *(n = 266) Source: Rojas and Pinto (2013)

granules allow for larger quantities of air to be introduced and exchanged, permitting a higher generation of air bubbles (Rojas *et al*., 2007).

The content of inverted sugars ranges from 10% to 35%. This variable expresses the quantity of sugar that initiates fermentation by unfolding or inversion; in other words, it can be used to determine the quality of carbohydrates. This parameter also permits quinoa to be classified as a food product appropriate for diabetics. The optimum percentage of inverted sugar is ≥ 25%. The accessions analysed comply with this requirement and can be used in mixtures with flour to produce bread, cereals etc. (provided all the external saponin is removed from the grain).

The variable "percentage of fused water" ranges from 16% to 66%. It measures the capacity of the starch to absorb water when making pasta, bread and other baked goods. The ideal value for this parameter for industrial application is ≥ 50%. In view of this characteristic, quinoa germplasm also constitutes an important source of genes for developing this product type.

Allowing for the concept of "genetic diversity" in the production of processed products will ensure that the genetic potential of quinoa is used in an appropriate manner. It is possible to select and obtain: varieties with higher protein percentages (≥ 18%) suitable for more attractive products; varieties with small starch granule diameters (≤ 3 µ) ideal for excellent, homogeneous popped/puffed grains; and varieties with stable percentages of amylase and amylopectin for the production of custard desserts, jellies, instant sauces and noodles. This immense range of ways to enjoy and use quinoa goes hand in hand with the conservation and use of genetic diversity.

Molecular characterization

In the Bolivian collection, between 2004 and 2008, it was possible to characterize 86% (2 701 accessions) of the germplasm, allowing the genetic fingerprinting of each quinoa accession. The information generated can therefore be used to group and differentiate accessions which are similar at molecular level. Seventeen microsatellite primers and ISSR markers were used for the typing. The polymorphic information content (PIC) for the quinoa collection showed values of between 0.73 and 0.95 with an average of 0.84; all the markers were found to be highly polymorphic (Veramendi *et al*., 2013). The microsatellites, QAAT074, QAAT076 and QAAT022, were found to be the most polymorphic and their values were higher than those reported by Mason *et al*. (2005) and Maughan *et al*. (2004).

In **Peru**, the 2 089 accessions in the *Universidad Nacional Agraria La Molina* were characterized

and evaluated, using the IBPGR quinoa descriptors (1981). The groups of characteristics are described below:

Morphological variables

Table 3 shows the most significant morphological characteristics recorded in the UNALM quinoa collection, which allows all morphological characteristics of variants to be identified. The plant tissue colour chart prepared by the Royal Horticultural Society of the United Kingdom was used to record the colours. In the grain, colours were evaluated in the quinoa pericarp (fruit-coat) and episperm (seed-coat).

The variables evaluated include: flowering, corresponding to the number of days from seedling emergence from the soil to 50% of plants with the first flower; maturation, corresponding to the number of days from seedling emergence until 50% of plants have dry stems and hard pasty grains; plant height, measured from the soil surface to the apex of mature inflorescences and expressed in centimetres.

The evaluation generally showed a predominance of earlier, shorter accessions from the Altiplano (Puno) and a greater predominance of later, taller accessions in other representative locations of the Inter-Andean valleys (Gómez and Eguiluz, 2011). When accessions were grouped by geographical origin (Table 4), no clear pattern of differentiation was identified between locations, considering the descriptors of plant height and days to flowering and maturation. This could be the result of the exchange of accessions between experimental stations and farmers.

The scale proposed by Solveig and Ames (2000) was used to evaluate the reaction of the germplasm to mildew, which is the most important disease of quinoa, caused by the fungus *Peronospora variabilis*. Table 5 shows an overview of the reactions of accessions to mildew under conditions in Valle de Mantaro – Junín, considered an area with a high incidence of the disease. This collection did not show total or qualitative resistance to the fungus. A selection was therefore carried out for partial or

Table 3. Variation in the morphological characteristics of the quinoa collection held by *Universidad Nacional Agraria La Molina (UNALM)*

Morphological characteristics	Peru (UNALM) ***
Leaf colour before flowering	Green, purple, mixture, red
Colour of leaf axils	Green, purple, red, pink
Colour of stem striae	Yellow, green, purple, pink, red
Colour of inflorescence at physiological maturity	Greenish-yellow, yellow, yellow-orange, orange, orange-red, red, red-purple, purple, purple-violet, violet, violet-blue, white, grey-white, yellow-white, white-orange, grey-yellow, grey-orange, grey-red, grey-purple, grey-green, grey-brown, brown, grey, black
Shape of inflorescence	Amarantiform, glomerulate and intermediate
Density of inflorescence	Compact, intermediate, lax
Colour of pericarp - seeds (fruit-coat)	yellow, yellow-orange, orange, orange-red, red, red-purple, white, white-yellow, white-orange, grey-yellow, grey-orange, grey-red, grey-purple, grey-green, grey- brown, brown, grey, black
Colour of episperm-seeds (seed-coat)	yellow, yellow-orange, orange, red-purple, purple, white, white-yellow, white-orange, white-grey, grey-yellow, grey-orange, grey-purple, brown, black

Source: Gómez and Eguiluz (2011)

Table 4. Range of variation in the agronomic characteristics of plant height, days to flowering and grain maturation in the *Universidad Nacional Agraria La Molina* (UNALM) quinoa collection.

Locations	N° of accessions	Height (cm)	Flowering (days)	Maturation (days)
Ancash	131	90 – 240	70 - 115	170 - 215
Apurímac	140	125 – 240	58 -110	170 - 210
Arequipa	17	64 – 140	85 - 115	170 - 220
Ayacucho	4	89 – 126	60 - 65	160 - 180
Cajamarca	46	77 – 165	55 - 110	150 - 215
Cusco	275	52 – 176	50 - 115	140 - 200
Junín- Huancavelica	6	75 – 141	68 - 80	160 - 190
Puno 2	1434	36 – 185	50 - 98	115 -185
Puno 1	138	75 – 205	46 - 80	130 - 175

Source: Gómez and Eguiluz (2011)

Table 5. Range of variation in response to the presence of mildew (Peronospora variabilis) for 2 089 quinoa accessions under conditions in the Valle del Mantaro - Junín, Peru.

Departments	Number of accessions evaluated	Range of variation (%)	Number of accessions evaluated with partial resistance
Puno	1466	10 - 100	74
Cajamarca	39	40 - 90	0
Arequipa	17	80 – 90	0
Ancash	131	20 - 90	14
Junín	6	30 - 60	1
Huancavelica	1	30	1
Ayacucho	4	40- 60	0
Apurimac	150	20 - 90	18
Cusco	275	30 - 90	12
Total	2089	10 - 100	120

Source: Gómez and Eguiluz (2011) *Grain quality variables.*

quantitative resistance, which made it possible to identify some accessions worth including in the improvement programme based on percentage severity and reproductive development of the pathogen.

Of the 2 089 accessions from the UNALM germplasm collection, 953 were characterized according to grain size, protein and saponin content.

For the grain size, the accessions were graded on the basis of grain size using meshes containing perforations with diameters of 1.4 mm (small grains), 1.7 mm (medium-sized grains) and 2.2 mm (large grains).

The procedure used to evaluate saponin was developed on the basis of a proposal by Koziol (1990), modified by Balsamo (2002). Koziol (1990) established 0.11% (wet basis) as the threshold for the detection of bitterness caused by saponins in quinoa. Quinoa accessions containing less saponin may therefore be considered sweet (0.7 cm foam height), while very bitter quinoas exceed a foam height of 6.6 cm – the equivalent of 1.69% (dry basis) of saponin.

Table 6 shows the information generated on these three descriptors associated with quality. The quinoas were grouped into sweet (0) and bitter (1)

on the basis of their saponin content (Gómez and Eguiluz, 2011).

The *Universidad Nacional del Altiplano* in Puno has characterized 1 029 accessions using eight phenotypic descriptors (stem colour, days to flowering, type of inflorescence, inflorescence colour and length, plant height, biomass and grain yield). Based on these characteristics, a "core collection" was built up comprising 103 accessions containing native ecotypes and varieties representing a large proportion of variation in the germplasm collection (Ortiz *et al*., 1988).

The Puno INIA characterized 536 quinoa accessions (68%) by applying the descriptors of plant colour, type of inflorescence, frost damage and grain yield. The results show that the plant colour (green, pink and purple) was observed in 149 accessions. The predominant inflorescence type is glomerulate with 380 accessions, 21 of which amarantiform and 135 intermediate. A total of 91 frost-tolerant accessions were identified. Grain yield varies widely (Bravo *et al*., 2010).

In **Chile**, there is currently an agronomic characterization for 28 accessions from the UNAP collection, using 11 morphological and productivity descriptors, (Fuentes and Bhargava, 2011). This characterization was carried out at low altitude, in the Canchines Experimental Station run by UNAP (20°26.562'S, 69°32.197'W; 1 005 m asl), near Iquique. The quinoa collection of the INIA base genebank, on the other hand, was regenerated and characterized in 2013 and the information is currently being processed (P. León-Lobos, unpublished data).

This involved evaluation of the genetic diversity of the 28 UNAP accessions plus 31 accessions from low altitude areas from different genebanks, using microsatellite markers (Fuentes *et al*., 2009). This study succeeded in detecting 150 alleles among the quinoa accessions evaluated, with an average of 7.5 alleles per locus. Based on an analysis of the main components, it was possible to separate the accessions into two separate groups: one containing accessions from the Chilean Altiplano (Salare ecotype); the other containing accessions from low altitude coastal areas (Coastal ecotype).

Procedures for regenerating and multiplying accessions

In general, even though the seeds are stored under optimum conditions, there is a decline over time in terms of quantity (due to use and distribution) and germination rate. According to Jaramillo and Baena (2000), aim of achieving an optimum seed sample size is known as "multiplication", while the aim of restoring viability is known as "regeneration or rejuvenation". This routine procedure is part of the process of managing a genebank: when accessions

Table 6. Occurrence of seeds germinated from INIAF quinoa accessions, Bolivia.

Locations	**Nº of accessions**	**Size** (diameter mm)	**Protein** (%)	**Saponin** (0=sweet 1= bitter)
Apurímac	145	1.2-1.7	10.3 -16.7	0 -1
Ayacucho	3	1.4	13.1-13.9	1
Cajamarca	12	1.4 -1.7	13.2-14.9	0 -1
Ancash	127	1.2 -2.2	10.3-16.5	0 -1
Cusco	133	1.4 -1.7	13.3 -18.6	0 -1
Junín	3	1.4	14.1-14.3	0 -1
Puno 1	138	1.4-1.7	7-24.4	0 -1
Puno 2 Bitter	220	1.4 -2.2	7.9 -23.7	1
Puno 2 Sweet	172	1.4 -1.7	7.1 - 23.2	0

fall below a threshold of quality (FAO, 2013) and quantity, they must be regenerated and multiplied.

In the INIAF collection in **Bolivia**, prior to regeneration, monitoring is carried out by means of germination tests to establish the seed germination rate, following the procedures established by ISTA (1993). The latest seed germination tests were carried out from 2010 to 2012 and involved 2 675 accessions. The aim was to monitor the behaviour of quinoa accessions and plan the germplasm regeneration on the basis of the results. In 2010, 200 accessions were analysed: for 31% of accessions, the germination rates were ≤ 80; for 69% the germination rates exceeded 80% (Table 7).

During 2011 and 2012, 2 475 accessions were analysed, and it was observed that the germination rates were ≤ 80 for 70.11% (in 2011) and 79.40% (in 2012) of the accessions; the germination rates were > 80% in 20.89% (2011) and 20.60% (2012) of accessions (Table 7). These results were used to plan the regeneration process, taking into account also the areas of origin of the accessions. As far as the seed quantity is concerned, it has been calculated that 60 g of quinoa is the minimum quantity that can be used as a parameter for the multiplication operation (Rojas and Bonifacio, 2001).

In the UNALM genebank in **Peru**, seed generation is carried out every 4–5 years. This period was calculated taking into account the effect of storage conditions on the viability of quinoa, which very easily loses its viability as a result of the climatic conditions under which it is stored.

The accessions are multiplied on the La Molina campus (located in mountainous conditions at

Table 7. Occurrence of seeds germinated from INIAF quinoa accessions, Bolivia.

		Seeds germinated					
Year	**Country**	**≤ 80 (%)**		**> 80 (%)**		**Total**	
		Accessions	**%**	**Accessions**	**%**	**Accessions**	**%**
2010	04 Bolivia	62	31.00	138	69.00	200	100.00
2011	02 Ecuador	5	62.50	3	37.50	8	100.00
	03 Peru	192	55.81	152	44.19	344	100.00
	04 Bolivia	617	75.89	196	24.11	813	100.00
	05 Chile	9	60.00	6	40.00	15	100.00
	06 Argentina	9	90.00	1	10.00	10	100.00
	07 Mexico	1	50.00	1	50.00	2	100.00
	11 No data	18	78.26	5	21.74	23	100.00
	Unidentified	3	100.00	0	0.00	3	100.00
	Total	**854**	**70.11**	**364**	**29.89**	**1218**	**100.00**
2012	02 Ecuador	8	61.54	5	38.46	13	100.00
	03 Peru	85	76.58	26	23.42	111	100.00
	04 Bolivia	891	79.84	225	20.16	1116	100.00
	05 Chile	1	100.00	0	0.00	1	100.00
	07 Mexico	1	50.00	1	50.00	2	100.00
	08 No data	2	100.00	0	0.00	2	100.00
	09 No datao	1	50.00	1	50.00	2	100.00
	10 No data	2	100.00	0	0.00	2	100.00
	Unidentified	7	87.50	1	12.50	8	100.00
	Total	**998**	**79.40**	**259**	**20.60**	**1257**	**100.00**
Total		**1914**	**71.55**	**761**	**28.45**	**2675**	**100.00**

3 200 m asl) in small groups to facilitate isolation. The main aims of multiplication are: to increase seed quantity for subsequent adaptation and yield studies in different locations; and to proceed further with quality studies, sometimes including destructive tests.

Care is taken to avoid genetic and physical contamination of accessions. Sowing for regeneration and/or multiplication is carried out in small, manageable groups that are interspersed with accessions of amaranth, corn, oats or rye; when necessary, the seeds are cultivated in complete isolation.

Documentation systems applied in the management of quinoa germplasm

The process of recording, organizing and analysing conservation data is known as documentation. It is essential for identifying the germplasm and making decisions with regards to its management. The value of the germplasm increases as more is known about it – hence the importance of ensuring it is well documented (Jaramillo and Baena, 2000).

The likelihood of accessions being used increases in direct proportion to the availability of information describing their characteristics and genetic potential. An accession cannot be identified as such if no information is available. For this reason, it is important to document the information in a systematic manner, including the maximum amount of possible detail.

In the INIAF quinoa collection in **Bolivia**, germplasm information is documented using one manual system and one electronic system. The data sets in which the quinoa germplasm information is organized are as follows: a) passport and collection data; b) characterization and evaluation data; and c) management data.

The electronic system is organized in different databases. In the pcGRIN system, provided by IPGRI (Hoogendijk and Franco, 1999), 2 701 quinoa accessions are documented with the following information: passport data, personnel data, geographical data, taxonomic data and characterization and evaluation data (Rojas and Quispe, 2001).

The information is organized using Microsoft Excel into double-entry tables; the database is interactive with an information flow structure, supported by pivot tables and menus for quick reference. Descriptive statistics of inventory, passport and viability data are generated, making it possible to make practical decisions (Figure 15).

Lastly, progress has been made with the DBGermo system, developed by INTA in Argentina. It organizes information on passport, characterization and evaluation data for the INIAF quinoa germplasm collection.

In **Peru**, the quinoa germplasm collection held by the *Universidad Nacional Agraria La Molina* has set up a database based on the quinoa passport and descriptive data published by IBPGR (1981). The program NTSYS Spc2.1 (Numerical Taxonomy System) is applied for the statistical analysis of information.

In **Chile**, institutions managing genebanks and working collections record the information manually and using computers (through the use of electronic aids such as Excel spreadsheets). INIA genebanks implement the Grin-Global database to curate their collections. INIA quinoa collection passport data are entered in this IT system and may be consulted online.

Experiences and links with *in situ* conservation work

The Andes is one of the most important mountain ranges in the world. In this ecoregion containing many special niches and a large number of plant associations, it has been possible for wild and cultivated quinoa to develop great genetic diversity. The plant is still found under natural conditions and growing as a crop in the fields of Andean farmers.

In the Andean region, it is possible to find agro-ecological areas housing quinoa with significant diversity and variability, displaying individual characteristics in terms of botanical, agronomic and crop adaptation traits. These areas have developed their own production systems based on the different individual agro-ecological conditions: Salare, Altiplano, Inter-Andean valleys, Coastal and Yunga (Lescano, 1989; Tapia, 1990; Rojas and Pinto, 2013).

In situ conservation is defined as the maintenance of crop genetic resources in their natural habitat and

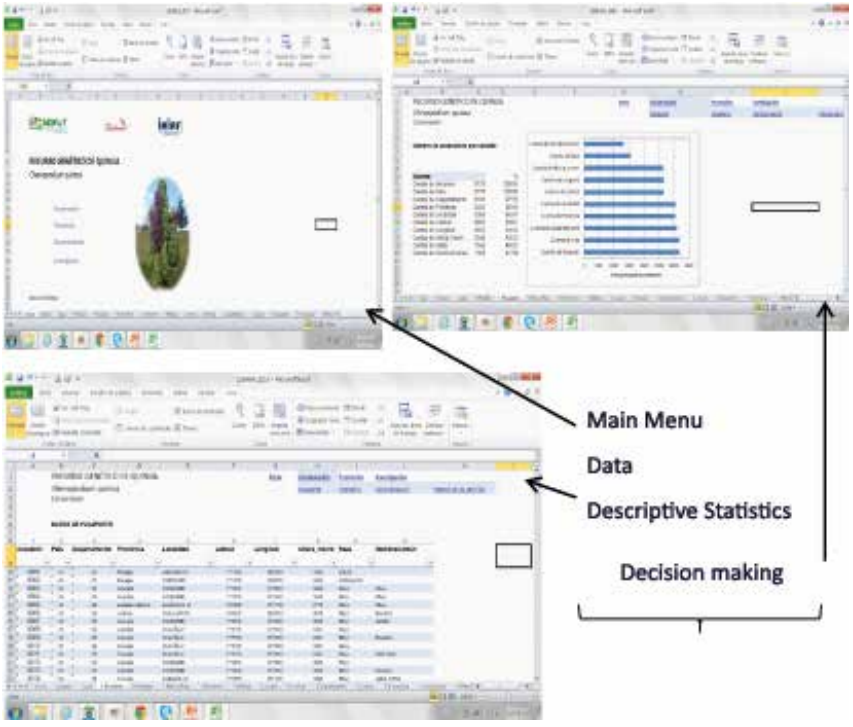

Figure 15. Microsoft Excel database of the INIAF quinoa collection, Bolivia

wild forms (Oldfield and Alcorn, 1987; Brush, 1991; Friis-Hansen, 1994). Traditional systems of cultivation – the *chacras* or farms – by means of which farmers traditionally conserve crop diversity, are also considered local spaces for *in situ* conservation of plant genetic resources for food and agriculture.

Traditional crop fields are a "mine of germplasm", where traditional varieties are maintained and where nature does its work of natural selection in conjunction with peasant farming traditions of seed propagation. Traditional knowledge is a key component of present-day agricultural biodiversity, and rural communities are responsible for its existence and evolution. Many factor, including knowledge of crops, use of food, associated culinary arts, agricultural management technologies and infrastructure, and local weather, are as important as the genetic resources themselves.

In this form of *in situ* conservation, farming families play an important role, with a number of interacting external and internal factors determining whether or not they will decide to continue planting a particular variety (landrace) and/or crop. These local dynamics occur in areas that are home to a wide diversity of crops and varieties, and where the ongoing management by families of the different local varieties will confer an evolutionary trend of adaptation to environmental, social and economic conditions by the planted materials.

While *ex situ* conservation is a model operating through genebanks that have been built up from biological material collected during prospecting operations conducted *in situ* and on farms, it is very unlikely that genebanks will contain the same material present *in situ* for various reasons (Wood and Lenne, 1997).

Local diversity is constantly evolving and accessions delivered to genebanks reflect a snapshot or image of a situation at a particular time or period. On the other hand, the same methodology has not always been applied when collecting samples from different quinoa-growing areas in widely varying geographical locations. As a result, genebanks do not fully reflect the variability present in a given region or country (Madrid *et al.*, 2011).

The great genetic diversity of quinoa comes from wide geographical diversity backed by a variety of farming practices and systems (Bazile and Negrete, 2009; Fuentes *et al.*, 2012). The perception and scale of this diversity must be considered in order

to appreciate the genetic diversity of quinoa and to support the maintenance of crop diversity for *in situ* conservation (Louafi *et al*., 2013), in particular through networks promoting and generating this biodiversity (Santonieri *et al*., 2011).

Support initiatives have been developed throughout the Andes to promote *in situ* conservation of quinoa. For example, in **Bolivia**, the first *in situ* conservation work with quinoa began in the area surrounding Lake Titicaca in 2002. It involved the study of varieties kept locally in traditional management systems. The results showed a reduction of up to 70% in locally conserved diversity compared with the diversity safeguarded in the genebank (Pinto *et al*., 2006; Pinto *et al*., 2007; Rojas *et al*., 2003b). Subsequently, preliminary findings from case studies showed that internal and external factors influenced families when deciding whether or not to continue planting quinoa varieties (Alanoca *et al*., 2004).

As part of the *ex situ–in situ* relationship, annual participative assessment studies have been performed using quinoa since 2003, including genebank material and local varieties. Seed diversity fairs were organized to promote the diversified use of quinoa (Pinto *et al*., 2010). Visits by farmers to genebanks were promoted, and genebank staff were encouraged to participate in various rural and urban fairs. In this way "community quinoa and cañahua genebanks" were set up within the framework of the National System of Genetic Resources for Food and Agriculture (SINARGEAA) and were implemented in the communities of Antarani, Patarani, Coromata Media and Rosapata near Lake Titicaca (Rojas *et al*., 2012).

In 2011, a network of "farmer custodians" was established, and "community genebanks" have since been implemented in eight communities (Cachilaya, Coromata Media, Antaquira, Pucamaya, Erbenkalla, Rosa Pata, Corqueamaya and Suruquiña) near Lake Titicaca as part of a strategy for the participative documentation and monitoring of agricultural biodiversity and traditional knowledge. This experience is conducted with an agricultural biodiversity approach and focuses its efforts on understanding and observing inter- and intraspecific diversity of crops useful for food, medicine and other applications. It also includes the development of a new method involving a red list for cultivated species (Padulosi *et al*., 2012).

The quinoa collection that INIAF is in charge of is linked to two microcentres of the area surrounding Lake Titicaca, located in the community of Cachilaya (province of Los Andes) and the community of Titijoni (province of Ingavi) in the northern Altiplano of La Paz (Figure 16). *In situ* conservation work is carried out in these microcentres, including monitoring and characterization of the genetic diversity of crops and varieties kept by families, taking into account local dynamics and interactions with the surroundings.

In situ conservation in **Peru** is mainly carried out

Figure 16. Microcentres: Titijoni (left) and Cachilaya (right), department of La Paz, Bolivia

in Puno, through the annual cultivation of quinoa in *Aynokas*or areas, where it shares space with its wild relatives. Traditional management practices ensure a food supply for family and community and effectively manage crop diversity, pests and diseases, thanks mainly to the adoption of a rotation system and the cultivation of the crop at different altitudes (Ichuta and Artiaga, 1986).

Mujica and Jacobsen (2000) reported the presence of systems where quinoa and its wild relatives are preserved under different names, such as *mandas* and *laymes*. Wild relatives are also found growing in isolation on the edges of fields or in places considered sacred (House of the Gentiles or *Phiru*). These species are prized by farmers as food (leaves consumed as a vegetable, or grain consumed roasted), for their medicinal value or for use in ancient rituals, especially in periods of climatic adversity.

Conclusions

Quinoa plant genetic resources are essential for food and nutrition security and sovereignty of peoples and they make a significant contribution to the basic needs of humanity. They are part of countries' ancestral and cultural heritage, especially the countries of the Andean region; their conservation and sustainable use are therefore the responsibility of society as a whole.

In Andean countries, policies for conservation of plant genetic resources are on the whole unclear. This is particularly the case for the *ex situ* conservation of quinoa germplasm collections. Bank activities are determined by the objectives or interests of the institution in charge and are often based on the individual interests of researchers. They should receive priority in budget allocation, because these resources must be handed down from one generation to the next as they have a vital role in supporting the very existence of the human species.

The genetic diversity of quinoa preserved *ex situ in different countries is relatively large considering the number of accessions in the collections and their ecogeographical origin.* More than 88% of this diversity is located in genebanks in the Andean region. Although this concentration could promote use of the resources, in reality, the extent of use of collections is inadequate and way below potential.

Despite the effort made, not all genebanks in the Andean region conserving quinoa have optimal storage conditions to ensure medium- and long-term preservation of germplasm. Technologies must be adopted to optimize the efficient and safe conservation of quinoa collections. It is important to rationalize the resources invested to maintain the collections and meet international standards for germplasm management.

Efforts must be made to develop or adapt protocols and procedures to optimize the management of quinoa collections. Management of the bank must also been streamlined: increasing the use of germplasm; creating links between genebanks; and making connections with potential users of conserved germplasm.

In general, the databases where the information generated by the banks is stored are off limits to bank staff, and there is no online access. This means that data are only circulated through technical reports, scientific publications and sometimes through germplasm catalogues. With the exception of INIA (Chile), there are no public Web sites with minimal information on the quinoa accessions conserved in genebanks.

There are a limited number of initiatives linking the activities of quinoa banks with *in situ* conservation work undertaken by farm families. It is important for *ex situ* and *in situ* work to be complementary, because the disadvantages of one are offset by the advantages of the other: the material preserved *in situ*, in particular, contains genes that are important for improvement.

It is necessary to develop protocols and/or lists of *in situ* descriptors to record agrobiodiversity managed in traditional farming systems, and to involve members of the community in carrying out this work in conjunction with local stakeholders, such as municipalities and other organizations.

In Bolivia INIAF is spearheading the drive to establish a national genetic resources system, with the participation of the various stakeholders in the country working with *ex situ* and *in situ* conservation, including farmers' organizations.

Annex 1. Details of countries and institutions in the world which maintain *ex situ* collections of quinoa (*Chenopodium quinoa, C. album, C. berlandieri, C. hircinum, C. petiolare, C. murale* and *Chenopodium* sp.).

N°	Countries	N° total of accessions	Code WIEWS	Institution	Acronym	Accessions by Institution
1	Bolivia	6721	BOL138	Instituto Nacional de Innovación Agropecuaria y Forestal - INIAF	BNGA	3178
			BOL094	Facultad de Agronomía UMSA	FA-UMSA	1370*
			BOL100	Facultad de Ciencias Agrícolas, Pecuarias y Veterinaria	FCAP-UTO	1780
			BOL318	Unidad Académica Campesina Tiahuanacu – Universidad Católica Boliviana San Pablo	UACT-UCB	257*
			BOL319	Carrera de Ingeniería Agronómica – Universidad Pública de El Alto	CIA-UPEA	136*
			BOL107	Centro de Investigación y Producción Comunal IRPANI	CIPROCOMI	262
2	Peru	6302	PER859	Estación Experimental Agraria Illpa, Banco Base Quinua	INIA-BB Quinua	1910
			PER014	Estación Experimental Agraria Illpa	INIA-EEA.ILL	789
			PER030	Estación Experimental Agraria Andenes	INIA-EEA.A	700
			PER012	Estación Experimental Agraria Baños del Inca	INIA-EEA.BI.	235
			PER041	Estación Experimental Canaán	INIA-EEC	123
			PER029	Estación Experimental Agraria Santa Ana	INIA-EEA.SA.	63
			PER002	Universidad Nacional Agraria La Molina	UNALM	2089
			PER007	Universidad Nacional del Altiplano	UNA	1873
			PER027	Universidad Nacional San Antonio Abad del Cusco	UNSAAC/CICA	430
3	Ecuador	673	ECU023	Departamento Nacional de Recursos Fitogenéticos y Biotecnología	DENAREF	673
4	Argentina	492	ARG1191; ARG1342	Facultad de Agronomía, Universidad de Buenos Aires; Banco Base de Germoplasma, Instituto de Recursos Biológicos, Instituto Nacional de Tecnología Agropecuaria	UBA-FA; BBC-INTA	492
			ARG1349	Banco Activo de Germoplasma del Noroeste Argentino (NOA)	BGNOA	40
			ARG1350	Banco Activo de Germoplasma de La Consulta	BGLACONSULTA	15
5	Chile	286	CHL028	Banco Base INIA Inihuasi	INIA INTIH	203
			CHL004	Centro Regional de Investigación INIA Carillanca	INIA CARI	84
			CHL003	Facultad de Ciencias Agrarias Universidad Austral de Chile	IPSV - UACH	15
			CHL142	Universidad Arturo Prat de Iquique	UNAP	31
			CHL006	Ingrid Van Baer de Temuco		91
6	Colombia	28	COL029	Centro de Investigación de La Selva, Corporación Colombiana de Investigación	CORPOICA	28
7	Germany	987	DEU146	Genebank, Leibniz Institute of Plant Genetics and Crop Plant Research	IPK	984
			DEU109	Greenhouse for Tropical Crops, Institute for Production and Nutrition of World Crops, Kassel University	GHK	3
8	India	294	IND001	National Bureau of Plant Genetic Resources	NBPGR	193
			IND032	Regional Station Shimla, NBPGR	NBPGR	98
			IND414	CSK HP Krishi Vishvavidyalaya, Palampur	CSK HPKV	3

N°	Countries	N° total of accessions	Code WIEWS	Institution	Acronym	Accessions by Institution
9	USA	229	USA020	North Central Regional Plant Introduction Station, USDA-ARS, NCRPIS	NC7	229
10	Japan	191	JPN003	Department of Genetic Resources I, National Institute of Agrobiological Sciences	NIAS	191
11	United Kingdom	65	GBR016	Genetic Resources Unit, Institute of Biological, Environmental & Rural Sciences, Aberystwyth University	IBERS-GRU	23
			GBR004	Millennium Seed Bank Project, Seed Conservation Department, Royal Botanic Gardens, Kew, Wakehurst Place	RBG	42
12	Australia	36	AUS048	Australian Tropical Crops & Forages Genetic Resources Centre	ATCFC	27
			AUS006	Australian Medicago Genetic Resources Centre, South Australian Research and Development Institute	AMGRC	9
13	Ethiopia	20	ETH013	International Livestock Research Institute	ILRI-Ethiopia	20
14	South Africa	19	ZAF001	Division of Plant and Seed Control, Department of Agriculture, Technical Service	PREPSC	5
			ZAF064	RSA Plant Genetic Resources Centre	PGRC	14
15	Hungary	17	HUN003	Institute for Agrobotany	RCA	17
16	Slovakia	15	SVK001	Plant Production Research Center Piestany	SVKPIEST	15
17	Spain	9	ESP003	Comunidad de Madrid. Universidad Politécnica de Madrid. Escuela Técnica Superior de Ingenieros Agrónomos. Banco de Germoplasma	UPM-BGV	7
			ESP004	Instituto Nacional de Investigación y Tecnología Agraria y Alimentaria. Centro Nacional de Recursos Fitogenéticos	INIA-CRF	1
			ESP109	Junta de Castilla y León. Instituto Tecnológico Agrario de Castilla y León. Centro de Investigación de Zamadueñas	ITACYL	1
18	Kenya	6	KEN015	National Genebank of Kenya, Crop Plant Genetic Resources Centre - Muguga	KARI-NGBK	6
19	Canada	5	CAN004	Plant Gene Resources of Canada, Saskatoon Research Centre, Agriculture and Agri-Food Canada	PGRC	5
20	Austria	5	AUT001	AGES Linz - Austrian Agency for Health and Food Safety / Seed Collection	BVAL	3
			AUT025	Office of the Styrian Regional Government, Department for Plant Health and Special Crops	WIEWS	2
21	Portugal	4	PRT102	Banco de Germoplasma - Universidade da Madeira	ISOPlexis	3
			PRT018	Departamento de Botânica e Engenharia Biológica, Instituto Superior de Agronomía	ISA	1
22	Czech Republic	3	CZE122	Genebank Department, Division of Genetics and Plant Breeding, Research Institute of Crop Production	RICP	3
23	Uruguay	3	URY003	INIA La Estanzuela	INIA LE	3
24	Zambia	3	ZMB030	SADC Plant Genetic Resources Centre	SRGB	3
25	Turkey	3	TUR001	Plant Genetic Resources Department	AARI	3
26	Lesotho	2	LSO002	Department of Agricultural Research		2
27	Brazil	1	BRA003	Embrapa Recursos Genéticos e Biotecnología	CENARGEN	1
28	Sweden	1	SWE054	Nordic Genetic Resource Center	NORDGEN	1
29	Romania	1	ROM007	Suceava Genebank	BRGV	1
30	Jordan	1	JOR006	National Centre for Agricultural Research and Technology Transfer	NCARTT	1
Total		**16422**	**59 banks**			**18787**

Source: Prepared with information from WIEWS 2013 and with the collaboration of experts working with ex situ collections of quinoa
* Data reported directly by the institution and not reflected in WIEWS

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