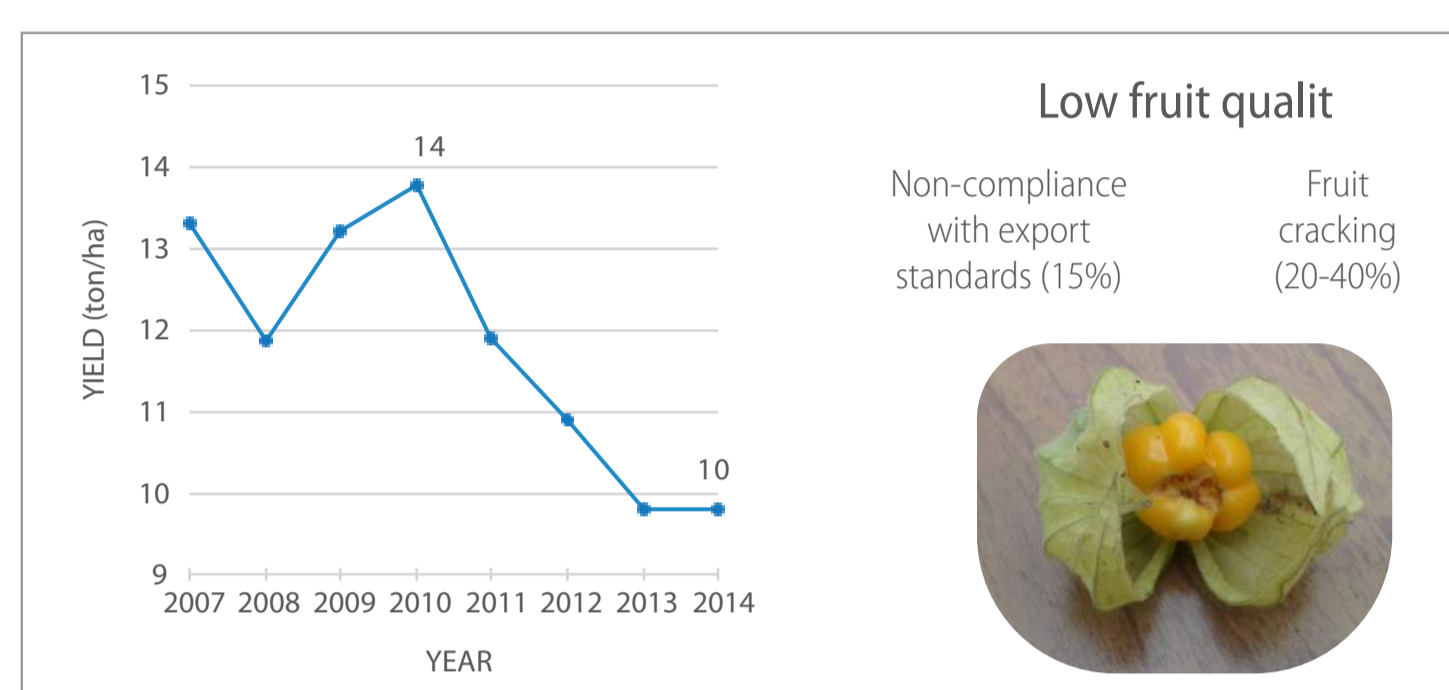


## Introduction

Cape gooseberry (*Physalis peruviana*, L.) is an exotic fruit that belongs to the Solanaceae family and it is well known for its nutritional value (high contents of vitamins A, C, B complex, phosphorus, calcium and iron), besides its health benefits as antioxidant, anti-inflammatory and anti-hepatotoxic activity (Ramadan et al., 2015). Colombia is the world's top producer of this fruit followed by South Africa and it is the second fruit in Colombian exports of fresh fruits, following the banana (Bonilla et al., 2009; Agronet, 2015). However, the yield and fruit quality do not satisfy the required standards for the market due the lack of high yield and cracking resistant varieties.

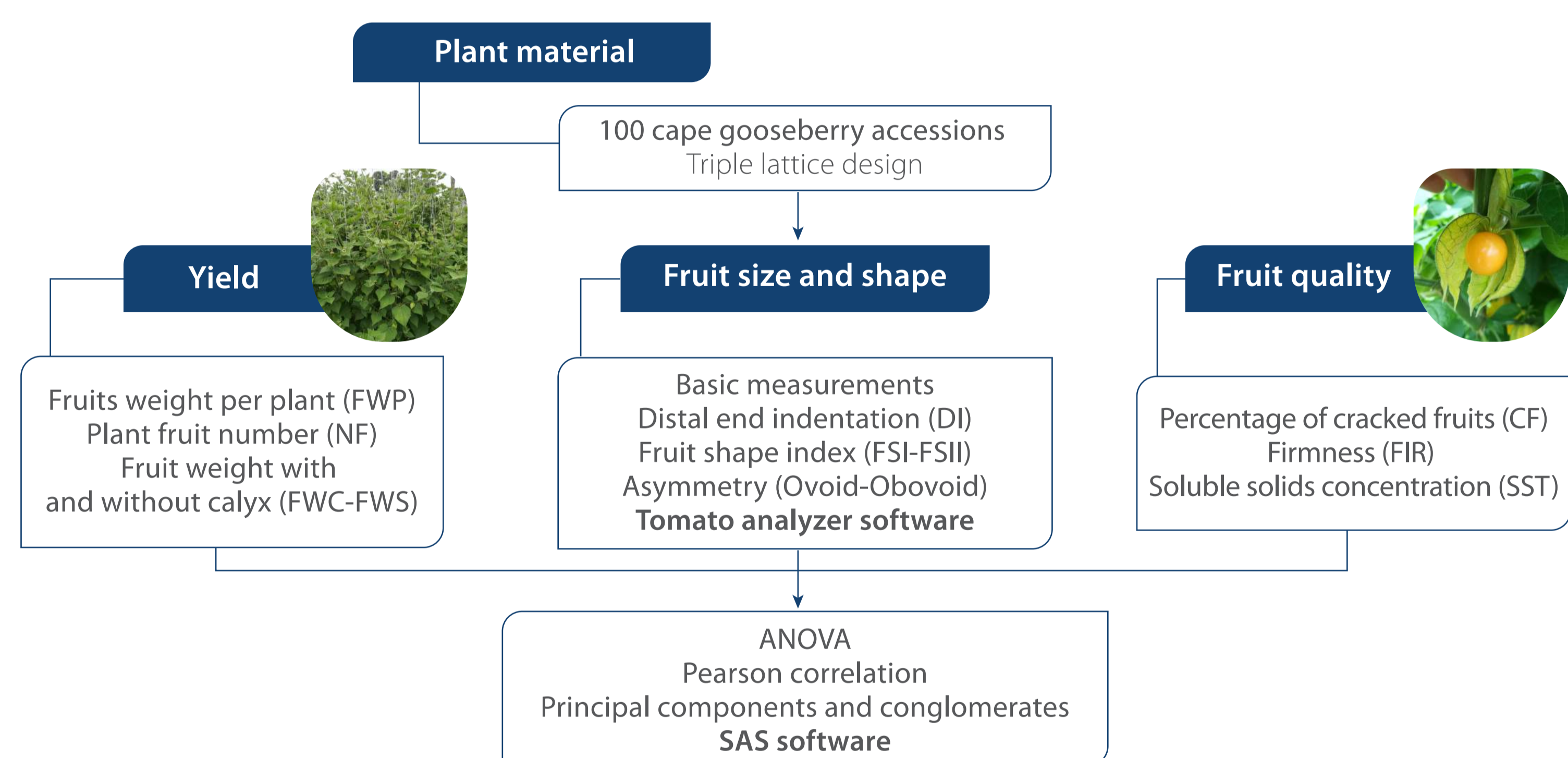
To understand genetic basis Increase the knowledge of genetic architecture of fruit quality and yield traits in cape gooseberry will provide advantages in the assessment of genetic diversity, cultivar identity and the development time of new varieties through the use of marker-assisted selection (MAS) (Chhetri et al., 2017; Favoretto et al., 2017).

The aim of the present study was to determinate molecular markers associated with yield, fruit size and quality through the evaluation of 18 phenotypic traits and genetic diversity of 100 cape gooseberry accessions from Corpoica's germplasm, as basis for future MAS and identify of promissory accessions that contribute to the cape gooseberry's breeding programs.

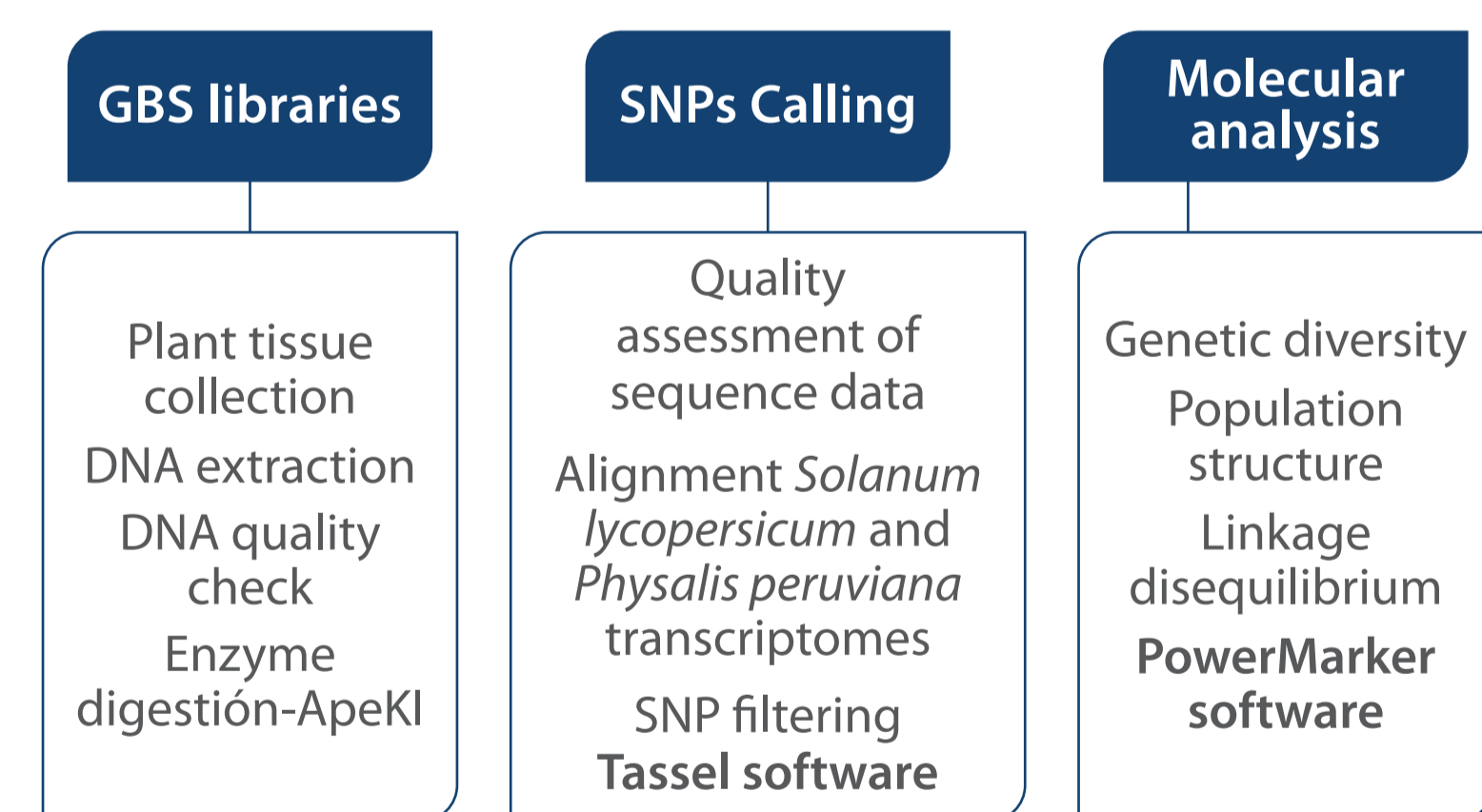


## Methodology

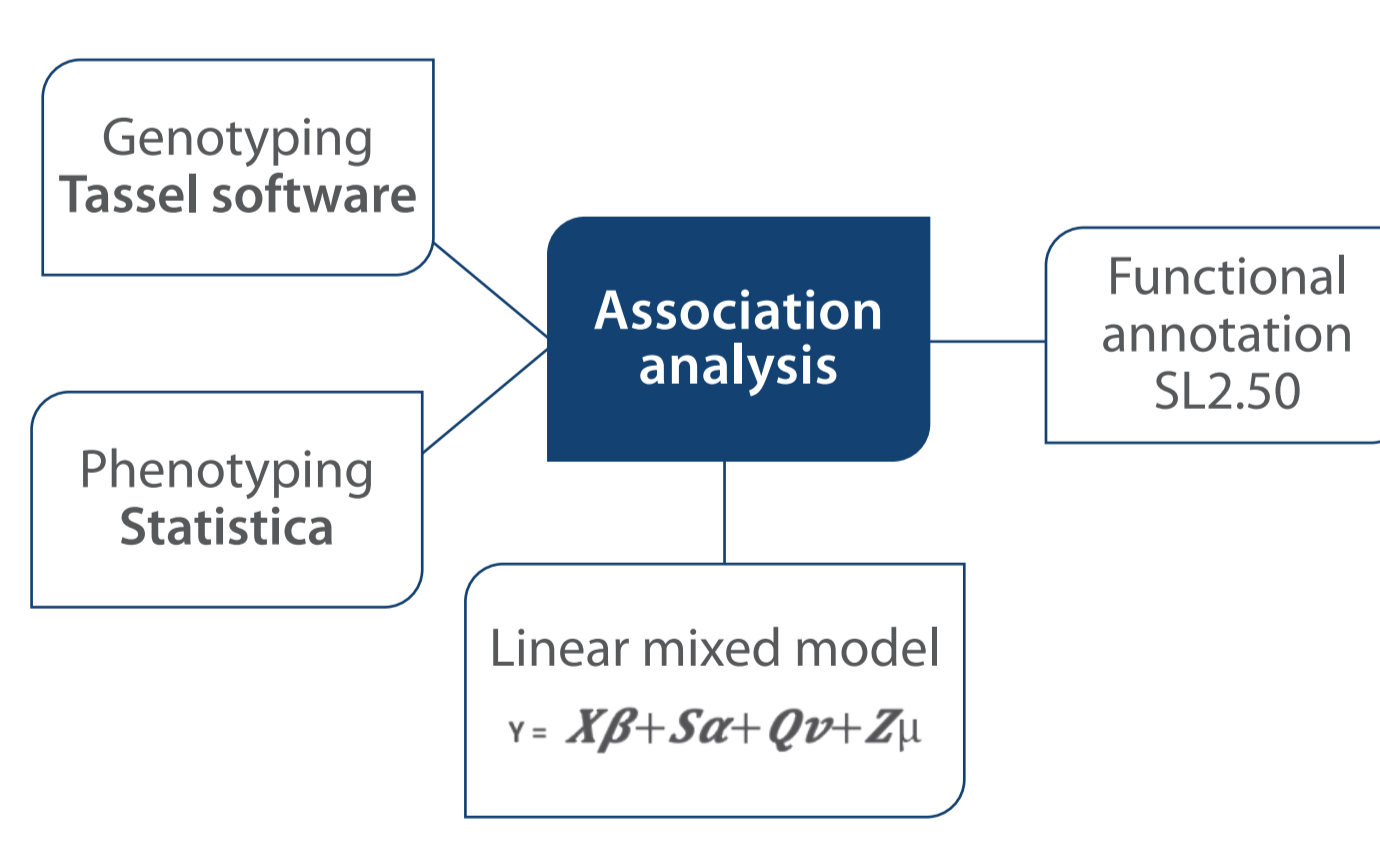
### Plant material and phenotyping



### Genotyping



### Association analysis



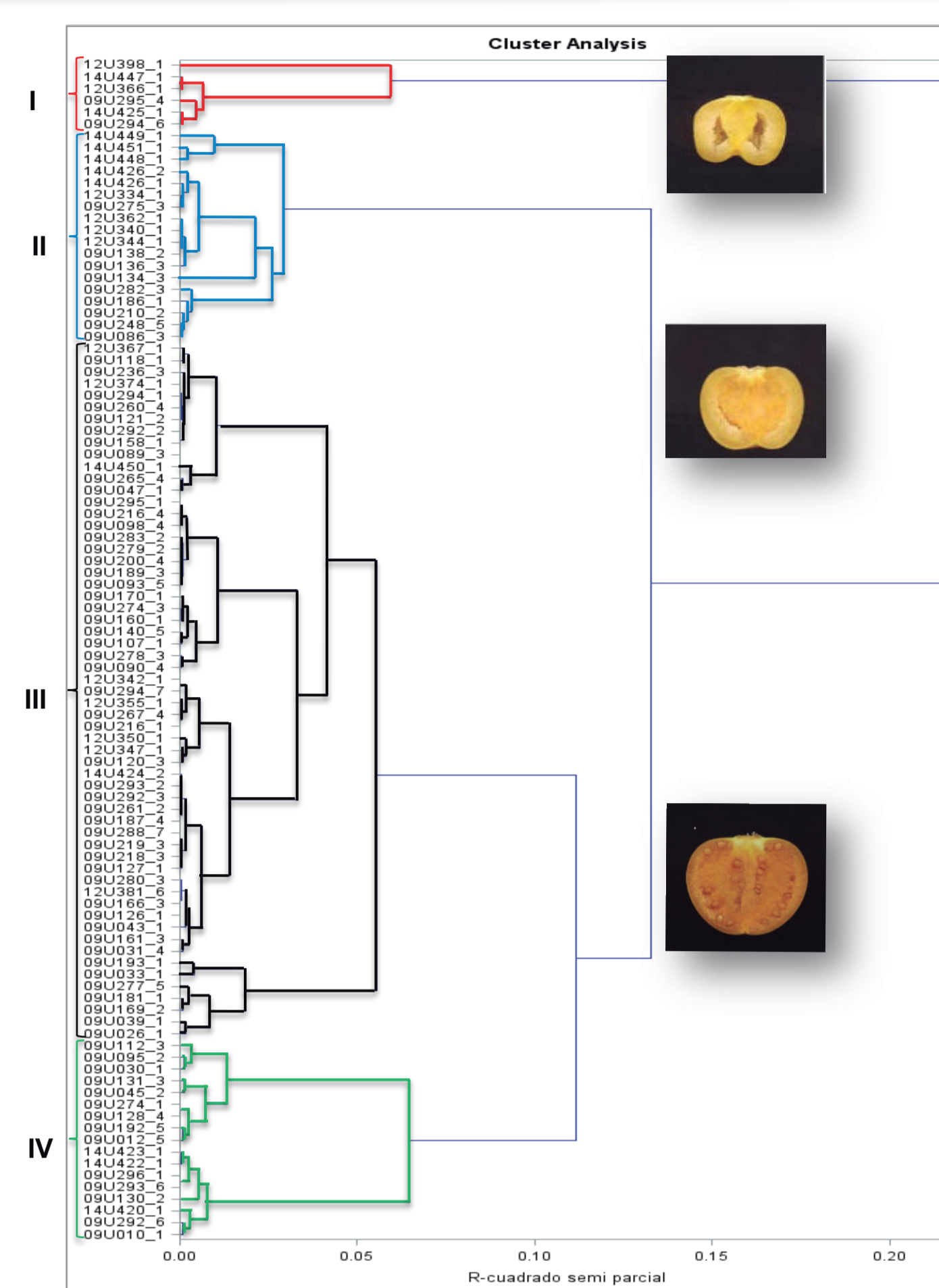
## Results

**Tabla 1.** Phenotypic variation of 18 traits analyzed in the entire collection

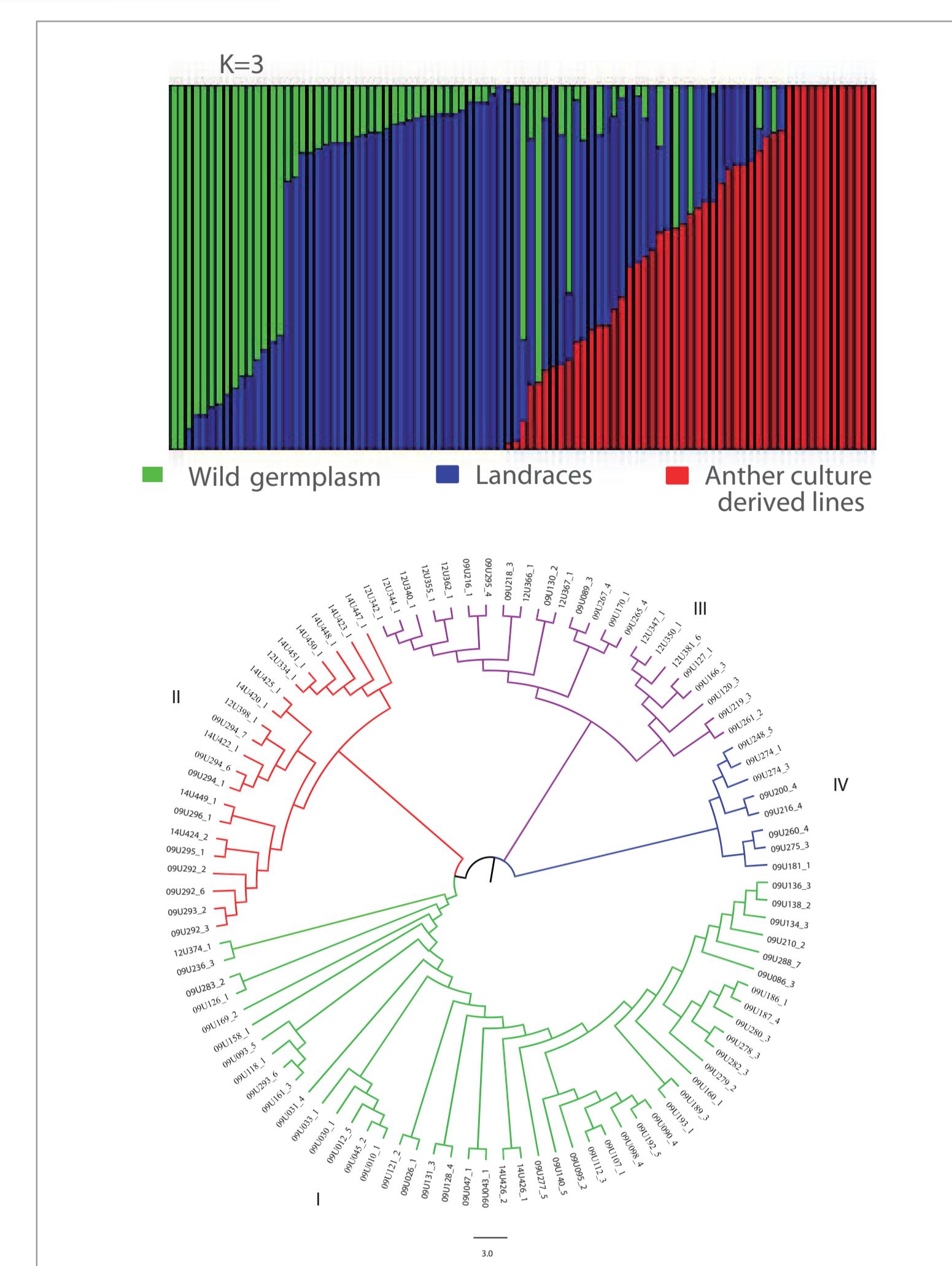
| Component     | Trait                                | Units           | Minimum | Maximum | Mean    | CV    |
|---------------|--------------------------------------|-----------------|---------|---------|---------|-------|
| Yield         | Fruits weight per plant (FWP)        | g/plant         | 22.44   | 8304.51 | 3863.45 | 47.45 |
|               | Number of fruits (NF)                | N°/plant        | 81.94   | 1471.79 | 685.25  | 46.18 |
|               | Weight of fruits with calyx (FWC)    | g/fruit         | 0.26    | 10.69   | 5.75    | 9.63  |
|               | Weight of fruits without calyx (FWS) | g/fruit         | 0.15    | 9.24    | 4.73    | 10.54 |
| Fruit size    | Fruit perimeter (FP)                 | cm              | 2.98    | 8.87    | 6.85    | 5.42  |
|               | Fruit area (FA)                      | cm <sup>2</sup> | 0.55    | 5.20    | 3.28    | 9.75  |
|               | Fruit maximum width (WM)             | cm              | 0.96    | 2.81    | 2.07    | 5.56  |
|               | Fruit width Mid-height (WHM)         | cm              | 0.93    | 2.78    | 2.06    | 5.54  |
|               | Fruit maximum height (HM)            | cm              | 0.76    | 2.3     | 1.93    | 4.50  |
|               | Fruit height mid-width (HMW)         | cm              | 0.63    | 2.25    | 1.90    | 4.51  |
| Fruit shape   | Distal end indentation area (DI)     | cm <sup>2</sup> | 0       | 0.18    | 0.0092  | 42.65 |
|               | Fruit shape index external I (FSI)   | -               | 0.70    | 1.06    | 0.93    | 3.17  |
|               | Fruit shape index external II (FSII) | -               | 0.68    | 1.06    | 0.92    | 3.56  |
|               | Asymmetry ovoid (OVO)                | -               | 0       | 0.21    | 0.15    | 9.51  |
|               | Asymmetry obovoid (OBO)              | -               | 0       | 0.18    | 0.0093  | 71.34 |
| Fruit quality | Cracked fruits percentage (CF)       | %               | 0       | 59.27   | 6.34    | 88.66 |
|               | Firmness (FIR)                       | lb-f            | 0.69    | 2.23    | 1.67    | 7.53  |
|               | Soluble solids concentration (SST)   | °Brix           | 13.12   | 17.27   | 14.85   | 3.47  |

**Tabla 2.** Genetic variability estimates of cape gooseberry collection

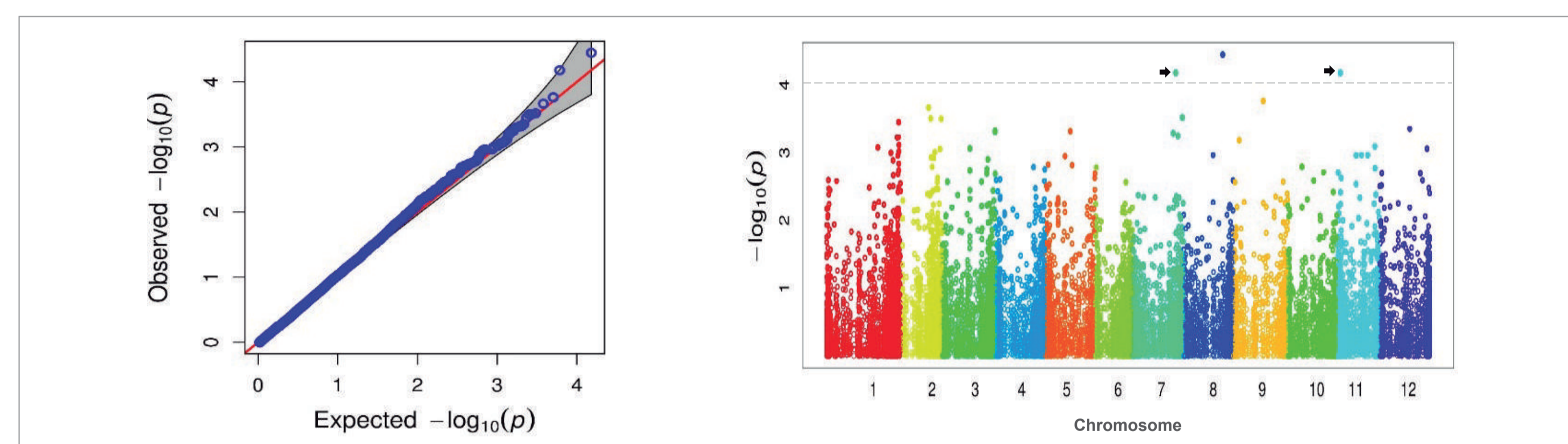
| Transcriptomes/genome reference | SNPs Default parameters | Filtered SNPs | H <sub>o</sub> | H <sub>e</sub> | PIC   |
|---------------------------------|-------------------------|---------------|----------------|----------------|-------|
| Leaf cape gooseberry            | 45,184                  | 27,982        | 0.731          | 0.447          | 0.343 |
| Root cape gooseberry            | 58,887                  | 36,142        | 0.733          | 0.449          | 0.344 |
| Tomato genome                   | 50,805                  | 30,344        | 0.711          | 0.439          | 0.338 |
| Media                           |                         |               | 0.725          | 0.445          | 0.342 |



**Figure 1.** Cluster dendrogram of cape gooseberry collection using 18 phenotypic traits based on ward method. Obtained from four principal components of yield, fruit shape, size and quality traits.



**Figure 2.** Population structure of cape gooseberry collection based on 30,344 SNPs markers.



**Figure 3.** Quantile-quantile (Q-Q) and manhattan plots showing significant associations for firmness.

**Table 3.** Association statistics of loci most significantly associated with cape gooseberry traits.

| Trait                             | SNP marker                   | Ch. | Locus            | Anotación                       | LOD Score | PVE         |
|-----------------------------------|------------------------------|-----|------------------|---------------------------------|-----------|-------------|
| Yield / Fruit weight / Fruit size | S03_52616353                 | 3   | Solyc03g082690.2 | U-box domain-containing protein | 4.0 - 4.7 | 17.9 - 21.4 |
| Fruit weight / size               | S03_70268245                 | 3   | Solyc03g123410.1 | Oxalate oxidase-like germin     | 4.1 - 4.6 | 17.8 - 20.6 |
| Fruit weight / size               | S06_2049586                  | 6   | Solyc06g008160.2 | Chloroplast FLU-like protein    | 4.0 - 4.7 | 17.4 - 21.4 |
| Fruit cracking                    | S06_45033846<br>S06_45033861 | 6   | Solyc06g073100.2 | GDSE esterase/lipase            | 4.01      | 15.23       |
| Fruit firmness                    | S07_57560621                 | 7   | Solyc07g043610.2 | Auxin response                  | 4.18      | 18.43       |

## Conclusions

The association mapping population used in this study showed high phenotypic and genetic variability and seven promissory accessions. The population were sub-divided into three sub-groups corresponding to wild, landraces and anther culture derived lines. The association analysis allowed the detection of 34 SNP markers related with the main fruit traits that can be useful in marker-assisted selection for cape gooseberry breeding program.

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