Genetic characterization of almond (Prunus dulcis) cultivars and natural resources
Hungary is a small country in Europe, but...

...is a geographical and historical link between the main growing countries in Western Europe and Asian gene centres of tree fruits.
Almond as an outbreeding species

- one of the oldest domesticated plants in Old World agriculture
- almond cultivars have been propagated by seeds until the 19th century
- strictly allogamous (GSI)
- ~50 S-alleles have been identified in USA, Spanish, Italian and French cultivars
- $S_f$ : allows for self-compatibility
Objectives of this study

• To estimate the level of local genetic diversity

• To compare Hungarian allelic profiles with genotypes from different geographic areas and elucidate phylogenetic relationships among accessions

• To analyse the impact of domestication

• To compare the genetic background of almond with those of apricot and peach
Plant material

Total of 110 genotypes

3 wild species (*Prunus tenella*, *P. webbii*, *P. arabica*)

Plant material

Tétényi-fennsík 12 accessions
Gellérthegy 11 accessions
Cegléd 10 accessions
Monor 3 accessions
+ 9 Hungarian cultivars
+ 3 Ukrainian cultivars
ILP - intron length polymorphisms

*in silico* sequence analyses

Methodology

1. ILP - intron length polymorphisms

   in silico sequence analyses

   1. intron region

   PaCons1-F

   EM-PC1consRD

   2. intron region

   EM-PC2consFW

   EM-PC3consRD

   RHV

Case 1

Case 2

Case 3

field pollination to validate phenotypically the molecular results
<table>
<thead>
<tr>
<th>Primer name</th>
<th>Locus type</th>
<th>Linkage group</th>
<th>Species</th>
<th>Reference</th>
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<tr>
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</tbody>
</table>

### Methodology

#### 3.

16 SSR primer pairs

**ABI PRISM 3100 Genetic Analyzer**

**Genotyper 3.7 software**

**GS500 LIZ size standard (Applied Biosystems)**

**Popgene 1.32**

**TREEVIEW program**

**STRUCTURE 2.3.4**

**STRUCTURE Harvester**
S-locus genotyping on almonds of Eastern Europe

S_{31H}

259 \quad 1340

344 \quad 1531

S_{36}

110 \quad 294

195 \quad 485

S_{37}

309 \quad 1347

394 \quad 1538

S_{38}

259 \quad 1078

344 \quad 1269

approx. 1460

S_{39}

195 \quad 1650

283

2nd intron

2000 bp

1500 bp

1000 bp

500 bp

250 bp

1st intron

750 bp

500 bp

250 bp

S_{31H} \quad S_{36} \quad S_{37} \quad S_{38} \quad S_{39}

S_{31H} \quad S_{36} \quad S_{37} \quad S_{38} \quad S_{39}

S_{10} \quad S_{28} \quad S_{11} \quad S_{11} \quad S_{28}

S_{6} \quad S_{6} \quad S_{6} \quad S_{6} \quad S_{6}

S_{6} \quad S_{6} \quad S_{13} \quad S_{13}

S_{6} \quad S_{6}

SzCs 58 SzCs 55 SzCs 55 SzCs 92 Vinosiwyi Öriás kagyló Öriás kagyló Eriane Marie Dupui Mold. 810 Mold. 812 Nik. 707 Nik. 3576 Nik. 2240 Pozényi Hybrid 1 Hybrid 2 Tét. ből Tét. rek. Tét. kem. Tét. kedv.
Genetic relationships among cultivars and genotypes of various origins
# Genetic diversity parameters

<table>
<thead>
<tr>
<th>Geographic groups</th>
<th>Hungarian cultivars</th>
<th>Gellért-hegy</th>
<th>Tétény-fennsik</th>
<th>Old Hungarian genotypes</th>
<th>Californian cultivars</th>
<th>Akdamar Island</th>
<th>Bademli region</th>
<th>Morocco</th>
<th>Self-compatible cultivars</th>
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</thead>
<tbody>
<tr>
<td>Number of alleles (na)</td>
<td>5.27</td>
<td>5.18</td>
<td>5.45</td>
<td>5.09</td>
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<td>4.05</td>
<td>5.09</td>
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<td>3.63</td>
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<tr>
<td>Shannon's Information index (I)</td>
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<td>1.41</td>
<td>1.45</td>
<td>1.35</td>
<td>1.02</td>
<td>1.06</td>
<td>1.28</td>
<td>1.60</td>
<td>1.06</td>
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<tr>
<td>Observed (Ho) heterozygosity</td>
<td>0.67</td>
<td>0.67</td>
<td>0.67</td>
<td>0.61</td>
<td>0.63</td>
<td>0.76</td>
<td>0.61</td>
<td>0.66</td>
<td>0.53</td>
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<tr>
<td>Expected (He) heterozygosity</td>
<td>0.71</td>
<td>0.75</td>
<td>0.75</td>
<td>0.71</td>
<td>0.63</td>
<td>0.64</td>
<td>0.66</td>
<td>0.75</td>
<td>0.64</td>
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<tr>
<td>Wright's fixation index ($F_{ST}$)</td>
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<td>0.52</td>
<td>0.52</td>
<td>0.54</td>
<td>0.45</td>
<td>0.34</td>
<td>0.52</td>
<td>0.55</td>
<td>0.50</td>
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<tr>
<td>Gene flow ($N_m$)</td>
<td>0.25</td>
<td>0.23</td>
<td>0.23</td>
<td>0.21</td>
<td>0.30</td>
<td>0.41</td>
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<tr>
<td>Number of samples</td>
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<td>11</td>
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<td>8</td>
<td>8</td>
<td>14</td>
<td>14</td>
<td>15</td>
<td>8</td>
</tr>
</tbody>
</table>

**case 1**

**case 2**

**case 3**
Case 1: Akdamar island

Akdamar island, Turkey
Genetic diversity

Number of different S-genotypes

Number of alleles from P. webbii
### Case 2: The erosive effects of modern breeding programs

<table>
<thead>
<tr>
<th>Pedigree of Californian cultivars</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Mission</strong></td>
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<tr>
<td><strong>Thompson</strong></td>
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<tr>
<td><strong>Nonpareil</strong></td>
</tr>
<tr>
<td><strong>Monterey</strong></td>
</tr>
<tr>
<td><strong>Ne plus ultra</strong></td>
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</tbody>
</table>
Evolution of self-compatibility in fruit trees - a case of domestication bottleneck
Distribution of the identified Prunus-specific miniature inverted repeat transposable elements, *Falling Stones* throughout the peach genome. Arrows indicate the orientation of the full length sequences and lines show fragmented copies. The approximate position of each centromere is indicated by an oval (not drawn to scale).
Genomic PCR analysis of 18 different Prunus species and 4 species outside the Prunus genus using the FaSt-specific primers.

Conclusions

- Our results supply long-awaited information on almond S-allele diversity from regions between the main cultivation centers and the centre of origin of this species.

- Almond showed huge level of allelic variability from Central Asia to California.

- Inter-specific hybridization contributes considerably to the maintaining of genetic diversity and geographical differentiation.
Reduced genetic variability can be effected by:

- geographical isolation (1st case)
- modern breeding programs (2nd case)
- self-compatibility (3rd case)

Breakdown of self-incompatibility has a powerful effect on shaping the genetic basis of a fruit tree species.

Our results contribute the knowledge on almond crop history.
This work was financed by
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and
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Vincent van Gogh:
Blossoming Almond Branch in a Glass with a Book