



Phenotypic and molecular analysis of sea-buckthorn accessions reveal promising genotypes and candidate genes associated with micronutrients



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Introduction

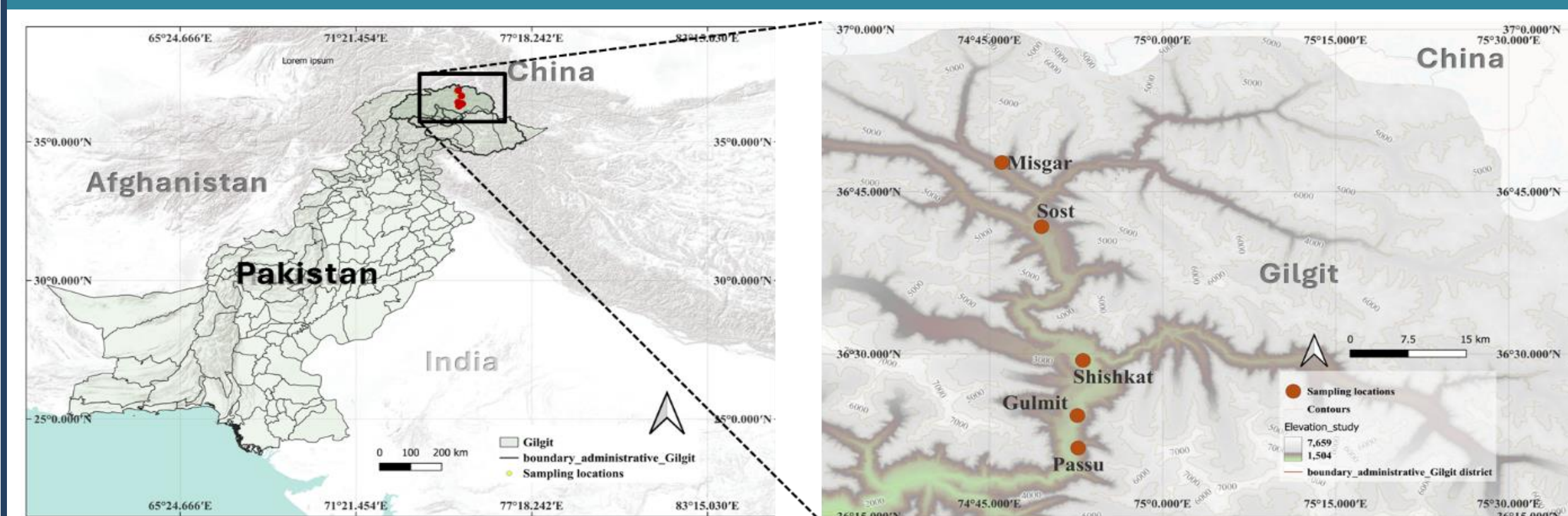


Fig. 1: Map of the studied sites in Gilgit region, Pakistan

Sea-buckthorn (*Hippophae rhamnoides*, family Elaeagnaceae), rich in vitamin C, anthocyanin, and minerals including iron (Fe)¹, is a potential candidate to combat micronutrient malnutrition. However, limited information exists on the genetic interplay between these nutrients, fruit morphology, and underlying genes. Aldo-keto reductase (AKR) gene family contributes to Fe/Zn uptake and vitamin C precursor synthesis.

Methodology

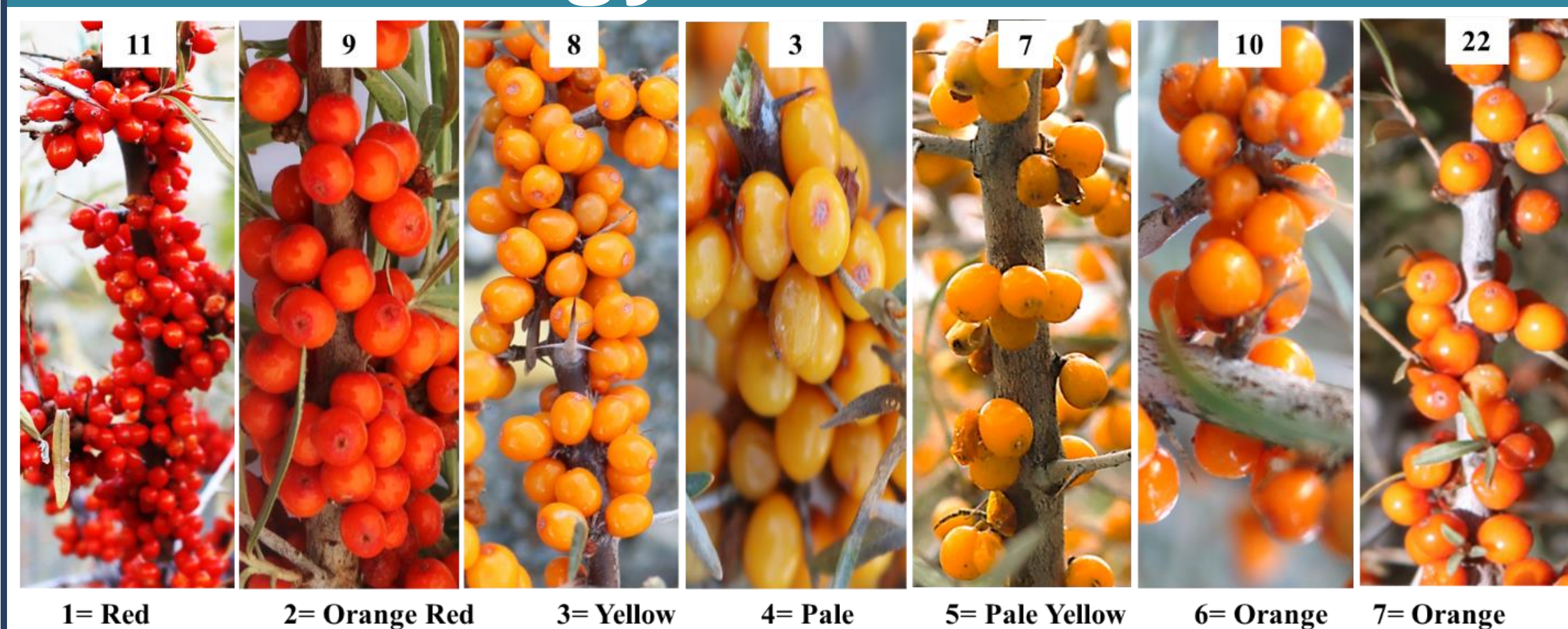
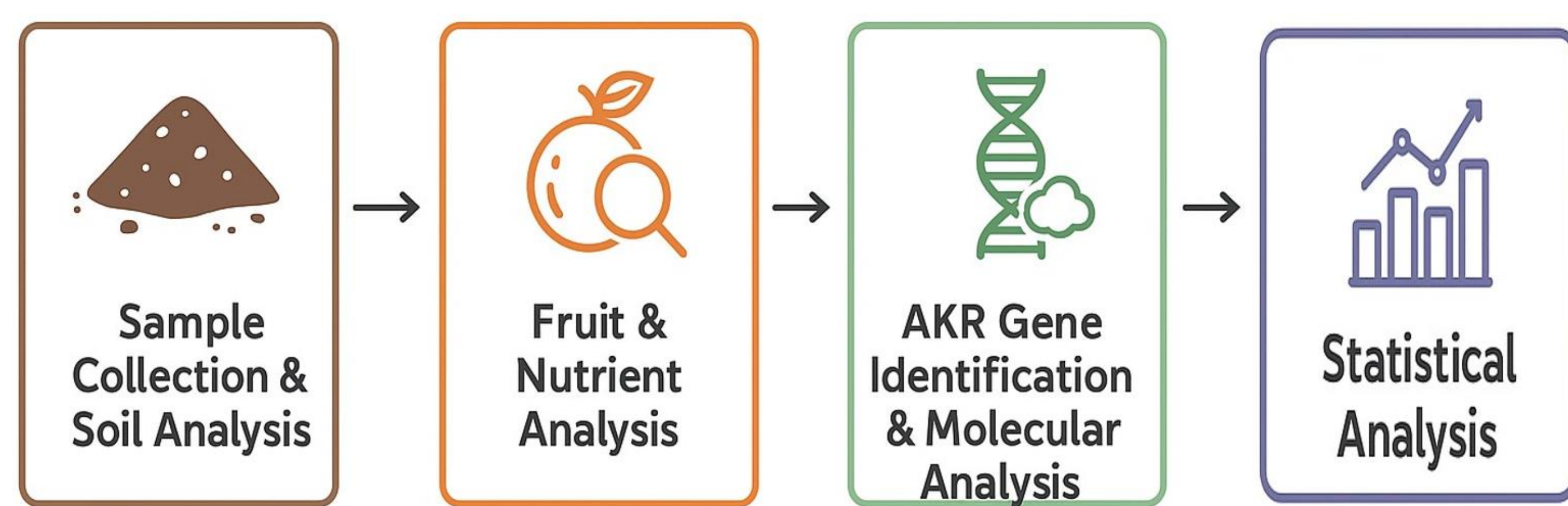


Fig. 2: Seven fruit colours observed in sea-buckthorn accessions (n = 70). Numbers in the white box represent frequency of accessions per colour tone



Results and Discussion

Fruit analysis

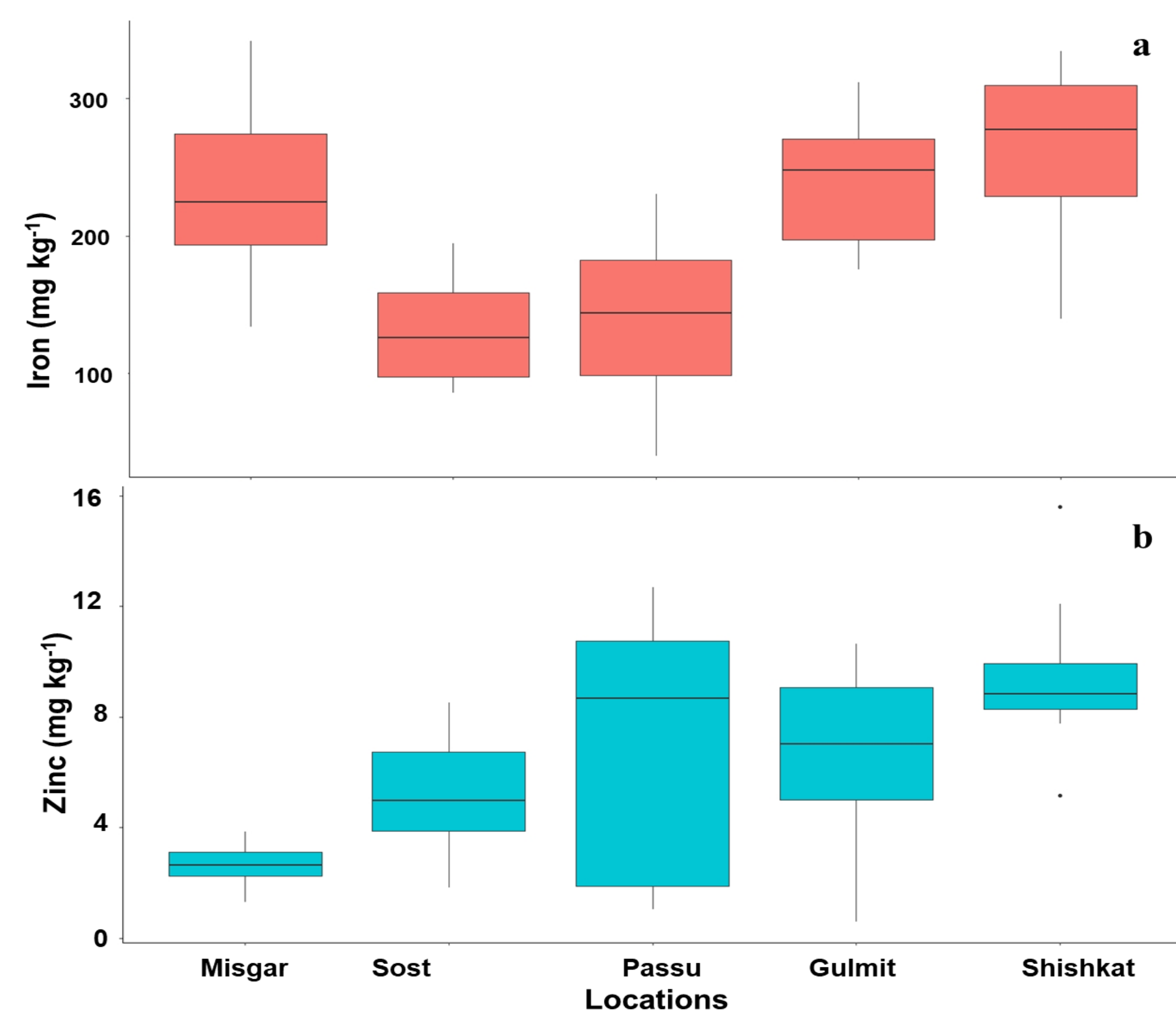


Fig. 3: Whisker box plots of Fe (a) and Zn (b) in descending altitude (l.-r.) in sea-buckthorn fruits (n=70)

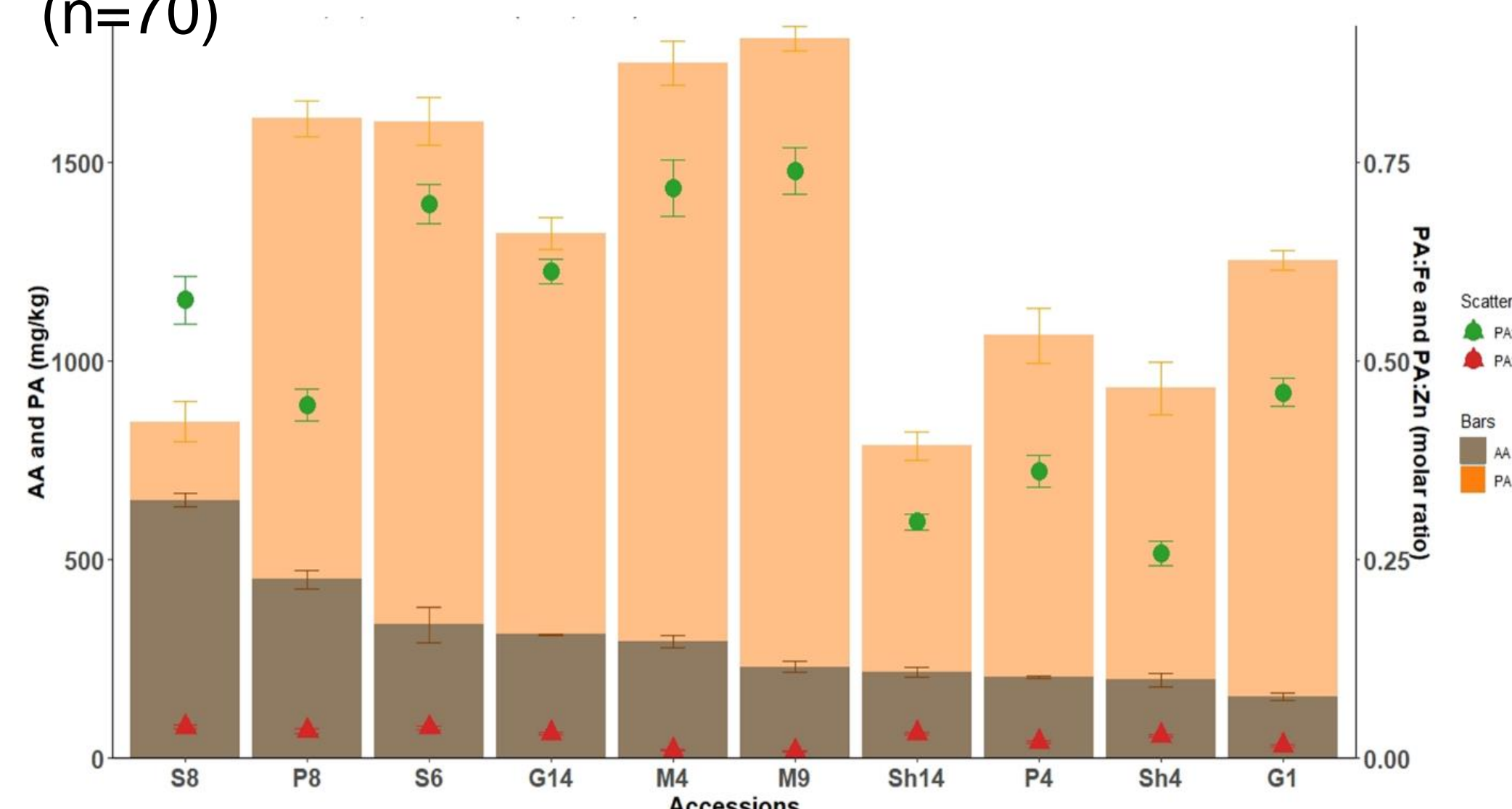


Fig. 4: Ascorbic acid, phytic acid, and bioavailability of ten sea-buckthorn accessions. PA: phytic acid, Fe: iron, Zn: zinc, AA: ascorbic acid, S: Sost, P: Passu, G: Gulmit, M: Misgar, Sh: Shihkat

Conclusions

Sost accessions had higher micronutrients, greater bioavailability, and stronger AKR gene expression. These findings suggest that AKR gene stacking could help improve the nutritional status of sea-buckthorn.

¹Wang Z, Zhao F, Wei P, Chai X, Hou G, Meng Q. Phytochemistry, health benefits, and food applications of sea buckthorn: A comprehensive review. Front Nutr. 2022; 9.

Results

- High diversity for Fe (40-342 mg kg⁻¹), Zn (1-13 mg kg⁻¹), vitamin C (40-595 mg 100g⁻¹)
- Shishkat accessions had highest concentrations of Fe (269 mg kg⁻¹), Zn (> 8 mg kg⁻¹; Fig. 3)
- Despite high PA levels (785-1811 mg kg⁻¹), low ratios for PA:Fe < 0.8, PA:Zn < 0.04, suggested high bioavailability (Fig. 4).
- Members of *H. rhamnoides* (18 *HrAKRs*) distributed among all six groups, indicating evolutionary divergence (Fig. 5).
- 10 *HrAKRs* confirmed by PCR in the studied accessions (Fig. 6).
- HrAKR08* consistently expressed across tissues, while *HrAKR02*, 05, and 14 expressed in highest number of accessions (Fig. 7).

AKR Analysis

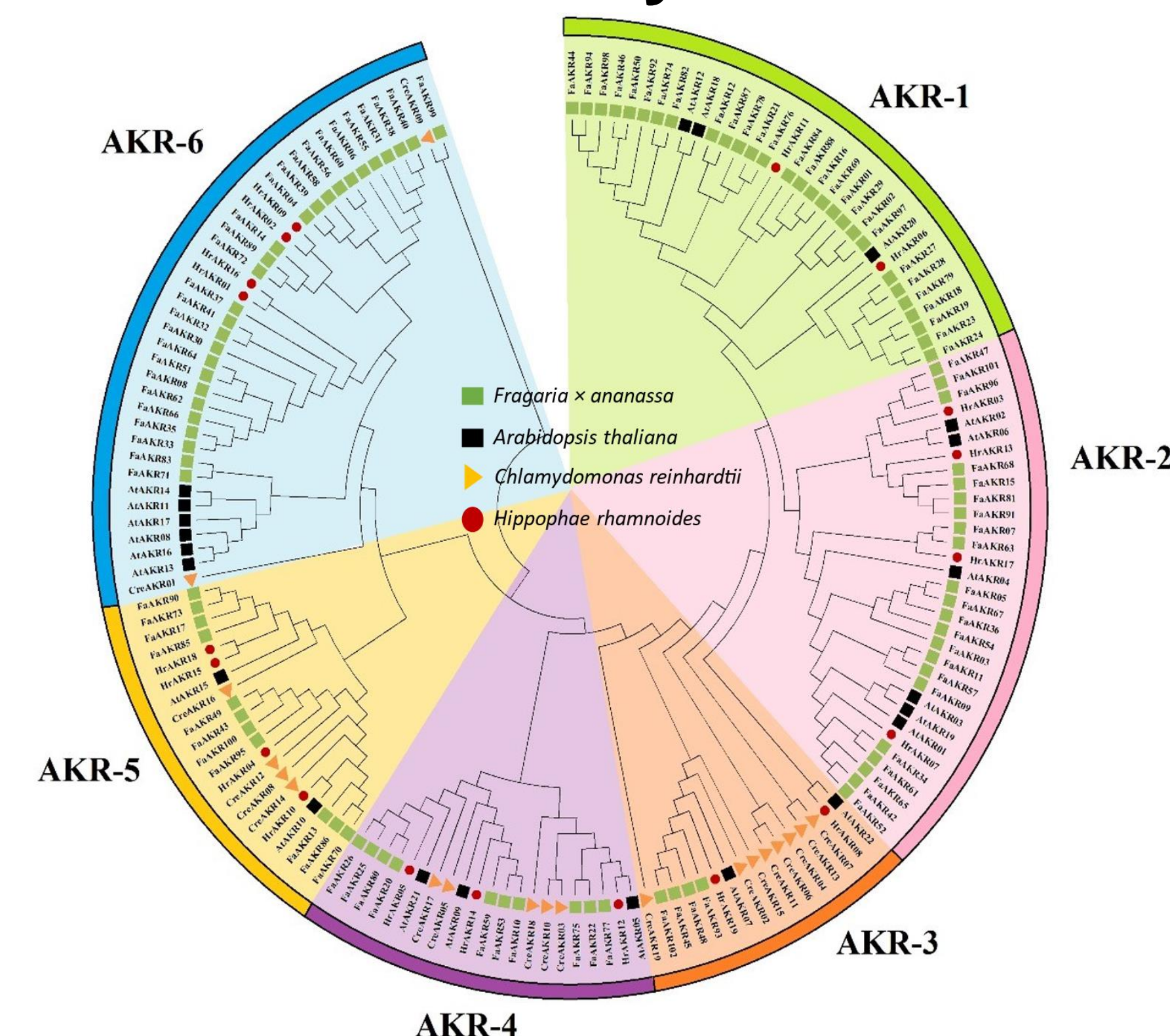


Fig. 5: Phylogenetic tree of *H. rhamnoides*, *A. thaliana*, *F. ananassa*, and *C. reinhardtii* AKR members. Most *HrAKRs* showed close association with *AtAKRs*.

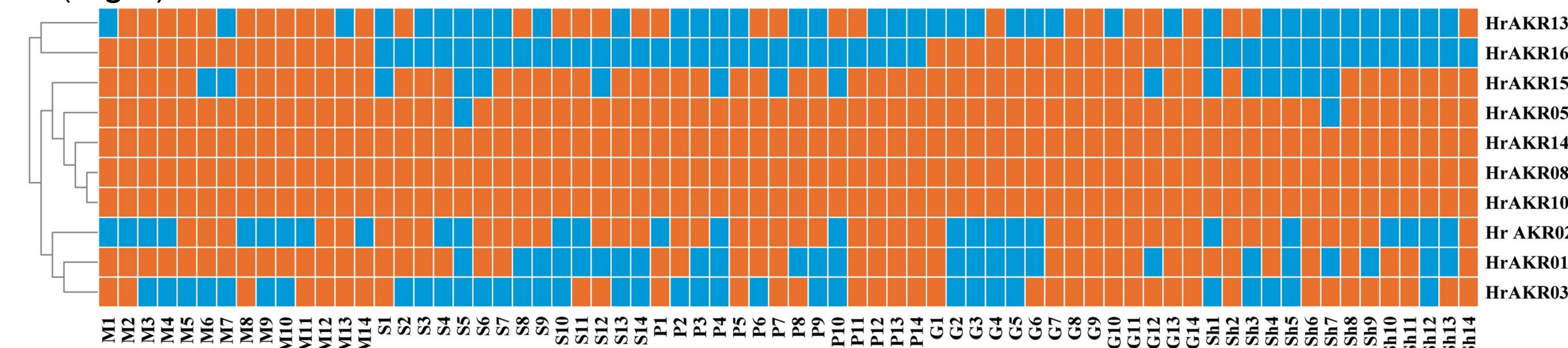


Fig. 6: Presence/absence of *HrAKRs* in 70 sea-buckthorn accessions. Gene IDs are presented vertically, accessions presented at the bottom. Orange color indicates presence while blue color indicates absence of the gene.

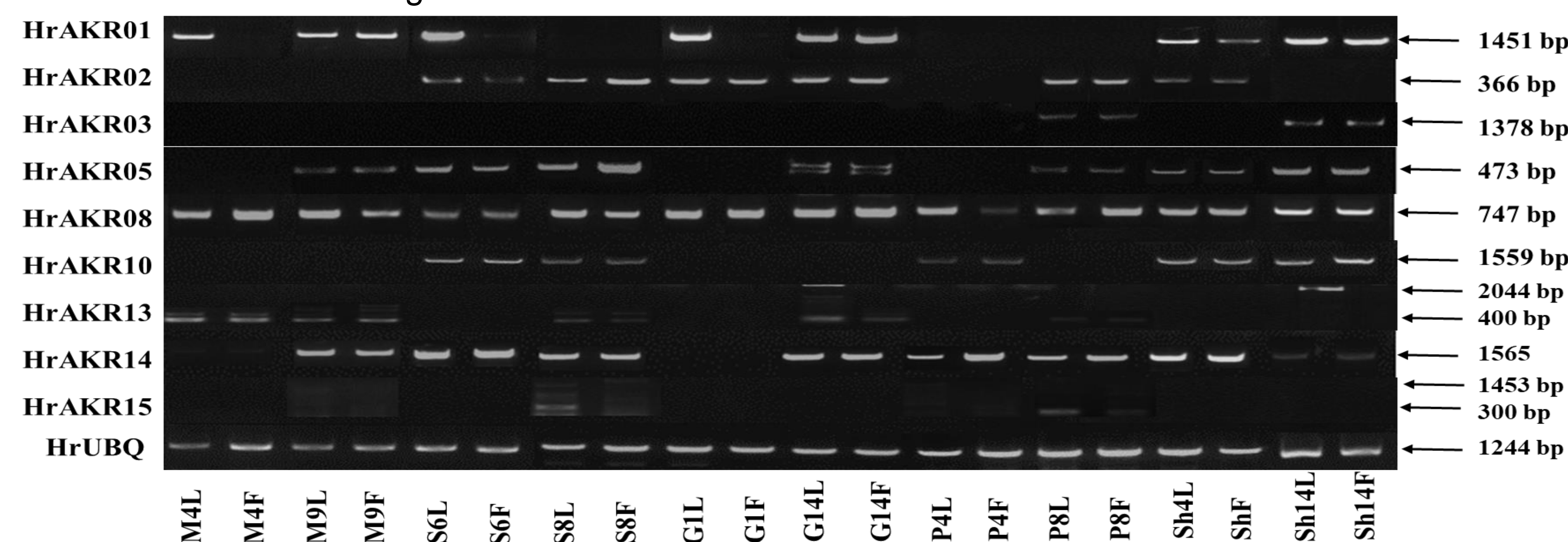


Fig. 7: Expression profile of *HrAKR01*, 02, 03, 05, 08, 10, 13, 14, 15 and *HrUBQ* in leaf and fruit tissues. F: fruit, L: leaf.