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Seed Storage Proteins in *Chenopodium Quinoa* Germplasm

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Abstract

Quinoa (*Chenopodium quinoa* Willd.) is a dicotyledonous pseudo-cereal from the Chenopodiaceae family that originated in the Andean Mountains of the South America region. In recent years, the production and consumption of quinoa seeds have increased. Cultivation has also spread to countries outside the original growing area, among others, to countries of temperate climate. However, the leading quinoa producers in the world are still Bolivia, Ecuador, and Peru. The main reason for the spread of quinoa is its remarkable adaptability to different climatic and soil conditions. Quinoa seeds are valued mainly for their relatively high content of gluten-free storage protein (14.6%). In addition, the composition of amino acids is very balanced and approaches an ideal protein with a quality equivalent to the milk protein casein. Quinoa grain also contains the essential amino acids lysine, methionine, and threonine, which are considered limiting factors in other crops. With the aim of analysing the band spectra of seed storage proteins and detailed characterisation of their polymorphism and genotype relationship, 35 quinoa genotypes of different geographical origins were analysed by SDS-PAGE. A total of 20 strong allelic positions were detected in the molecular weight range from 10 to 175 kDa. The protein bands differed in intensity, and the main variability in band position among genotypes was found in the positions around 30 and 60 kDa. The evaluated samples showed some degree of heterogeneity at the level of overall seed protein polymorphism. Electrophoretic analysis of seed storage protein proved to be a helpful tool to discriminate quinoa genotypes as a first step in evaluating quinoa genetic resources, contributing general and specific valuable knowledge for breeding and selecting perspectives of quinoa genotypes.

Keywords: *Chenopodium quinoa*, genetic resources, total protein, variability