Comparing results of phenotypic characterization and genetic fingerprints for traditional sweet cherry varieties

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Cherry Projects BOKU
Old regional cultivars

• 2011: Stoob, Burgenland
• Sweet cherry collection BOKU

• 2012: Leithaberg, Burgenland
• 2012: Survey community Purbach
• 2013: Scharten, Upper Austria
• 2013: Anthocyanins in cherry juice
Methods Survey and phenotypic characterization
Selection of stable parameters

Fruit description

- Fruit form index
- Pedicel length
- Pedicel width
- Pedicel removal force
- Stone index
- Stone:fruit ration

Methods Fingerprinting

STSM – East Malling Research

• 10 of 16 markers recommended by ECPGR*
• 2 markers for fruit size**
• ECPGR* and US standard cultivars
• Multiplex PCRs: size of fragments: small + large, medium
• Fragment length on ABI-Sequencer
• Genotyper, GeneScan, R

**Olmstead et al. (2008) Construction of an intra-specific sweet cherry (Prunus avium L.) genetic linkage map and synteny analysis with the Prunus reference map. Tree Genetics & Genomes, 4.
Zhang et al. (2010) Fruit size QTL analysis of an F_1 population derived from a cross between a domesticated sweet cherry cultivar and a wild forest sweet cherry. Tree Genetics & Genomes, 6:25-36
Data analysis

Phenotypic data:
SPSS 21: cluster analysis (squared Euclidean distance) dendrogram

Genotypic data:
Excel -> R, package poppr*
Dendrogram UPGMA with Bruvo’s distance

Genotype vs. phenotype
Conclusions

- Probable Synonyms „Schneiders-Type“
- Cultivar identification verified by genetic fingerprint
- Distinct similarity-distribution in dendrogram phenotype vs. genotype
- Groups of the same variety cluster in both dendrograms
Thank you for your attention!