

Universal biological bar-code for determining the geographical origin of fruits by using PCR-DGGE

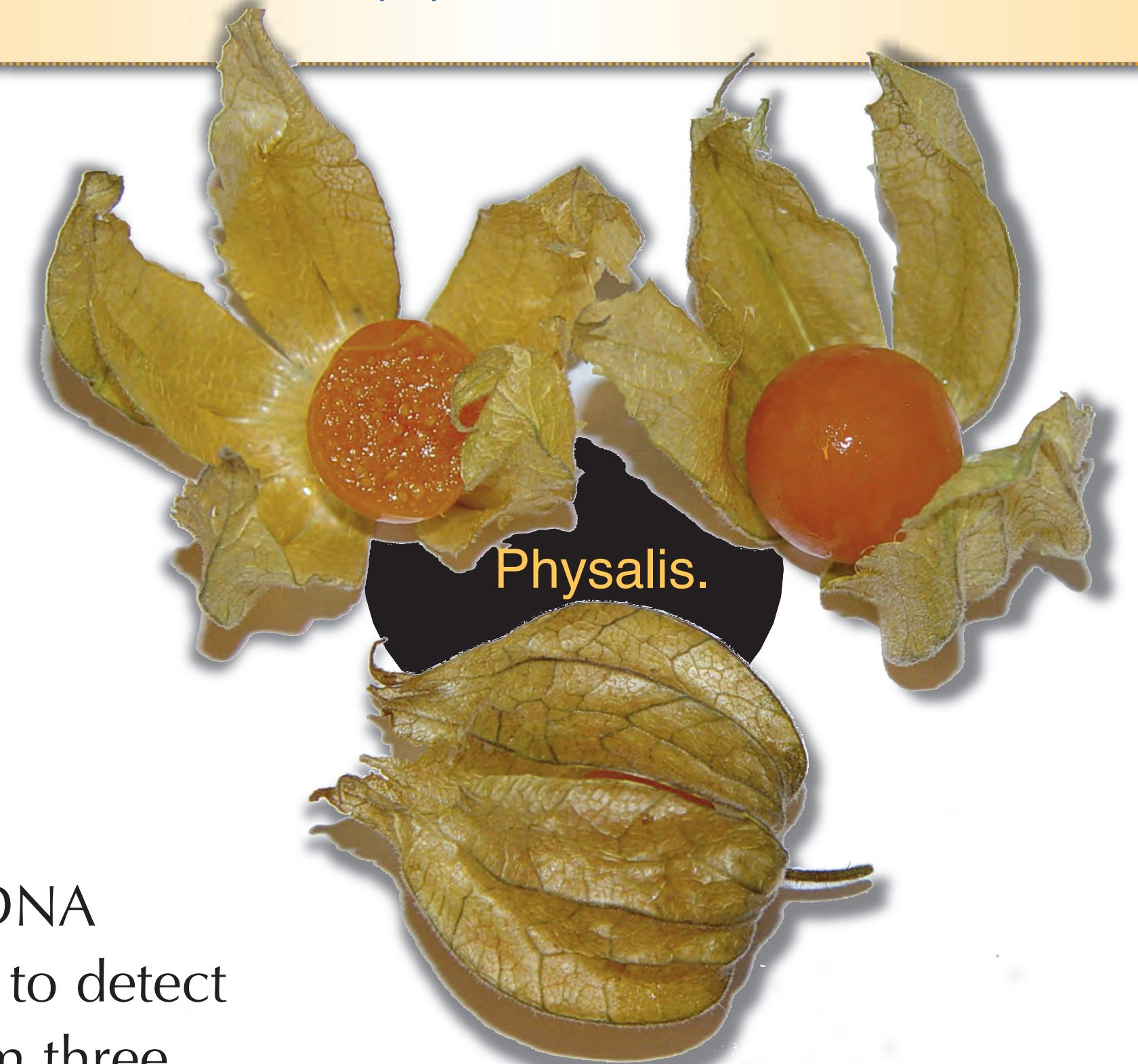
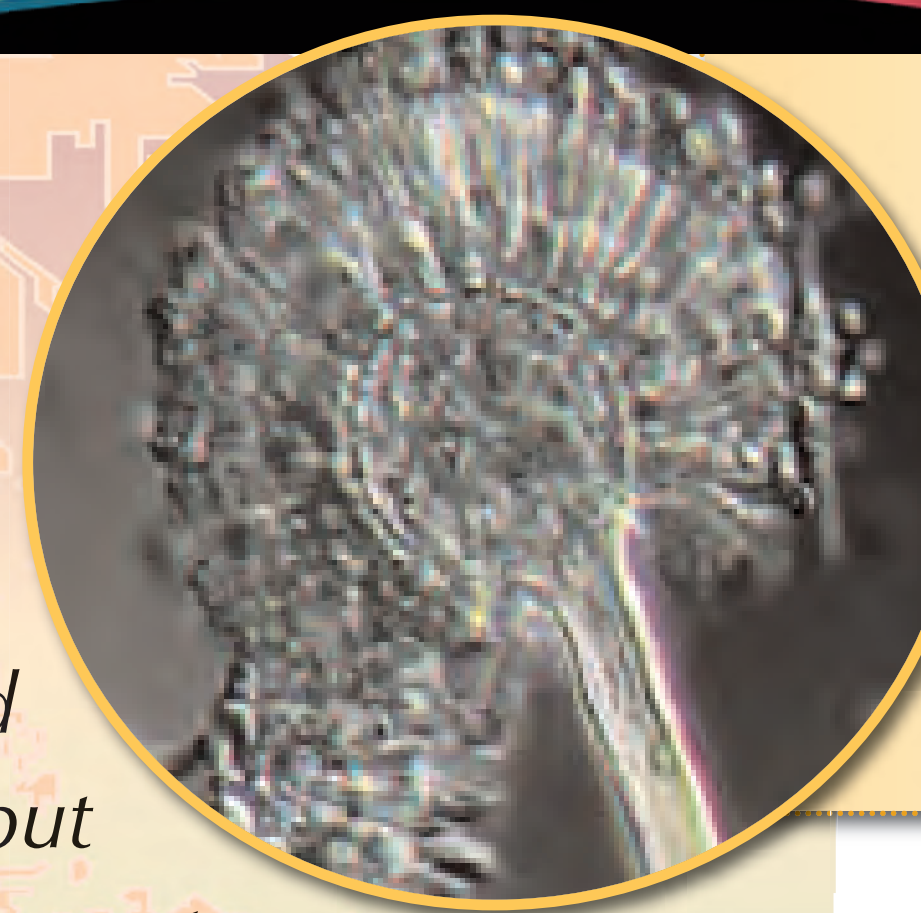
The determination of geographical origin is a demand of the traceability system of import-export foodstuff. One hypothesis of tracing the source of a product is by analyzing in a global way the microbial communities of the food and links statistically this analysis to the geographical origin of the food (1). *Physalis* is included in the priority list of many governments' horticulture and fruit export plan. It is exported from several countries including Colombia, Egypt, Zimbabwe and South Africa, but Colombia stands out as one of the largest producers, consumers and exporters. Colombia exports of *Physalis* in 2004 were worth 14 million USD (2). Shea tree fruits, only seven countries have statistics. Nigeria accounts for more than 60% of the production of Shea butter in 2005. It is followed by Mali, Ghana and Burkina Faso, which together account for just under a third of world production in 2005. In Europe, Shea butter is used mainly (95%) by the chocolate industry (3).

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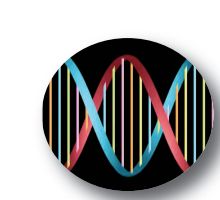
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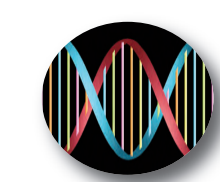
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Methodology



We applied an innovative molecular technique employing 28S rDNA profiles generated by PCR-DGGE as a new traceability technique to detect the variation in fungal community structures of *Physalis* fruits from three countries (Colombia, Uganda, Egypt) (4), and Shea tree fruits from three countries (Cameroon, Mali, Senegal) (5).



This novel technique was created by El Sheikha et al. (4, 5) and take into account the method of El Sheikha et al. (1).



Shea tree fruits.

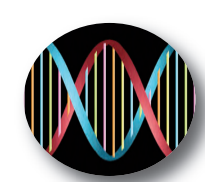
Results



The DGGE gels showed some significant differences in the migration patterns. However, the duplicates for each sampling location gave statistically similar DGGE patterns throughout the study (Fig. 1, Fig. 2).



The band profiles from different countries were different and were specific for each country and could be used as a bar code to discriminate the origin of the fruits.



When the 28S rDNA profiles were analyzed by multivariate analysis, distinct microbial communities were detected (Fig. 3, Fig. 4, Fig. 5, Fig. 6).

Fig. 1. PCR-DGGE 28S rDNA profiles of *Physalis*.

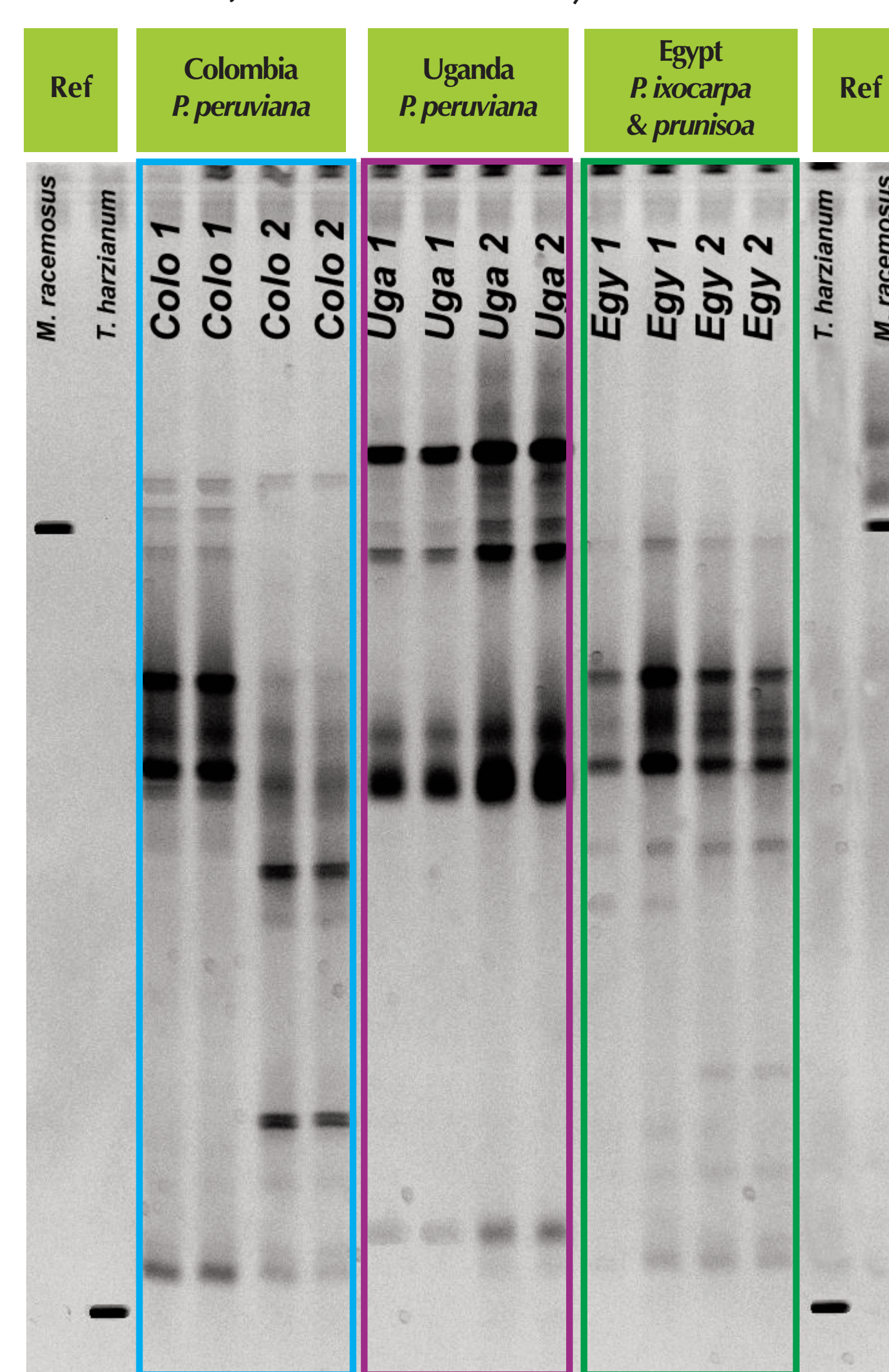


Fig. 2. PCR-DGGE 28S rDNA profiles of Shea tree fruits.

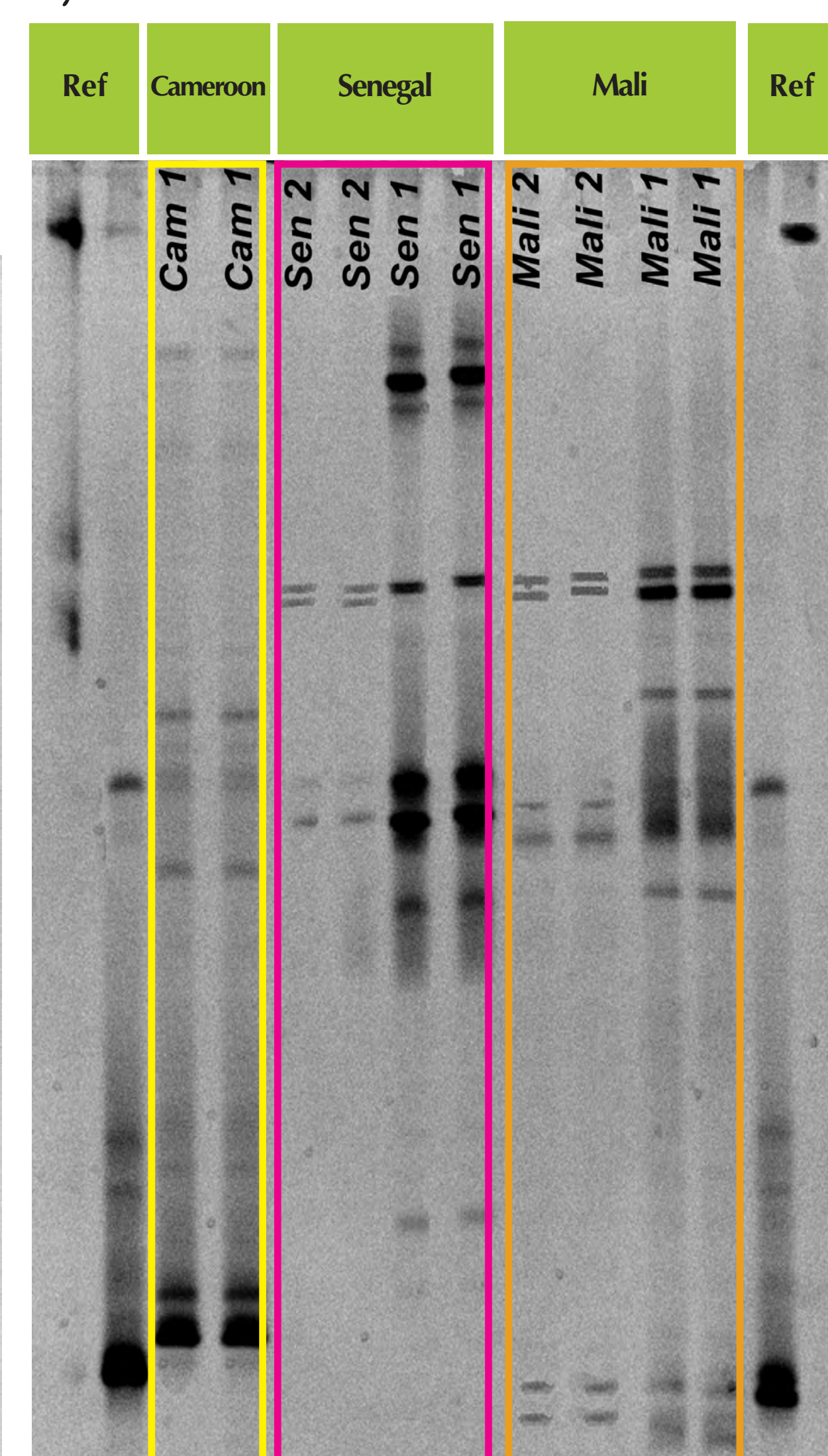


Fig. 3. Factorial variance analysis of 28S rDNA profiles of *Physalis*.

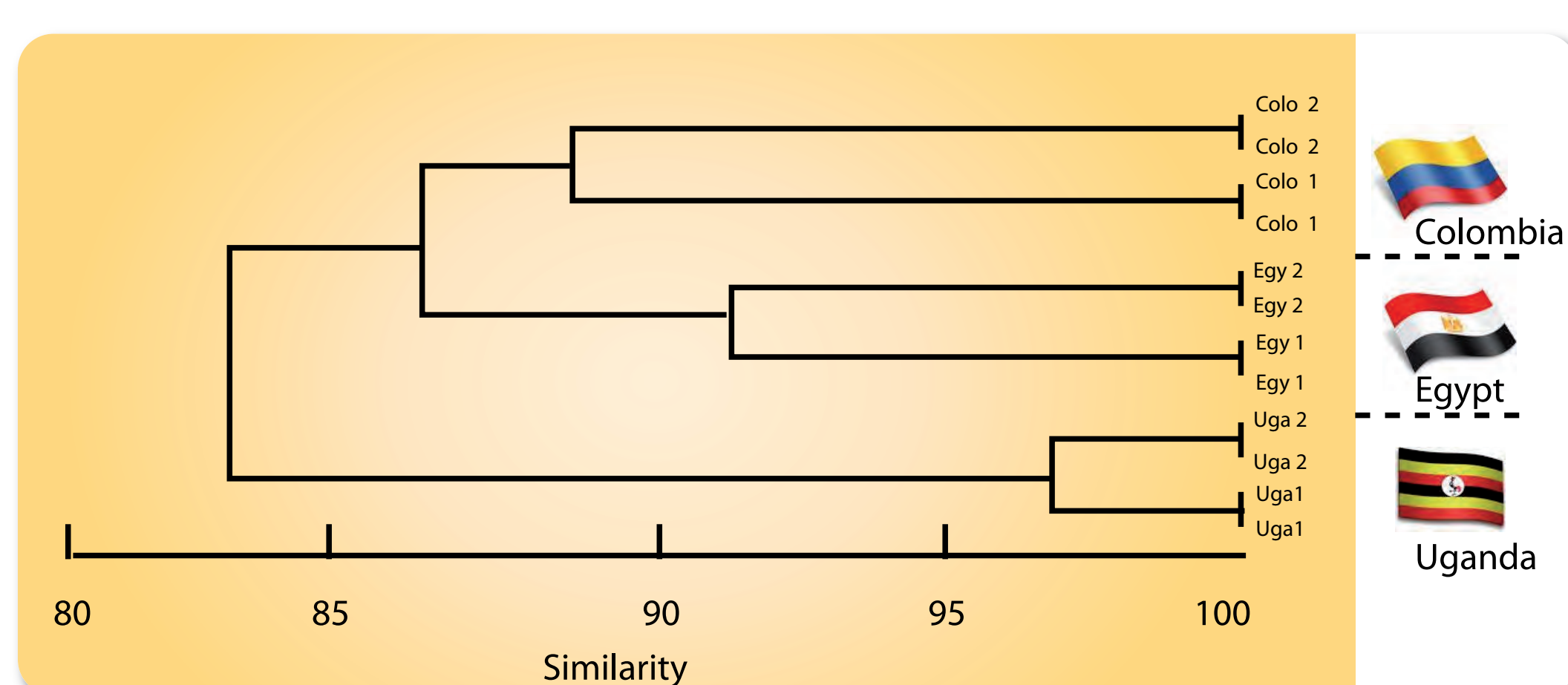


Fig. 5. Factorial variance analysis of 28S rDNA profiles of Shea tree fruits.

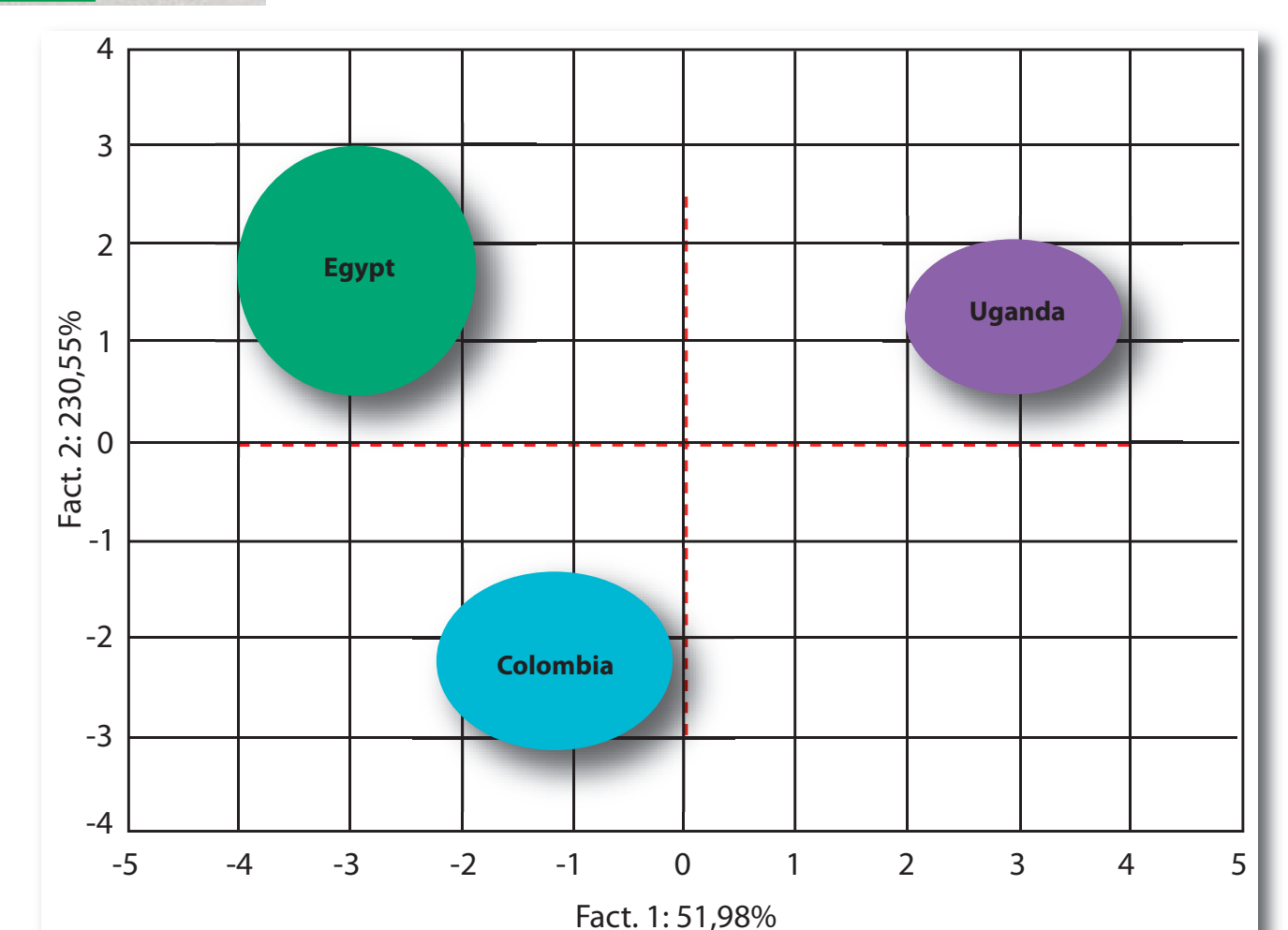
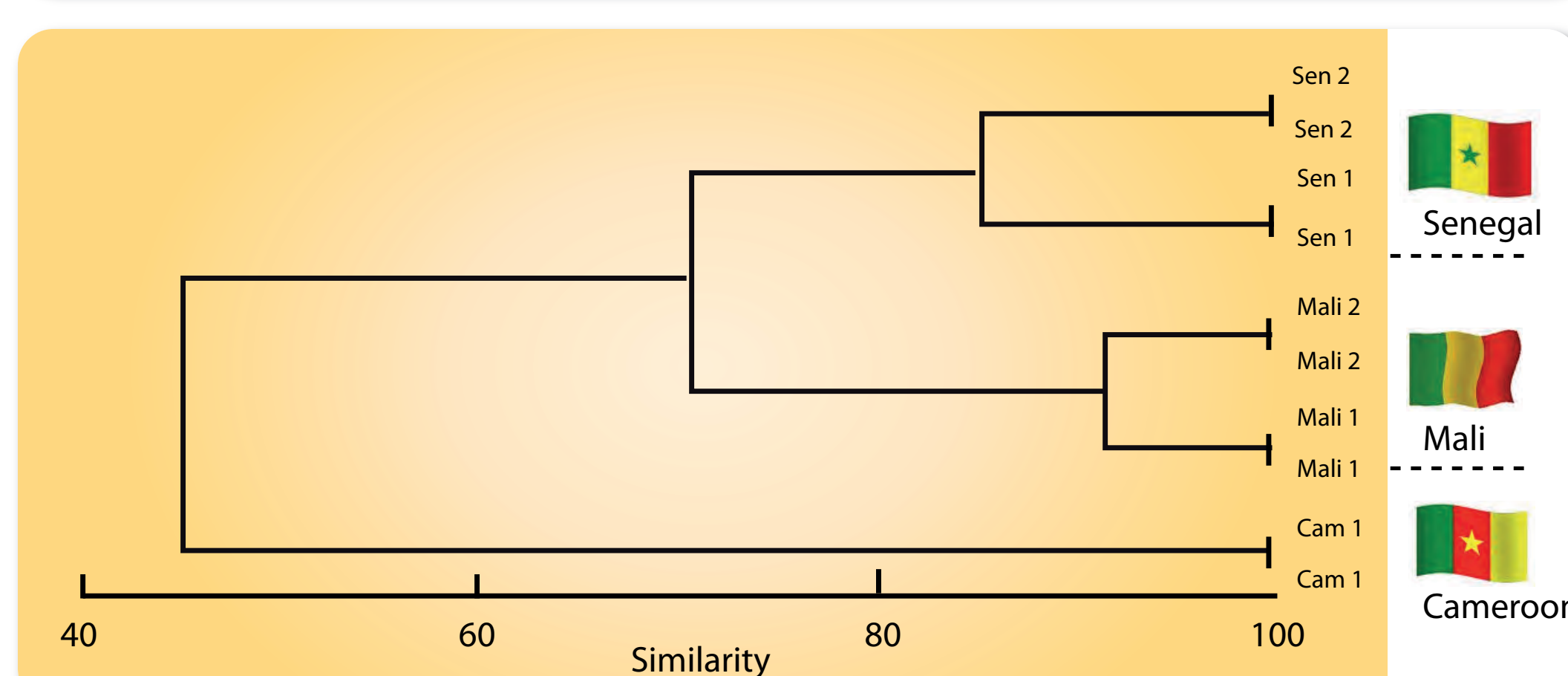


Fig. 4. Cluster analysis of 28S rDNA band profiles of *Physalis*.

Conclusion

We demonstrated that there was a link between the fungi populations and the geographical area. This method is a new traceability tool which provides fruit with a unique bar code and makes it possible to trace back the fruits to their original countries.

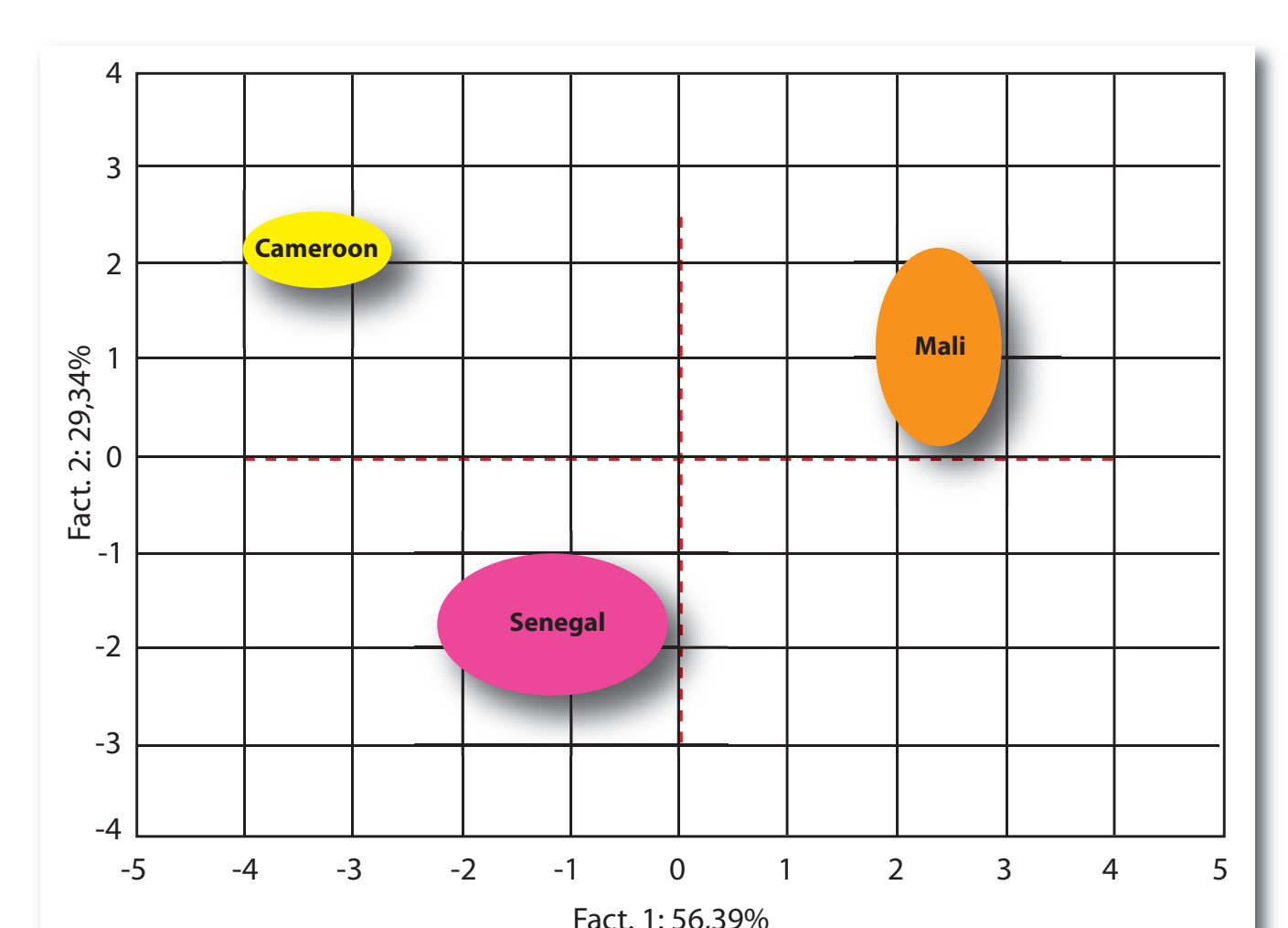


Fig. 6. Cluster analysis of 28S rDNA band profiles of Shea tree fruits.

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