



# Compiling unused *Vitis sylvestris* genetic data – update and further steps

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10.10.2023, Kavala



# Workshop recap: 29.11.2022 - 01.12.2022

The standard set comprises the 20 SSR markers:

VVS2, VVMD5, VVMD7, VVMD21, VVMD24, VVMD25, VVMD28, VVMD27, VVMD32, VrZAG62, VrZAG79, VMC1b11, VVIb01, VVIIn16, VVIh54, VVIIn73, VVIp31, VVIp60, VVIv37 and VVIq52.

It was decided to remove four SSR markers:

- Extremely polymorphic markers VVIV67 and VMC4F3.1 are difficult to adapt
- VrZAG67 and VrZAG83 are not often applied, resulting in too many missing data
- Already published datasets were integrated
- Allele sizes were harmonized across datasets

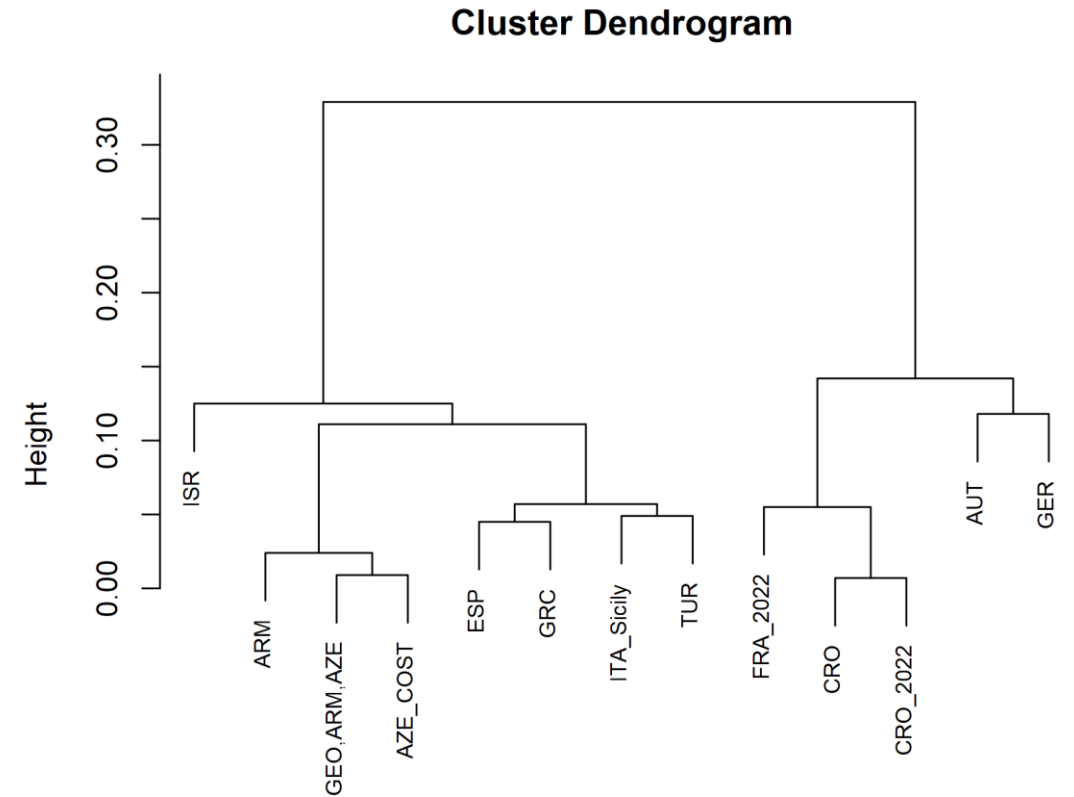
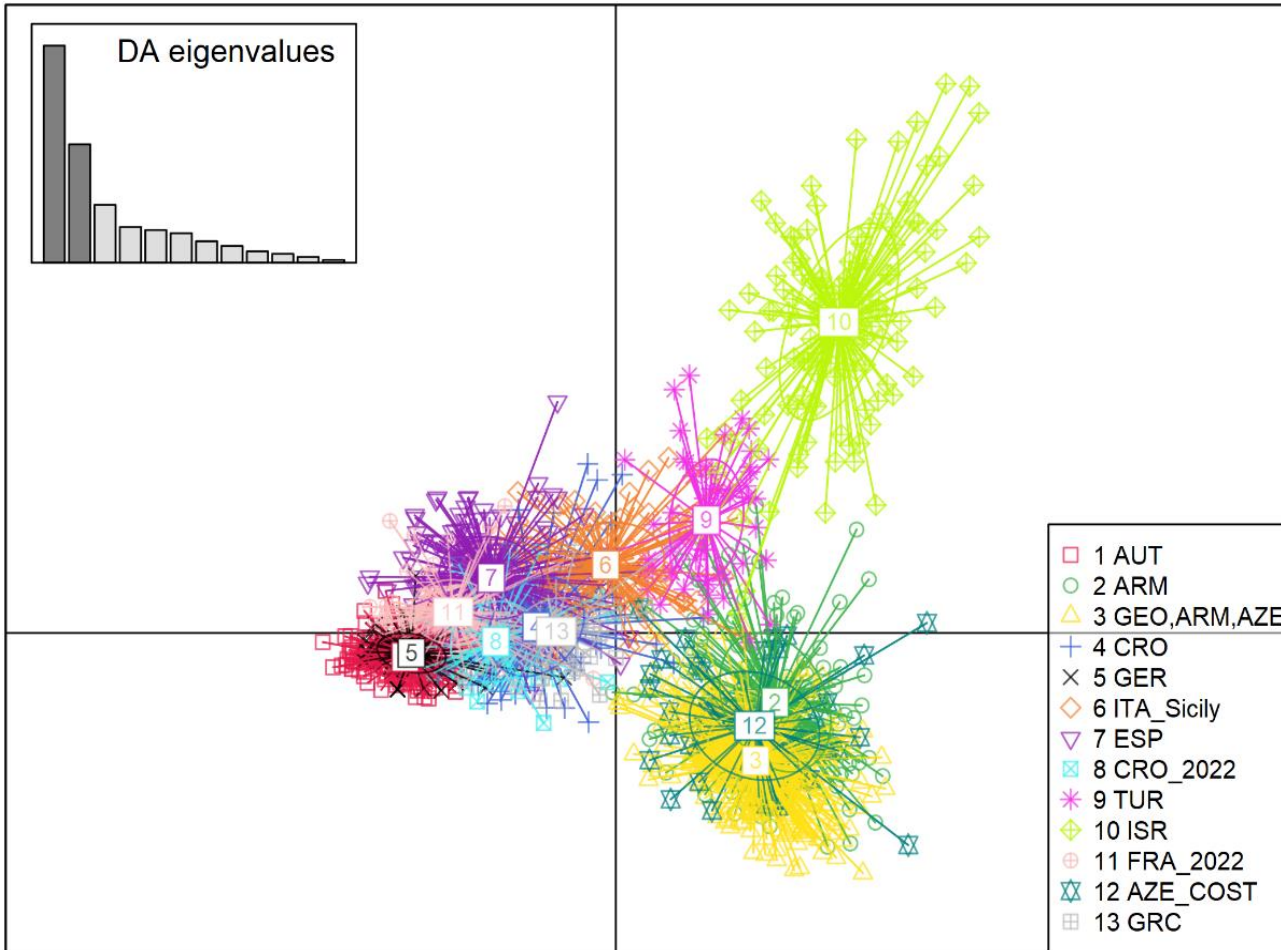


# Data sources

Data source	Published	Population name	Sample number
AUT_Danube (JKI-intern)	no	Pop1	179
ARM (Margaryan et al. 2021)	yes	Pop2	135
GEO,ARM,AZE (Riaz et al.2018)	yes	Pop3	371
CRO_etc.-Zdunic_2020_Riaz_2018	yes	Pop4	109
<b>France (Riaz et al. 2018)</b>	<b>yes</b>	<b>Pop5</b>	<b>46</b>
GEO_ (Imazio et al. 2013)	yes	Pop6	44
DEU_Ketsch (JKI-intern)	no	Pop7	74
<b>ITA_Peninsula_Biagini_2014 (Riaz et al. 2018)</b>	<b>yes</b>	<b>Pop8</b>	<b>286</b>
ITA_Sicily _de Michele_2019	yes	Pop9	121
ESP_de Andres_2011	yes	Pop10	192
CRO_2022 (Zdunic)	no	Pop11	52
TUR (Uzun)	no	Pop12	58
ISR: Drori et al. 2017; Rahimi et al. 2021	yes	Pop13	127
France_2022 (V. Laucou)	no	Pop14	109
AZE_COST Action_FA1003	no	Pop15	54
GRC (G. Merkouropoulos; only 9 markers)	no	Pop16	52
<b>Total</b>			<b>2009</b>

- Not all considered due to doubtful data quality

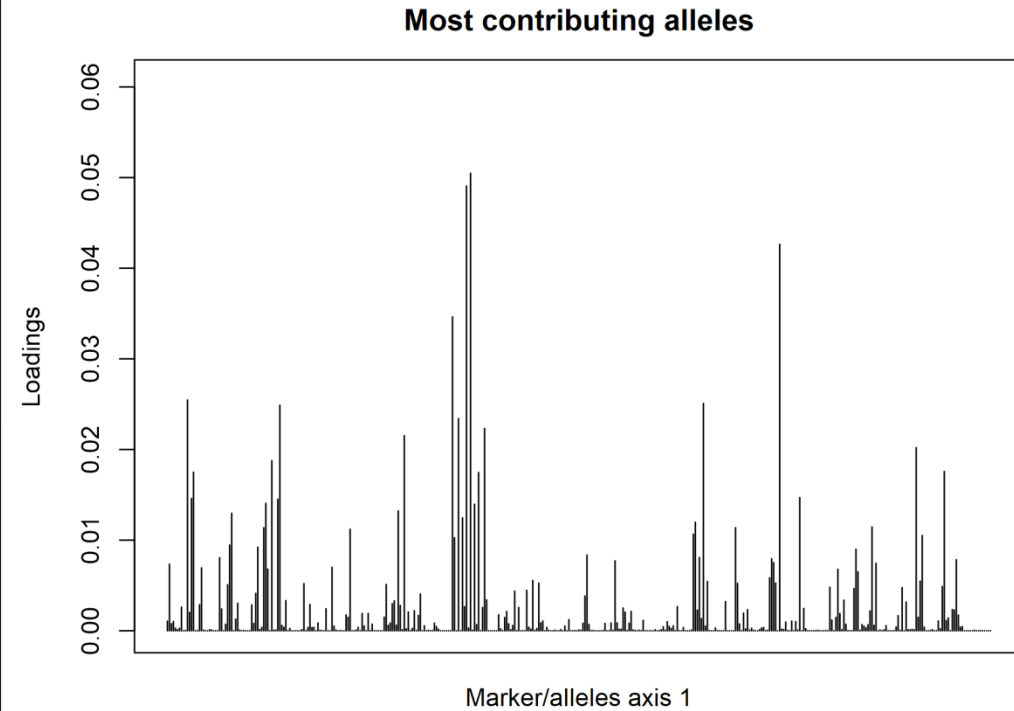
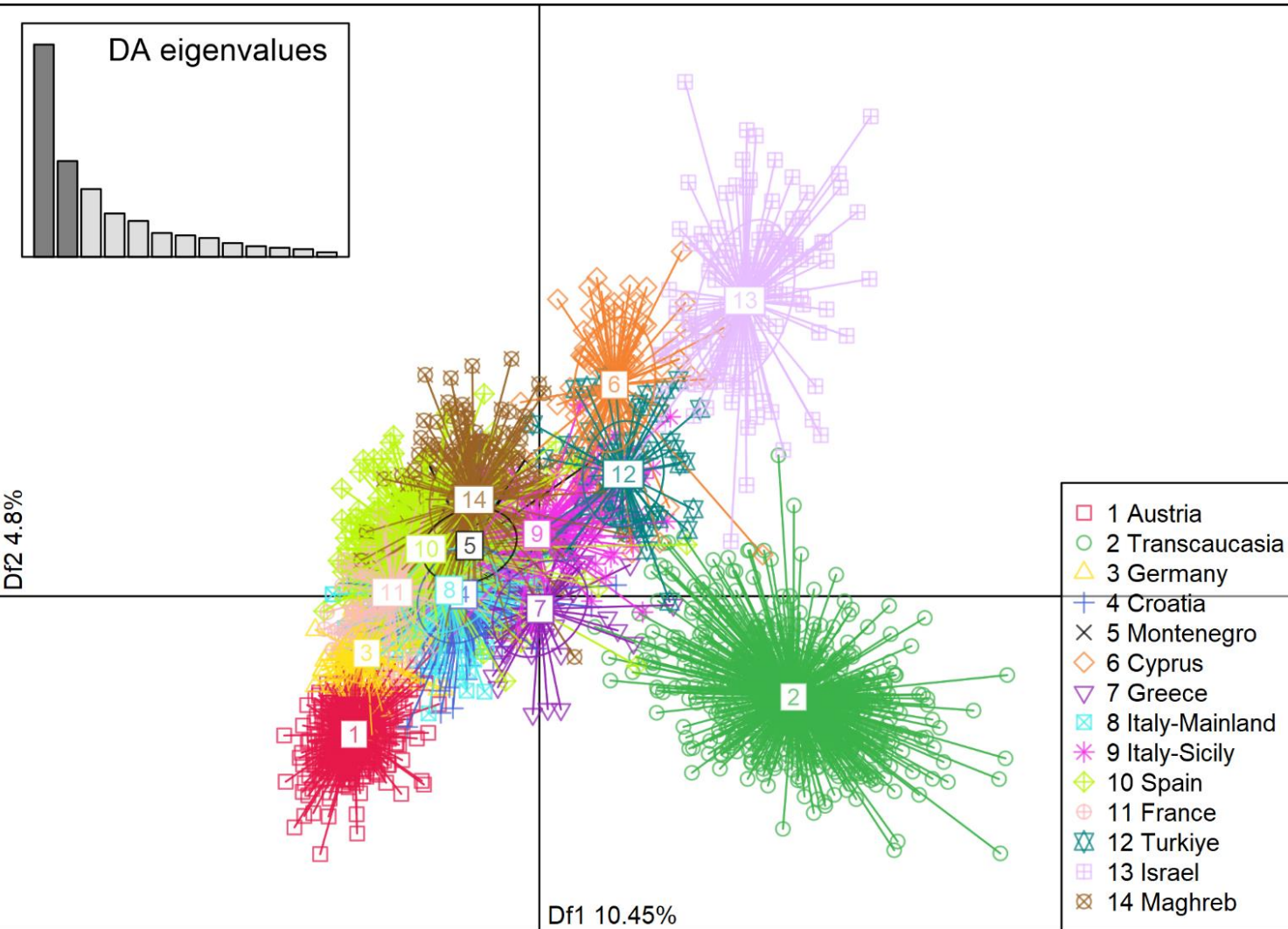
# First results



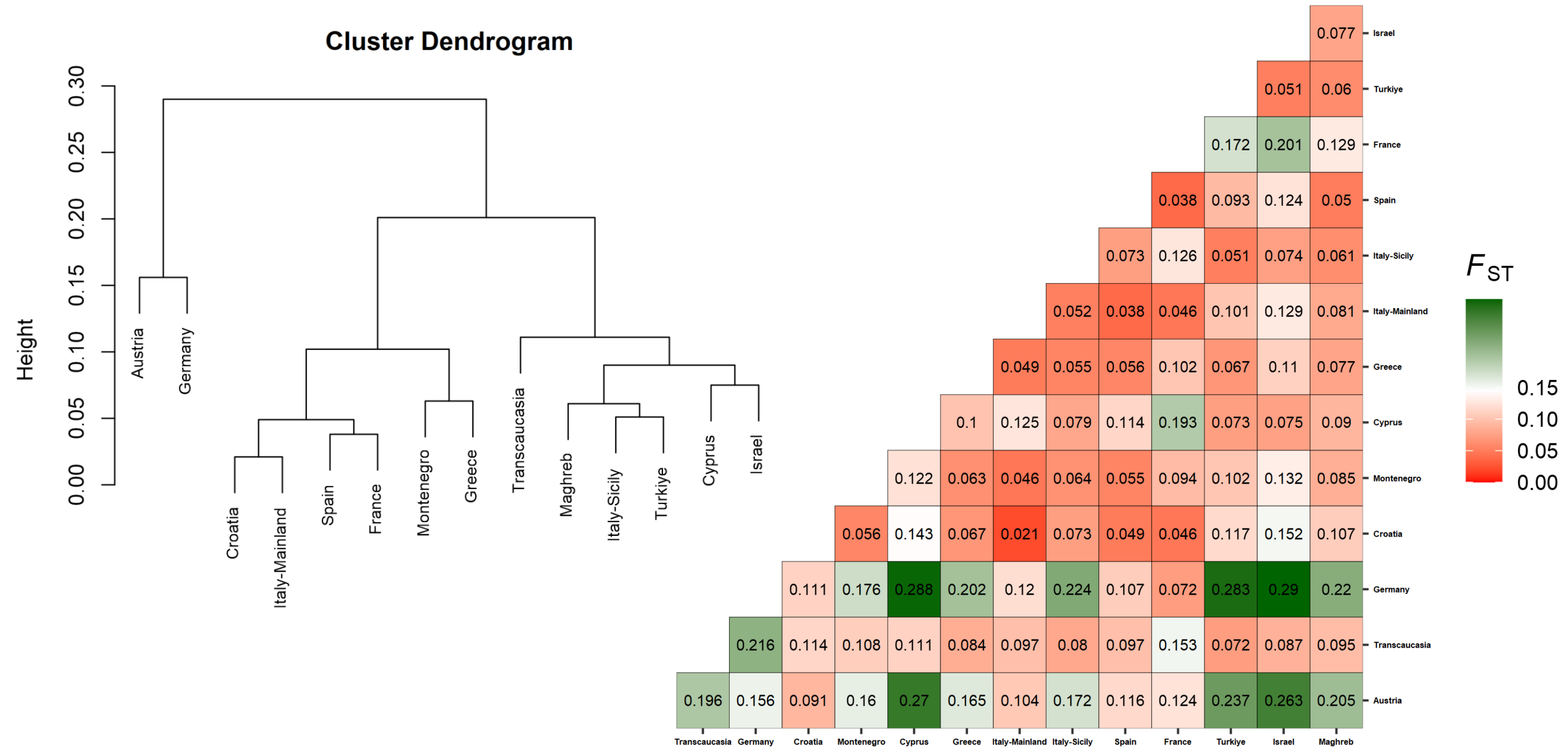
# Data sources now – October 2023

Country / Region	Pop-nr	Size	Source / Remark	Published
Austria	Pop1	350	177+173 samples; Danube; E. Maul & F. Röckel	no
Transcaucasia	Pop2	610	134+371+54+51 samples; Margaryan2021; Riaz2018; CostFA1003; Imazio2013	partly
Germany	Pop3	93	Ketsch; E. Maul & F. Röckel	no
Croatia	Pop4	161	109+52 samples; Zdunic2020+Riaz2018; G. Zdunic	partly
Montenegro	Pop5	55	J. Tello (Maras2020)	yes
Cyprus	Pop6	93	S. Savvides, E. Maul & F. Röckel	no
Greece	Pop7	52	G. Merkouropoulos	no
Italy-Mainland	Pop8	155	15+140 samples; A. Schneider; G. de Lorenzis & G. Pelissetti	no
Italy-Sicily	Pop9	125	121+4 samples; deMichele2019; G. de Lorenzis & G. Pelissetti	partly
Spain	Pop10	468	192+134+142 samples; deAndres2011; J. Tello; G. Munoz	partly
France	Pop11	115	V. Laucou (Dong2022; André2017; Barnaud2010)	yes
Turkiye	Pop12	58	I. Uzun & E. Maul	no
Israel	Pop13	127	Drori2017 & Rahimi2021	yes
Maghreb	Pop14	178	30 TUN J. Tello (Ghaffari2013) / 33 TUN V. Laucou / 8 DZA V. Laucou / 107 MAR V. Laucou	partly
<b>Total</b>		2640		

# Intermediate results - DAPC



# Intermediate results – $F_{ST}$



# Discussion – Results/Figures/Tables

- Map with contributing countries  
→ Highlighting sample size, what else?
- Genetic diversity analysis  
→ Structure, DAPC (dependent / independent grouping),  
F-statistics, hierarchical clustering, ancestry values etc.
- Pooling of datasets for non-overloaded figures (not at first)?  
Based on  $F_{st}$ ?  
→ Maghreb, Transcaucasia, Italy-Sicily, SW/N-Spain?





# Discussion – Results/Figures/Tables

- Possible migration routes / heritage modelling
  - Remixture, TreeMix, SOM
- Core collection for preservation
  - Calculating is easy, but it is feasible?
  - How much individuals? Is there an interest to plant?
  - How much genotypes are still available?
- What else?



# Outlook / further steps

Upcoming data:

- ~100 samples from Greece / Albania / Romania (G. Merkouropoulos)
- What else? Portugal, J. Cunha? Slovenia, A. Perko?
- **Deadline for data contribution 31.01.2024**
  - I will finalize the dataset afterwards
  - Online meeting in March/May to present/discuss results
- Publication will be written during 2024





**THANK YOU**