MICROSATELLITE DIVERSITY OF DALMATIAN SAGE POPULATIONS FROM THE BALKAN AND APENNINE PENINSULAS

Zlatko Šatović
University of Zagreb, Faculty of Agriculture, Zagreb, Croatia
Centre of Excellence for Biodiversity and Molecular Plant Breeding (CoE CroP-BioDiv), Zagreb, Croatia
E-mail: zsatovic@agr.hr

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CoE CroP-BioDiv

Host Institution

University of Zagreb, Faculty of Agriculture
Institute for Agriculture and Tourism Poreč
University of Zagreb, Faculty of Science
Agricultural Institute Osijek
Institute for Adriatic Crops Split
University of Osijek, Faculty of Agriculture

+ 5 Member Institutions
**OBJECTIVES**

- **Conservation of PGR**
- **Phenotyping**
- **Genotyping**
- **Bioinformatics**
- **Dissemination**

Conservation of Plant Genetic Resources >> increase the benefits
Phenotyping >> high-throughput phenotyping (HTP) platforms
Genotyping >> next-generation sequencing (NGS) techniques
Bioinformatics >> genome-wide association studies (GWAS)
Dissemination >> workshops, summer schools
MODEL PLANT SPECIES

Major Crops
- Maize
- Wheat
- Soybean

Traditional Crops
- Grapevine
- Olives

Promising Crops
- Brassicas
- Alliums
- Common bean
- Dalmatian pyrethrum
- Dalmatian sage

Promising Crops
MICROSATELLITE DIVERSITY OF Dalmatian Sage Populations from the Balkan and Apennine Peninsulas
(1) Natural distribution
(2) Genetic diversity
(3) Genetic structure
(4) Ecological niche modelling
NATURAL DISTRIBUTION OF DALMATIAN SAGE
- **samples:**
  
  62 populations / 1,350 plants
  
  Italy (13), Slovenia (2), Croatia (23), Bosnia and Herzegovina (2), Montenegro (7), Serbia (2), Albania (5), Macedonia (1), Greece (7)

- **molecular analysis:**
  
  8 microsatellite markers
  191 alleles
(1) Natural distribution
(2) Genetic diversity
(3) Genetic structure
(4) Ecological niche modelling
## GENETIC DIVERSITY

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Mean</th>
<th>Range</th>
</tr>
</thead>
<tbody>
<tr>
<td>Allelic richness ($N_{ar}$)</td>
<td>6.669</td>
<td>1.35-10.11</td>
</tr>
<tr>
<td>Observed heterozygosity ($H_O$)</td>
<td>0.665</td>
<td>0.081-0.832</td>
</tr>
<tr>
<td>Expected heterozygosity ($H_E$)</td>
<td>0.683</td>
<td>0.087-0.846</td>
</tr>
</tbody>
</table>

### Allelic richness ($N_{ar}$)

<table>
<thead>
<tr>
<th>Country</th>
<th>Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>ITA</td>
<td></td>
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<tr>
<td>SVN</td>
<td></td>
</tr>
<tr>
<td>HRV</td>
<td></td>
</tr>
<tr>
<td>BIH</td>
<td></td>
</tr>
<tr>
<td>MNE</td>
<td></td>
</tr>
<tr>
<td>SRB</td>
<td></td>
</tr>
<tr>
<td>ALB</td>
<td></td>
</tr>
<tr>
<td>MKD</td>
<td></td>
</tr>
<tr>
<td>GRC</td>
<td></td>
</tr>
<tr>
<td>Br.</td>
<td>Population</td>
</tr>
<tr>
<td>-----</td>
<td>------------</td>
</tr>
<tr>
<td>P38</td>
<td>Konavle</td>
</tr>
<tr>
<td>P41</td>
<td>Vrbanj</td>
</tr>
<tr>
<td>P35</td>
<td>Pelješac</td>
</tr>
<tr>
<td>P40</td>
<td>Mostar</td>
</tr>
<tr>
<td>P39</td>
<td>Međugorje</td>
</tr>
<tr>
<td>P34</td>
<td>Hvar</td>
</tr>
<tr>
<td>P45</td>
<td>Rumija</td>
</tr>
<tr>
<td>P28</td>
<td>Šparadići</td>
</tr>
<tr>
<td></td>
<td><strong>N_{ar} &gt; 9</strong></td>
</tr>
<tr>
<td>P59</td>
<td>Arta</td>
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<tr>
<td>P03</td>
<td>Maratea</td>
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<td>P04</td>
<td>Cilento</td>
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<tr>
<td>P52</td>
<td>Prespa</td>
</tr>
<tr>
<td>P01</td>
<td>Pollino 2</td>
</tr>
<tr>
<td>P02</td>
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</tr>
<tr>
<td>P06</td>
<td>Savoia</td>
</tr>
<tr>
<td>P10</td>
<td>d'Antino</td>
</tr>
<tr>
<td>P14</td>
<td>Novokračine</td>
</tr>
<tr>
<td>P11</td>
<td>M. Salviano</td>
</tr>
<tr>
<td>P12</td>
<td>Maiella</td>
</tr>
</tbody>
</table>
(1) Natural distribution
(2) Genetic diversity
(3) Genetic structure
(4) Ecological niche modelling
Bayesian model-based clustering method for inferring population structure

Assumption:
- there are K populations of origin each of which is characterized by a set of allele frequencies at each locus

Goal:
- assign individuals to populations of origin in such a way that within each population the departures from:
  (1) Hardy-Weinberg equilibrium (HWE) and
  (2) linkage equilibrium (LE) are minimized
- proportions of membership (Q) of each individual plant in each of the two clusters (populations of origin):
  - each individual plant is represented by a single vertical line divided into colors representing different clusters
  - the length of the colored segment shows the individual's estimated proportion of membership in that cluster
- the cluster B (Balkan) is at K = 3 split into two clusters according to geographical locations:
  North-West: Slovenia-Croatia-BiH
  South-East: Montenegro-Albania-Macedonia-Greece
\( K = 4 \)

\( K = 3 \)

Apennines

Balkans

Northern Adriatic

Southern Adriatic

Albania

Greece
GENETIC CLUSTERS

Cluster

A  Southern Apennines
B  Central Apennines
C  Northern Adriatic
D  Southern Adriatic
E  Albania Greece

Clusters

Clusters

Clusters

Clusters
Distance measure: net nucleotide distance
Tree algorithm: Neighbor-Joining

A: Southern Apennines
B: Central Apennines
C: Northern Adriatic
D: Southern Adriatic
E: Albania/Greece
(1) Natural distribution
(2) Genetic diversity
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ECOLOGICAL NICHE MODELLING

- species distribution modelling (SDMs)
  - estimate the relationship between species records at sites and the environmental characteristics of those sites
  - predict the suitability of sites for occupation or persistence of the species

- input data:
  (1) geographic distribution
      68 data on occurrence (evenly distributed)
  (2) environmental characteristics of the sites
      19 bioclimatic variables (WorldClim database)
Suitability:
- 0.23 - 0.45
- 0.45 - 0.68
- 0.68 - 0.90

ENM: PRESENT DAY CONDITIONS
(1) Balkans
- Leptosols
  Shallow soils over limestone

(2) Apennines
- Cambisol
  Moderately developed brown soil
Collaborators:
Danijel Škrtić
Ivan Radosavljević
Marija Jug-Dujaković
Romeo di Pietro
Zlatko Liber