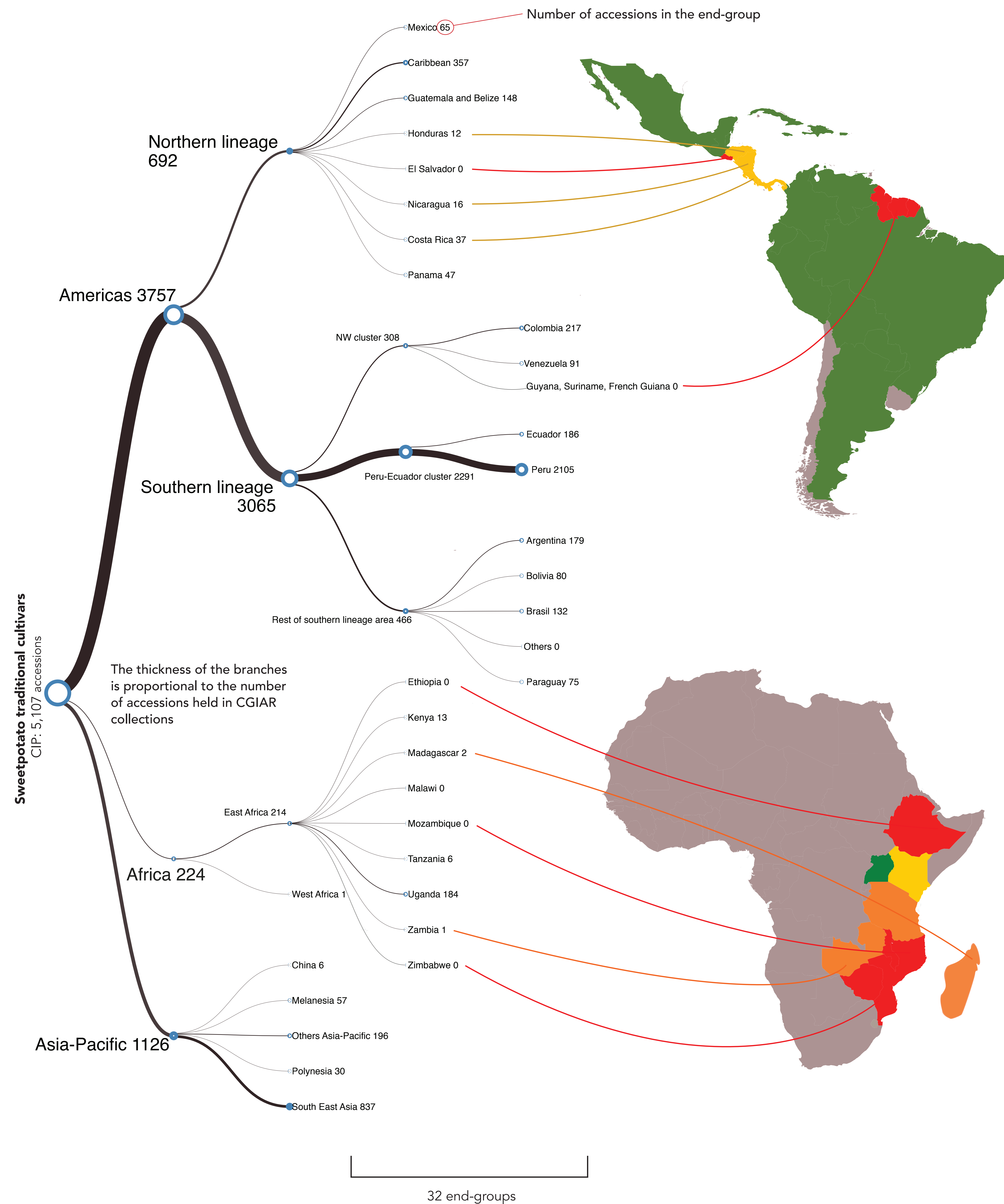




# Sweetpotato native cultivars diversity in the CGIAR collections: Finding and filling the gaps

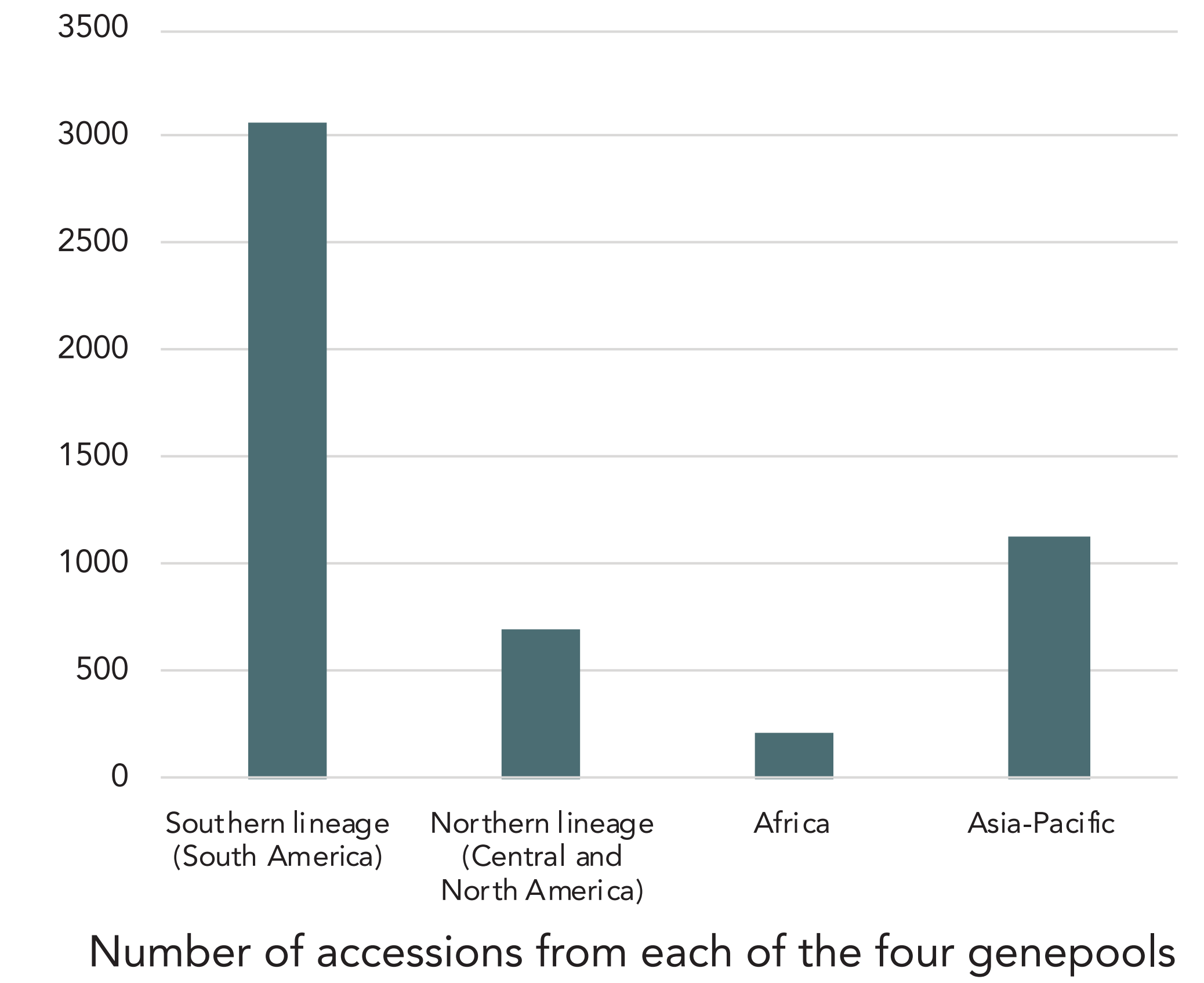
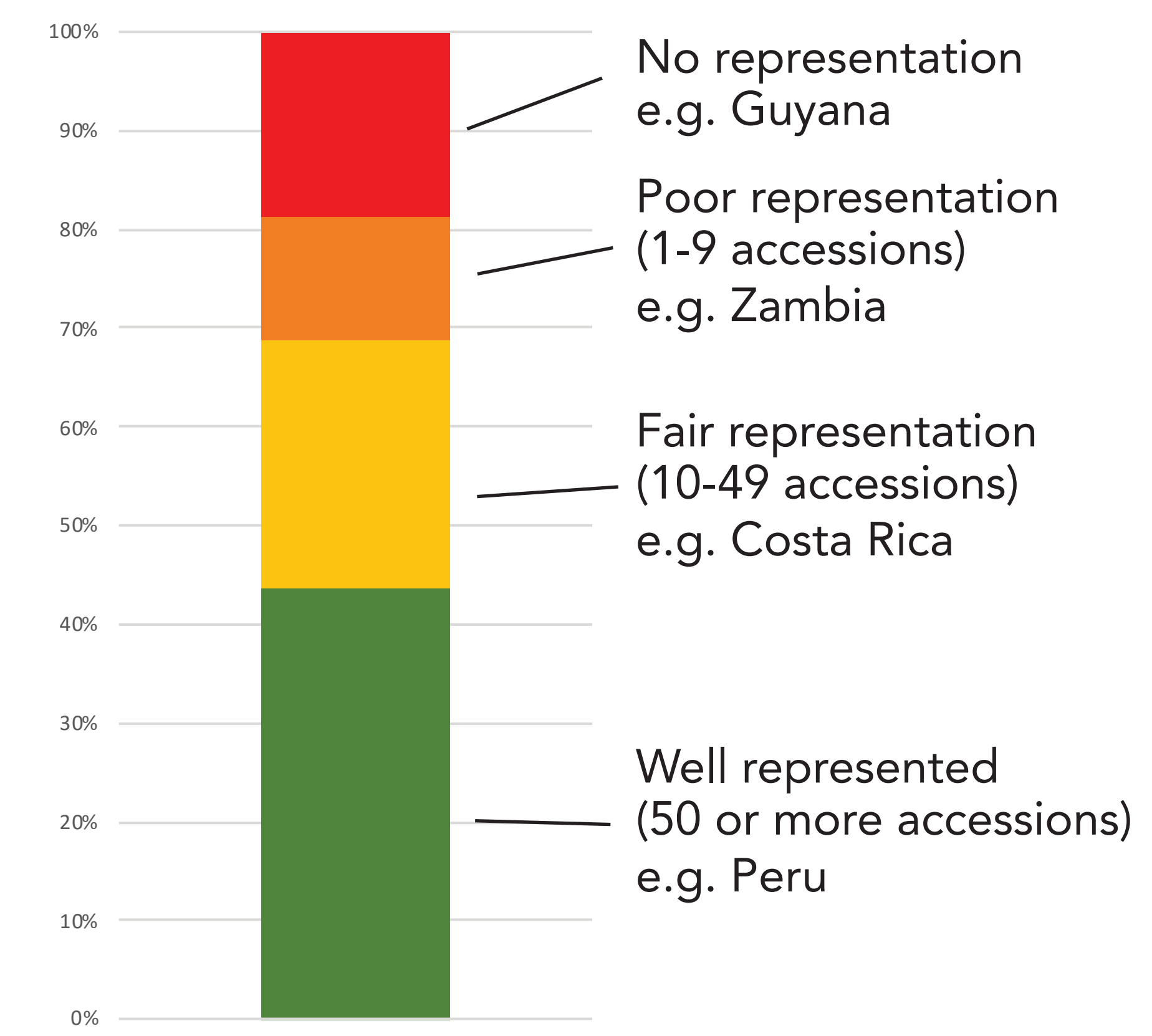


**1** The Sweetpotato Diversity Tree is a representation of the structure of the sweet potato gene pool obtained by dividing it into hierarchical clusters (Van Treuren et al 2009).

**2** Accessions conserved at CIP were mapped onto the groups in the Tree and against the political map of Central and South America, and East Africa.

**3** 44% of the end-groups in the Sweetpotato Diversity Tree are well represented in the CIP collection (in terms of coverage of allelic diversity), but 19% are not represented at all.

**4** The CIP collection covers well the Southern lineage of the American gene pool, while the Northern lineage of the American gene pool, and the African gene pool are less well represented.



## 5 How does your national collection complement these CGIAR collections?

**Reference**  
Van Treuren, R., Engels, J. M. M., Hoekstra, R., and Van Hintum, T. J. 2009. Optimization of the composition of crop collections for *ex situ* conservation. *Plant Genetic Resources*, 7(2), 185–193.

For more information, visit <http://bit.ly/sweetpotato-tree> or scan the below QR code



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