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# Assessment of Genetic Diversity in the USDA and CIP-FAO International Nursery Collections of Quinoa (*Chenopodium quinoa* Willd.) Using Microsatellite Markers [Abstract]

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**Assessment of Genetic Diversity in the USDA and CIP-FAO International Nursery Collections of Quinoa (*Chenopodium quinoa* Willd.) Using Microsatellite Markers**  
**[Abstract]**

Quinoa (*Chenopodium quinoa* Willd.) is a staple food crop for millions of impoverished rural inhabitants of Andean South America where it has been cultivated for millennia. Interest in quinoa, due largely to its superior nutritional characteristics, is fuelling a growing export market and has led to an increased focus on genetic research and the development of quinoa breeding programmes throughout South America. The success of these breeding programmes will rely heavily on the development of core germplasm collections and germplasm conservation. We report the development of a set of fluorescence-tagged microsatellite molecular markers that can be used to characterize genetic diversity within quinoa germplasm and we use this set of 36 microsatellites markers to genetically characterize the diversity of 121 accessions of *C. quinoa* held in the USDA germplasm bank, 22 accessions from the CIP-FAO international nursery collection and eight accessions representing parents from genetic mapping populations. A total of 420 alleles were detected among the quinoa accessions with an average of 11 alleles detected per microsatellite locus. Genetic heterogeneity was observed in 32% of the quinoa accessions at a given locus and suggests that many of these accessions represent heterogeneous seed lots or landraces. Both unweighted pair-group method with arithmetic averages (UPGMA) and principle components analysis (PCA) analyses partitioned the quinoa accessions into two main clusters. The first major cluster consisted of accessions from the Andean highlands of Peru, Bolivia, Ecuador, Argentina and extreme northeastern Chile. The other main cluster contained accessions from both the lowlands of Chile and a set of USDA accessions with no known passport data, collected by Emigdio Ballón. Using the patterns of genetic diversity detected within the *C. quinoa* accessions we discuss hypotheses regarding quinoa's centre of diversity, including highland and lowland ecotype clustering patterns, origin of lowland varieties, origin of domestication, and diversity levels in the USDA and CIP-FAO collections.