



The HARNESSTOM repository of promising tomato genotypes selected for direct cultivation by farmers



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Background

During the last years significant efforts have been made within the framework of European publicly funded research projects to characterize the genetic diversity of cultivated tomato¹. As a result phenotypic databases have been published, but their complexity renders difficult for farmers to “navigate” and select among thousands of accessions. **In order to facilitate the transfer of superior genotypes to farmers, chefs and citizens we reviewed the phenotypic and genotypic information collected for more than 3,000 accessions, including crop wild relatives, landraces and breeding lines. The selected genotypes will be included in an open-access repository to be transferred to farmers, chefs and citizens throughout participatory strategies (Participatory Plant Breeding² and Citizen Science).**

References: ¹Asins et al., 2015, Theor. Appl. Gen., 128:667-679; Barchi et al., 2019, Front. Plant Sci.,10:1005; Blanca et al., 2022, J. Exp. Bot., 73:3431-3445; Bouzayen et al., 2017, Impact, 1:31-33; Pons et al., 2022, Hortic. Res., uhac112; ² Ceccarelli et al., Euphytica, 2007, 155:349-360.

Methodology

We reviewed the phenotypic data of accessions characterized in the TRADITOM (1,700 accessions), TOMGEM (658), G2PSOL (435), ROOTPOWER (150), and BRESOV (404) projects. Six selection criteria were applied separately in each project (Figure 1) and the best accessions were selected. Subsequently, the first draft of the repository was analyzed in order to study its phenotypic diversity, to check for duplicates, and to identify under-represented phenotypes.

Phenotypic data:
3,000 accessions

Selection criteria (6) used to select
“promising genotypes”



- breeder's notes
- phenotypic data
- renowned landraces
- pathogen resistance
- heat stress tolerance
- use as rootstock

Figure 1. Tomato collections screened in this study and selection criteria applied.

Results: the HARNESSTOM repository of promising genotypes

As a result of the collaborative selection process, a repository has been created with 241 accessions selected from the BRESOV (56), G2PSOL (60), ROOTPOWER (3), TOMGEM (32), and TRADITOM (90) projects. Most of the accessions have been selected based on qualitative evaluations made by breeders in the field (35.3%), on the re-analysis of the phenotypic data (29.0%) or because of the presence of resistance to diseases or tolerance to heat stress (24.5%) (Figure 2). 24 accessions have been selected by using 2 criteria at the same time, being potentially superior genotypes. The selected accessions belong to the different tomato horticultural groups (processing, 17.8%; cherry, 6.2%; LSL, 15.8%; fresh market, 50.6%), and display a wide phenotypic diversity for plant, fruit and quality traits (fruit weight: 1.5-700.9 g; SSC, 2.7-9.6 °Brix) (Figures 3-4). A total of 39 accessions (16.2% of the selected ones) have tolerance or resistance to different diseases that affect the tomato crop (*Fusarium*, *Verticillium*, ToMV, TYLCV, TSWV, *Pseudomonas*, *Phytophthora*).

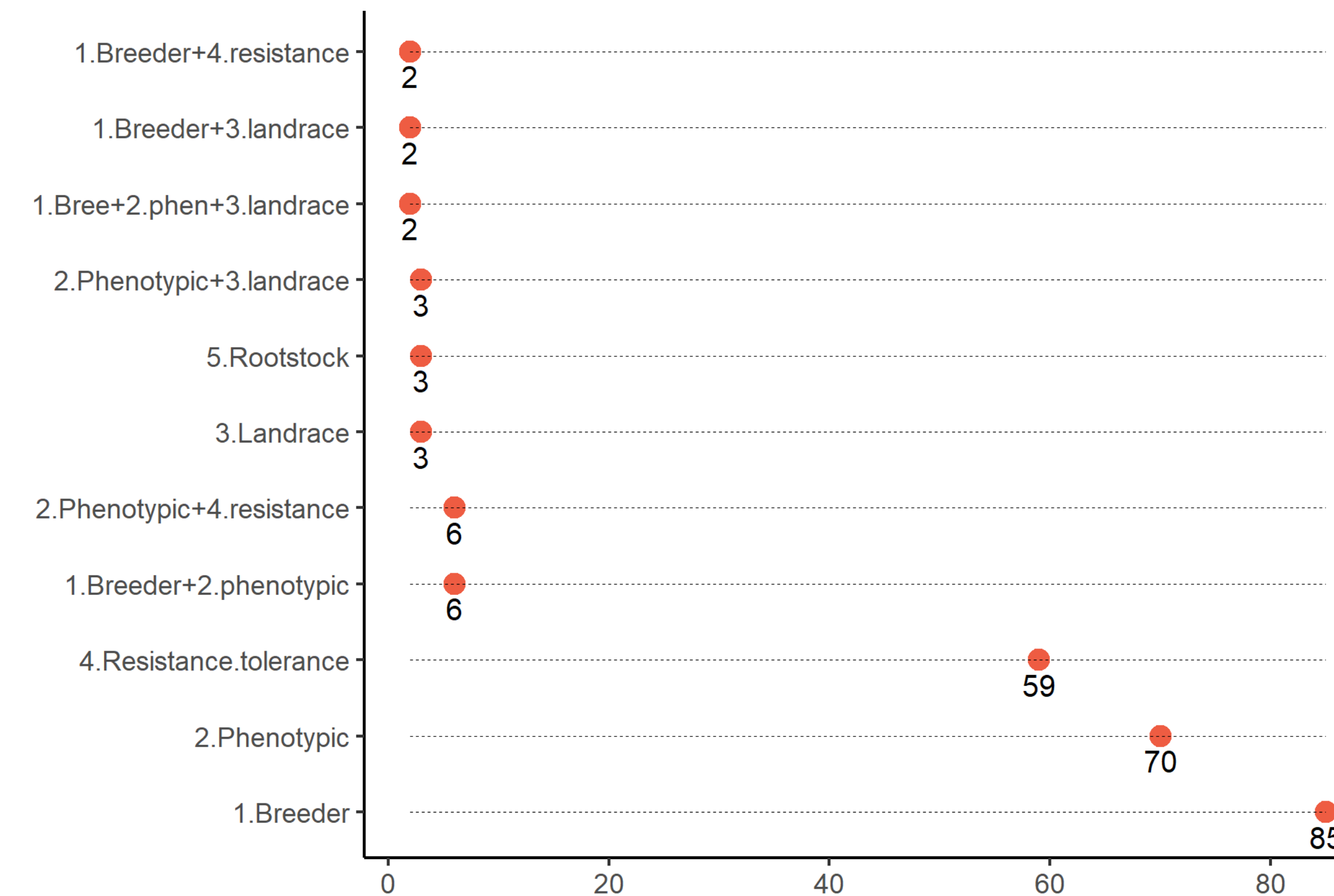


Figure 2. Number of accessions selected for each criterion.

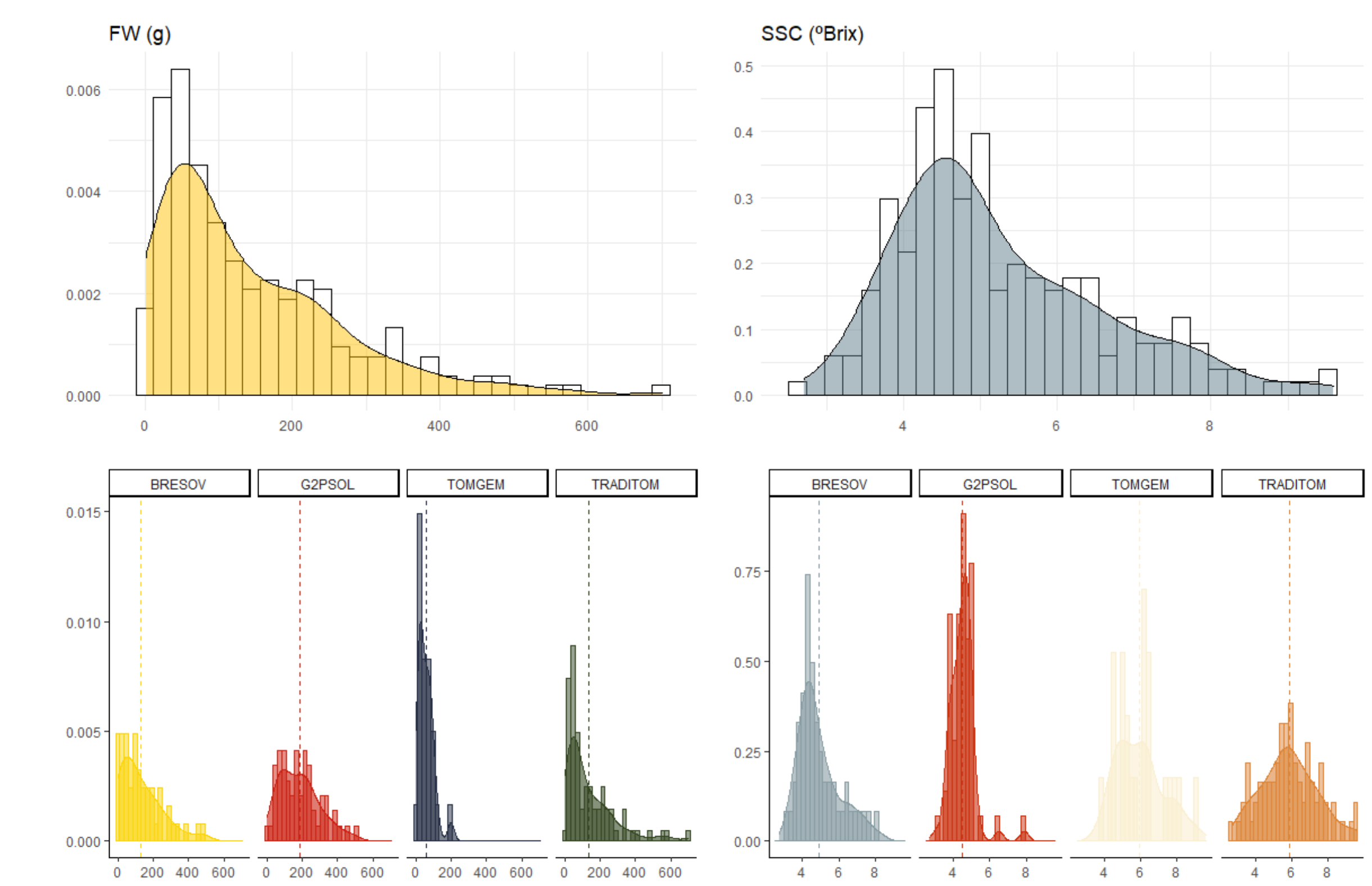


Figure 3. Fruit weight (FW) and Soluble Solids Content (SSC) diversity in the HARNESSTOM repository: whole collection (above) and diversity from each project (below).



Figure 4. Variability in fruit traits in some selected landraces from the G2P-SOL project.

CONCLUSIONS

The re-analysis of the phenotypic data of 3,000 accessions from former EU-projects enabled us to select 241 tomato genotypes based on 6 selection criteria. Participatory Plant Breeding (PPB) and Citizen Science (CS) methodologies are being deployed in order to transfer these materials and their phenotypic information to farmers, chefs and citizens. In parallel, the collection will be genotyped in order to gain knowledge on the genetic diversity and structure of the repository.