

Development of a genetic map of grape (*Vitis vinifera* L.) backcross offspring using high-throughput genotyping

Lytkin K.F.^{1*}, Grigoreva E.A.^{1,2,3}, Potokina E.K.^{1,2}

¹Saint-Petersburg State Forestry University, St Petersburg, Russia

²All-Russian National Research Institute of Viticulture and Winemaking “Magarach” RAS,
Yalta, Russia

³ITMO University, St Petersburg, Russia

*e-mail: kirill.lytkin@mail.ru

Introduction

The Crimean autochthonous grape varieties are a valuable source for breeding new cultivars with increased salt and frost resistance, as well as high quality berries.

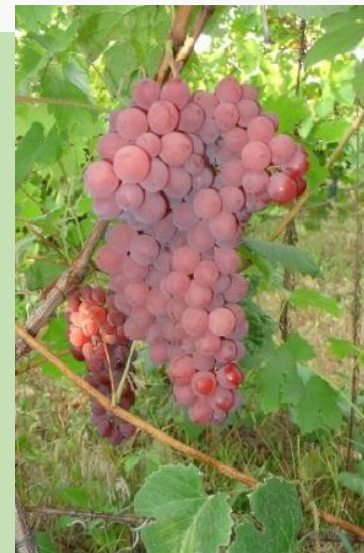
However, they suffer from fungal pathogens, such as oidium and mildew.

An increase in the resistance of Crimean grape varieties is currently achieved through interspecific hybridization.

In this study we report the first attempt to construct linkage maps for two hybrid populations obtained using *Vitis* interspecific hybrid 'Magarach 31-77-10' as a female parent and donors of the resistance genes carrying introgressions from *Muscadinia rotundifolia* - the immune North American species.

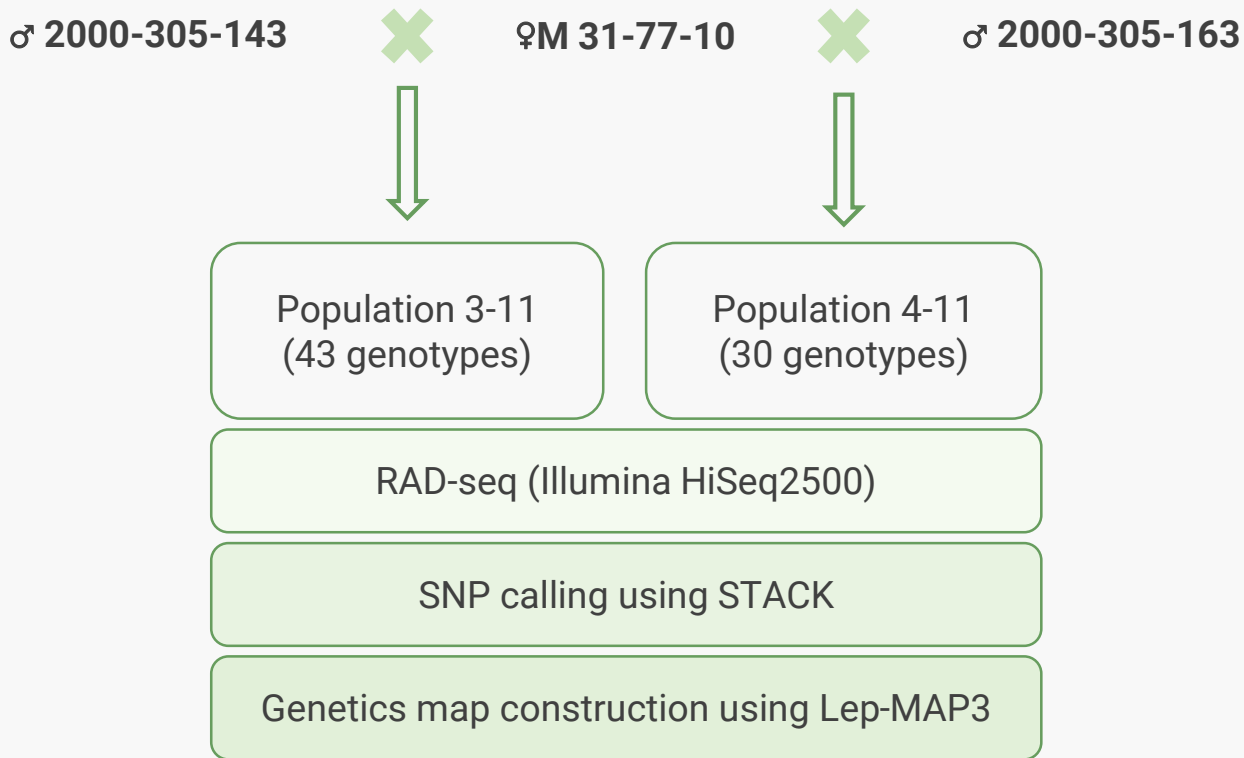


V. rotundifolia, 2n=40
Muscadinia rotundifolia



V. vinifera, 2n=38

Experimental design



Aim & Tasks of the study

Aim:

Construction of linkage maps using the high-throughput SNP genotyping of two hybrid populations from the cross the elite breeding line ♀M.Nº31-77-10 and two male parents, carrying introgressions from *Muscadinia*:

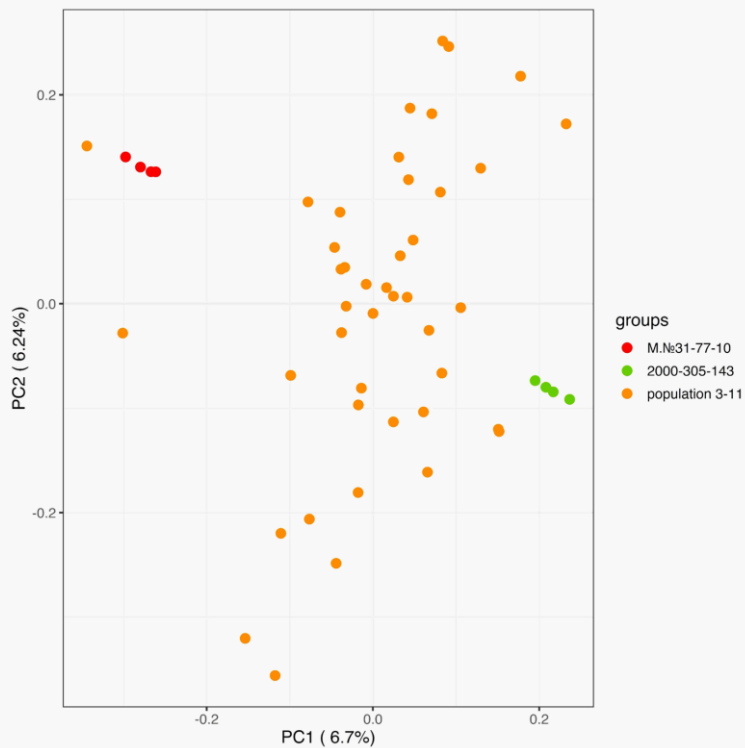
Population 3-11 = ♀M.Nº31-77-10 x ♂2000-305-143.

Population 4-11 = ♀M.Nº31-77-10 x ♂2000-305-163.

Tasks:

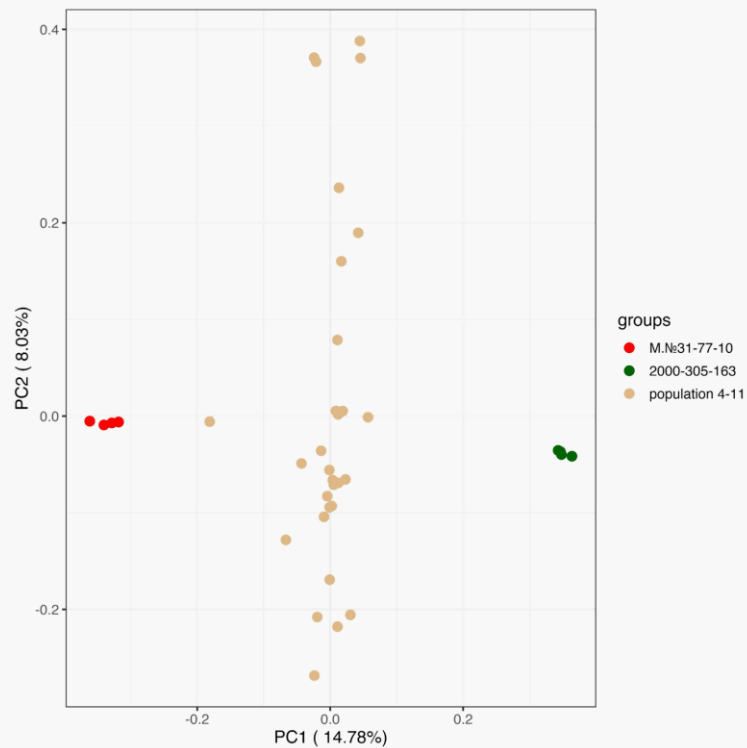
- DNA extraction
- GBS libraries construction
- SNP calling (STACK)
- Filtration (VCFtools)
- Chi-Square test
- Genetics map construction (Lep-MAP3)

Results of SNP calling



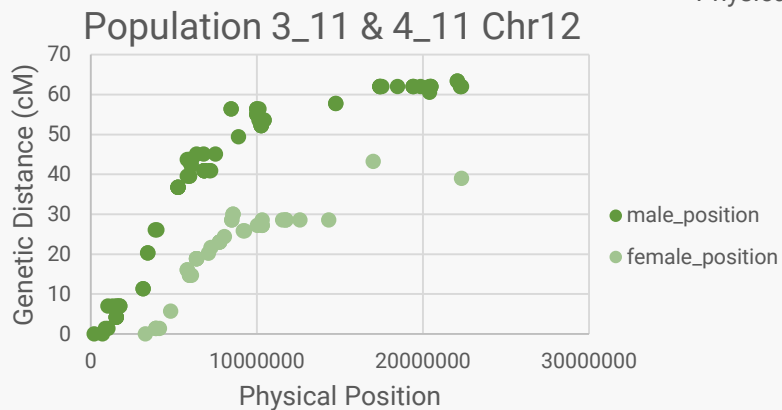
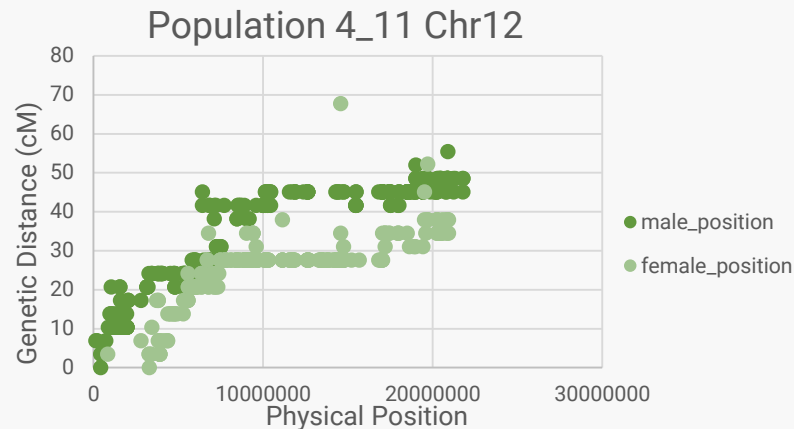
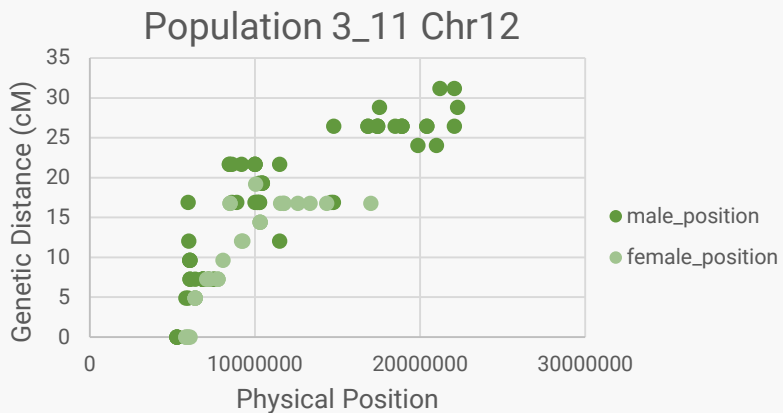
49275 filtered SNPs (MAF < 0.01 & missings < 0.5)

Pictures constructed by Grigoreva E.



41601 filtered SNPs (MAF < 0.01 & missings < 0.5)

Results of genetic maps constriction



Conclusions

Six linkage maps were constructed for hybrid backcross populations for chromosome 12, where the possible introgressions from *Muscadinia rotundifolia* are located. Since grapevine is the cross-pollinated species, for each cross two maps were created - for the female (F) and male (M) parents:

For population 3-11 in total 31 and 64 SNPs were involved for the F and M maps.

For population 4-11 - 250 and 262 SNPs respectively

When two populations were merged - the number of SNPs increased by 39 and 80.

The linkage maps constructed can further serve as the potential source for deeper study of genetic loci affecting resistance to fungal pathogens of grapevine varieties adapted to the ecological conditions of Crimea.

Thank you for your attention!



Российский
научный фонд

The research was funded by Russian Science
Foundation (project No. 20-16-00060).