

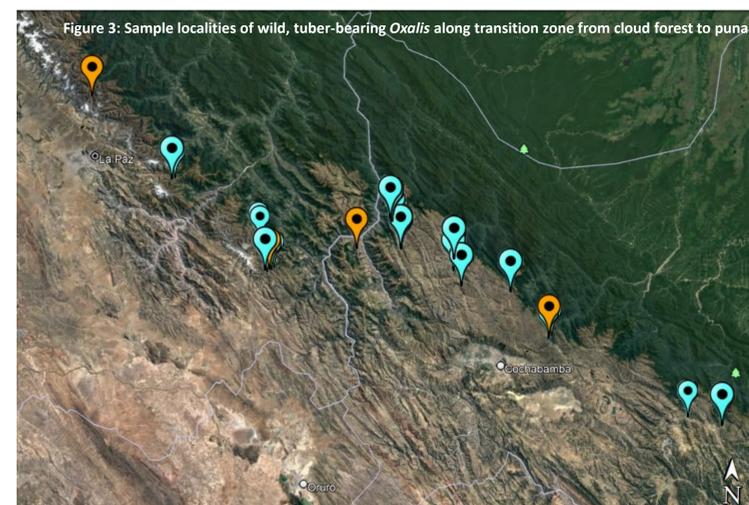
# Distributions of wild, tuber-bearing *Oxalis* in the central Andes, and their bearing on the origin of domestication of *Oxalis tuberosa*

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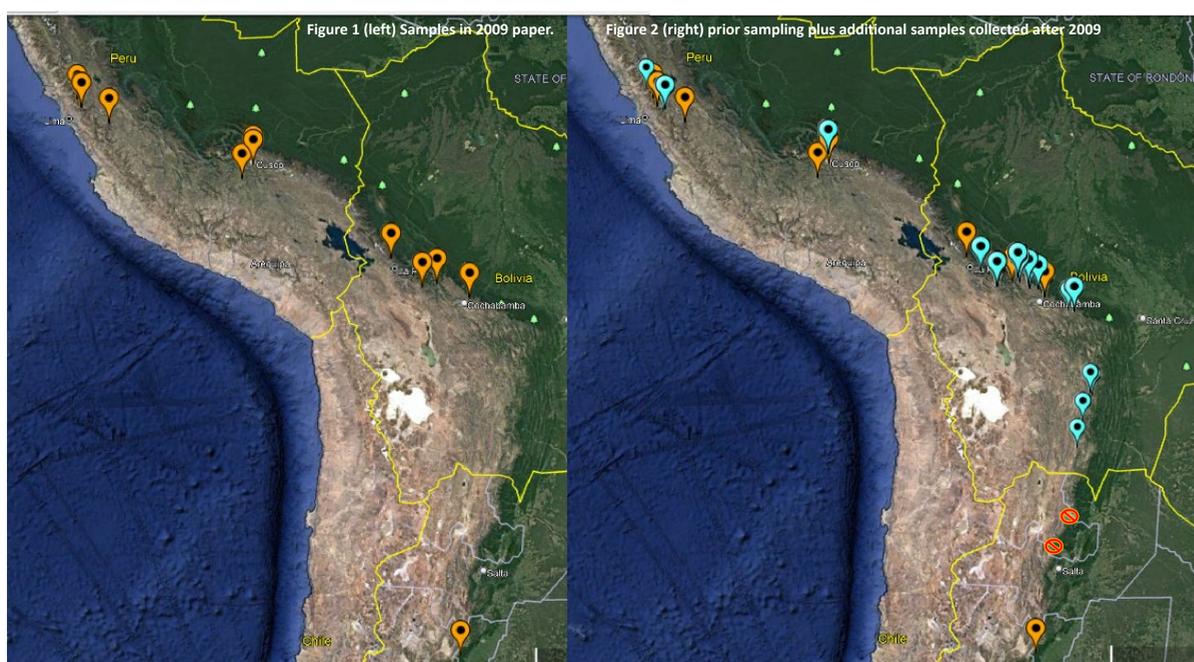
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Since our previous study of AFLP data in wild, tuber-bearing *Oxalis* populations from Peru, Bolivia, and Argentina (Emshwiller, et al. 2009), we have continued collecting to improve the geographic representation of sampling of these taxa. The distributions of the Bolivian and Argentinian taxa may be continuous, and their distinctiveness from each other is in question. These were the populations supported as most similar to cultivated *Oxalis tuberosa* in their AFLP profiles in the previous study. From 2013 to 2022, we have been revisiting and expanding the areas where these taxa were previously found, to improve geographical representation of our sampling for future studies with next generation sequencing methods. The populations in central Peru and southern Peru are separated from each other, and their ranges are now better understood. None of current ranges of the populations overlap with the archaeological site of Guitarrero Cave in Ancash Region of Peru, supporting the domesticated nature of the ancient tuber remains found in that site.

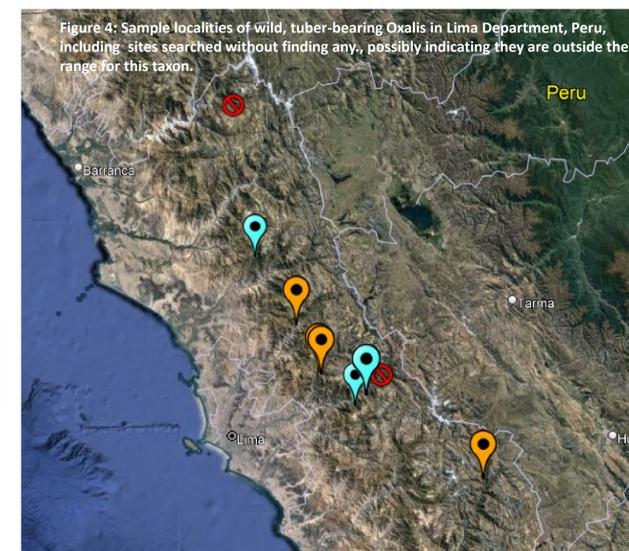
Our previous work on the origins of the octoploid Andean tuber crop oca, *Oxalis tuberosa* Molina, included DNA sequencing of two genetic regions for members of the clade to which oca belongs, the “*Oxalis tuberosa* Alliance” (Emshwiller & Doyle 1998, 2002) followed by AFLP data of wild, tuber-bearing *Oxalis* populations found in four Andean regions of Peru, Bolivia, and Argentina (Emshwiller, & al. 2009). There were some differences in the findings from the different data sources, and limited sampling of the wild, tuber-bearing *Oxalis* from each of four regions. To continue studies of the origins of polyploidy and domestication of oca, we have been revisiting the regions of Bolivia, central and southern Peru, and northwestern Argentina to improve the geographic representation of our sampling. We now have HiFi whole genome sequence data (via Pacific Biosciences, PacBio) in the process of alignment for cultivated octoploid *Oxalis tuberosa* and also a closely related diploid species, *Oxalis oulophora* Lourteig, of Bolivia. We plan to use targeted sequencing (Hyb-Seq, Schmickl & al. 2016) as well as long read PacBio sequencing in the case of polyploids, to improve our phylogenetic estimates of the “*Oxalis tuberosa* alliance” clade. We will use the results to understand how tuber formation and oxalic acid concentration are related to polyploidy and to domestication, and the distribution data may contribute to conservation efforts to preserve these crop wild relatives of oca as genetic resources.



The greatest number of samples were collected from Bolivia, thanks to a Fulbright Award during parts of 2013 to 2016 (see table below). The wild, tuber-bearing *Oxalis* in Bolivia are found just above the transition zone from “Yungas” cloud forest vegetation to high elevation “puna” grasslands (see dark green and tan areas in Figure 3 above). In April 2022 we tried, unsuccessfully, to find more tuber-bearing *Oxalis* in northwestern Argentina, also by seeking the transition from cloud forest to puna. We had hoped to fill in the gap between our previous sampling in Tucumán and the frontier with Bolivia (see symbols in Figure 2 indicating areas visited in Jujuy Province). In the case of Lima Department, we found the tuber-bearing *Oxalis* in some areas visited but not others (Figure 4 below). This provided some information about the limits of the range of these populations, as some locations may have been beyond the northern limits of the distribution, and others at too high elevation (see symbols in Figure 4).



Number of samples included for each region	in 2009 paper	additional samples now available
Central Peru (Lima)	3	5
Southern Peru (Cusco + Apurimac)	3	5
Bolivia	4	52
Argentina	5	0



Emshwiller, E and J. J. Doyle. (1998). Origins of domestication and polyploidy in oca (*Oxalis tuberosa*: Oxalidaceae): nrDNA ITS data. American Journal of Botany, 85(7): 975-985.; Emshwiller, E. and J. J. Doyle. (2002). Origins of domestication and polyploidy in oca (*Oxalis tuberosa*: Oxalidaceae). 2. Chloroplast-expressed glutamine synthetase data. American Journal of Botany, 89(7):1042-1056.; Emshwiller, E., T. Theim, A. Grau, V. Nina and F. Terrazas. (2009). Origins of domestication and polyploidy in oca (*Oxalis tuberosa*: Oxalidaceae) 3: AFLP data of oca and four wild, tuber-bearing taxa. American Journal of Botany, 96(10):1839-1848.; Schmickl, R., Liston, A., Zeisek, V., Oberlander, K., Weitemier, K., Straub, S. C., Cronn, R.C., Dreyer, L.L. & Suda, J. (2016). Phylogenetic marker development for target enrichment from transcriptome and genome skim data: the pipeline and its application in southern African *Oxalis* (Oxalidaceae). Molecular Ecology Resources, 16(5), 1124-1135.