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Conservation Dynamics of Roots and Tuber Crops under On-Farm Management

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Understanding the conservation dynamics of smallholder managed landrace populations requires understanding their human ecology and the selective pressures that farmers exert when they manipulate diversity. Ongoing evolution of crop genetic resources in their center of origin and diversity, where they are exposed to a dynamic state of management, environmental stress, proximity to crop wild relatives among other forces of natural and human selection, is commonly considered an essential contribution of farmer-driven conservation. It is hypothesised to lead to adaptable evolution that reconfigures diversity to contemporary cropping environments and societal needs. In this process some diversity may get lost, while new diversity may be created.

At least four pathways contribute to conservation dynamics. First, geneflow among landraces and/or compatible wild relatives and the eventual incorporation of new genotypes into farmer landrace stocks (Bonnave *et al*., 2015). Second, the collection of selected semi-wild genotypes that are brought into cultivation. Third, mutations leading to intra-clonal variation. Fourth, Darwinist selection based on exposure of landrace pools to stressors and other selection pressures resulting in a 'survival of the fittest' of best-adapted genotypes, changes in phenology, and/or shifts in agro-ecologies (Vigouroux *et al*., 2011). Vegetatively propagated roots and tuber crop landraces are genetically fixed once created. This facilitated the study of their conservation dynamics on-farm (McKey *et al*., 2012), even though the lack of time series data, geographical benchmarking, and other factors still pose challenges for field-based crop evolutionary studies.

Methodology

In this paper we explore the four mechanisms outlined above for potato and cassava based on our own research findings and comparisons with the global literature have been discussed. We make use of several multi-year studies that were conducted by the International Potato Center (CIP), International Center for Tropical Agriculture (CIAT) and partners, involving additionally multiple (inter) national research institutes and farmer communities. Some of the studies contributing to the "big picture" are specified in Table 1.

Discussion

Geneflow and feral capacity: geneflow between wild and cultivated potatoes readily occurs (Scurrah *et al*., 2008). The subsequent steps of successful (A) germination of botanical seed, (B) seedling establishment, (C) naturalisation though advantageous feral capacity, and (D) subsequent farmer "discovery" and incorporation into landrace stocks are essential. Our finding, involving 55 hybrids exposed to natural conditions (3 environments), showed that steps A to C do occur at low frequencies

Table 1. Summary description of selected studies conducted

Study	Period	Country	Methodologies included
a. Geneflow in landraces and wild relatives (potato)	2002-2007	Peru	Pollinator identification, ALFP and SSR markers
b. Feral capacity of interspecific hybrids (potato)	2011-2014	Peru	Population ecology, GxE interaction trials
c. Population genetics and phenology of Araq (potato)	2011-2015	Peru	Phenological characterisation, SSR markers
d. Diversity monitoring in selected hotspots (potato)	2012-2016	Bolivia, Peru	Morphological and SSR marker characterisation, pGIS
e. Impact study of varietal releases (cassava)	2014-2015	Colombia	SNP markers, extensive varietal sampling
f. pGIS and spatial diversity transitioning (potato)	2012-2016	Bolivia, Peru	Extensive varietal sampling, cartography, pGIS

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till at least 3 years after establishment. Naturalisation rates were genotype and environmentally determined, but particularly hybrids between *Solanum tuberosum* landraces (tetraploid Andigenum group) and interspecific hybrids of *S. tuberosum* (diploid Andigenum group) with wild *S. chiquidenum* showed high survival rates. Similarly, geneflow and pathways leading to the use of new cassava hybrids have been shown in the literature (Deputié, 2008).

Use of semi-wild genotypes: Araq potatoes are a folk taxon with considerable cultivar diversity that is commonly found as a weed in Andean maize fields. These semi-wild potatoes are altitudinally separated from cultivated landraces. A characterisation experiment aimed at comparing the phenology of 6 Araq cultivars, 11 cultivated Andigenum landraces and 1 outgroup (*S. Juzepczukii*) showed that tuber skin thickness and vegetative reproduction through few and large tubers were significantly different. These characters in combination with prolonged dormancy and early bulking provide incentives for farmers to collect and consume Araq in times of food scarcity. Incorporation of selected cultivars into cultivated landrace stocks is uncommon, but has been observed by the authors. A SSR-marker based population genetic study involving 668 Araq cultivars from Peru's Huanuco region and 23 primers shows that considerable allelic and clonal diversity exists, with some sub-populations (Fig. 1) being genetically very distinct from the cultivated Andigenum landraces present in CIP's ex situ reference collection. Even low-level frequencies of smallholder incorporation of Araq cultivars can have a significant effect on the overall novel diversity influx into *on-farm* managed landrace stocks.

Mutations: The presence of numerous potato landraces that are morphologically alike (except for tuber skin and/or bud colour), showed close similarity based on SSR-markers and belong to consistent farmer recognized cultivars groups are numerous. The occurrence of so-called "sports", or skin/bud colour variants, of well-known bred potato varieties such as Yungay (Peru) provides evidence that even recent cultivars undergo simple point mutations. Such event, which are difficult to track without detailed knowledge of time-tagged landraces diversity, are numerous for original domesticates that have been continually exposed for centuries to intense UV radiation at high altitude. The role of simple mutations in cassava and resulting chimerical

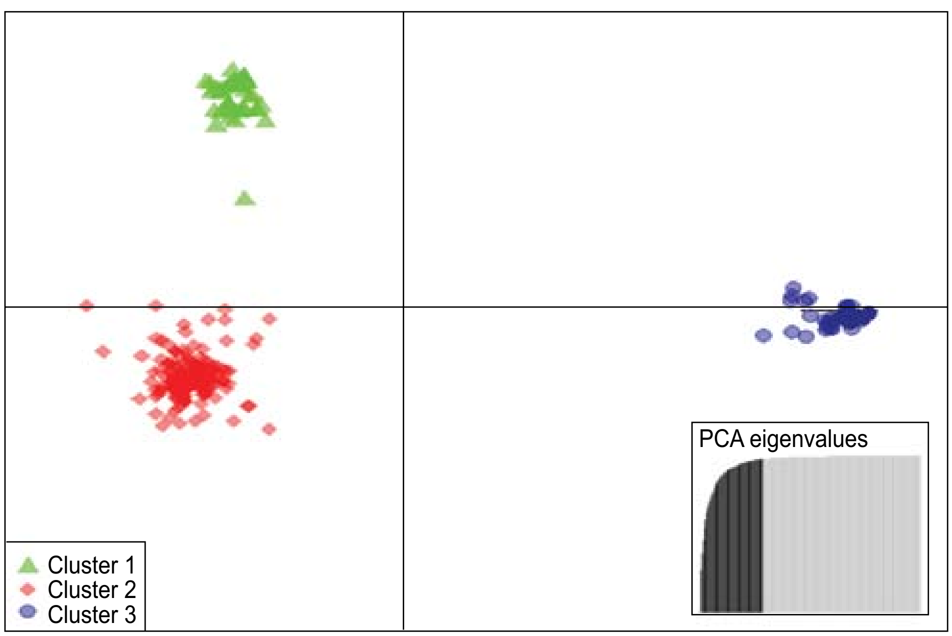

Fig. 1. Discriminant analysis of principal components (DAPC*) showing three discriminant clusters of semi-wild Araq potatoes (n=668), providing infrequent influxes into cultivated landrace stocks

*** DAPC (Jombart *et al*., 2010) evidenced 3 discriminant clusters. Cluster 1 included 117 samples (85% from Huamalíes province, 15% from Yarowilca province), cluster 2 included 357 samples (62% from Yarowilca province, 38% from Huamalíes province), and cluster 3 included 214 samples (all of them from Ambo province). Bayesian inference confirmed there are at least 3 different (sub) populations**

variants is less documented compared to other root and tuber crops.

Temporal–spatial shifts: geographically delimited comparisons of landrace diversity in key hotspots with sizeable landrace diversity frequently show an influx and outflow of cultivar and allelic diversity. This dynamic state may be the result of a classic Darwinist selection process in which individual landraces need to comply with (changing) environmental conditions and anthropogenic use rationales. Shifts in the agroecological distribution patterns of landrace diversity are concurrent. For example, potato landrace production zones throughout the Andes have gone up 300 m in altitude during the last 50 years. Recent studies by CIAT and CIP have shown that novel landrace diversity, frequently uncovered in genebanks, is abundantly found in close proximity to the research stations where collection efforts and breeding were most intense.

Conclusions

We show that farmer managed diversity is actively changing and continues to produce novel and unique diversity. An important implication is that the global community should more systematically monitor farmer-managed landrace populations in centers of crop genetic diversity to be able to track their conservation status and eventually increase ex situ coverage based on quantitative gap analysis. Essentially *on-farm* "conservation" projects should ideally not only elucidate temporal and spatial change patterns of the diversity itself (landraces, alleles), but also the processes that contribute to adaptive evolution in times of accelerated global change.

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