

Identification of haplotypes controlling seedless by genome resequencing of grape

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Why seedless grape research in Korea?

- Among the three major uses for grapes, which are wine making, fresh fruit (table grapes), and dried fruit (raisins) production, most of grapes produced in Korea are for the table grapes
- Grape market size in Korea is approximately 400 million \$
- Because of concern of safety of gibberellin treatment, demands for stenospermocarpic seedlessness grapes are increasing



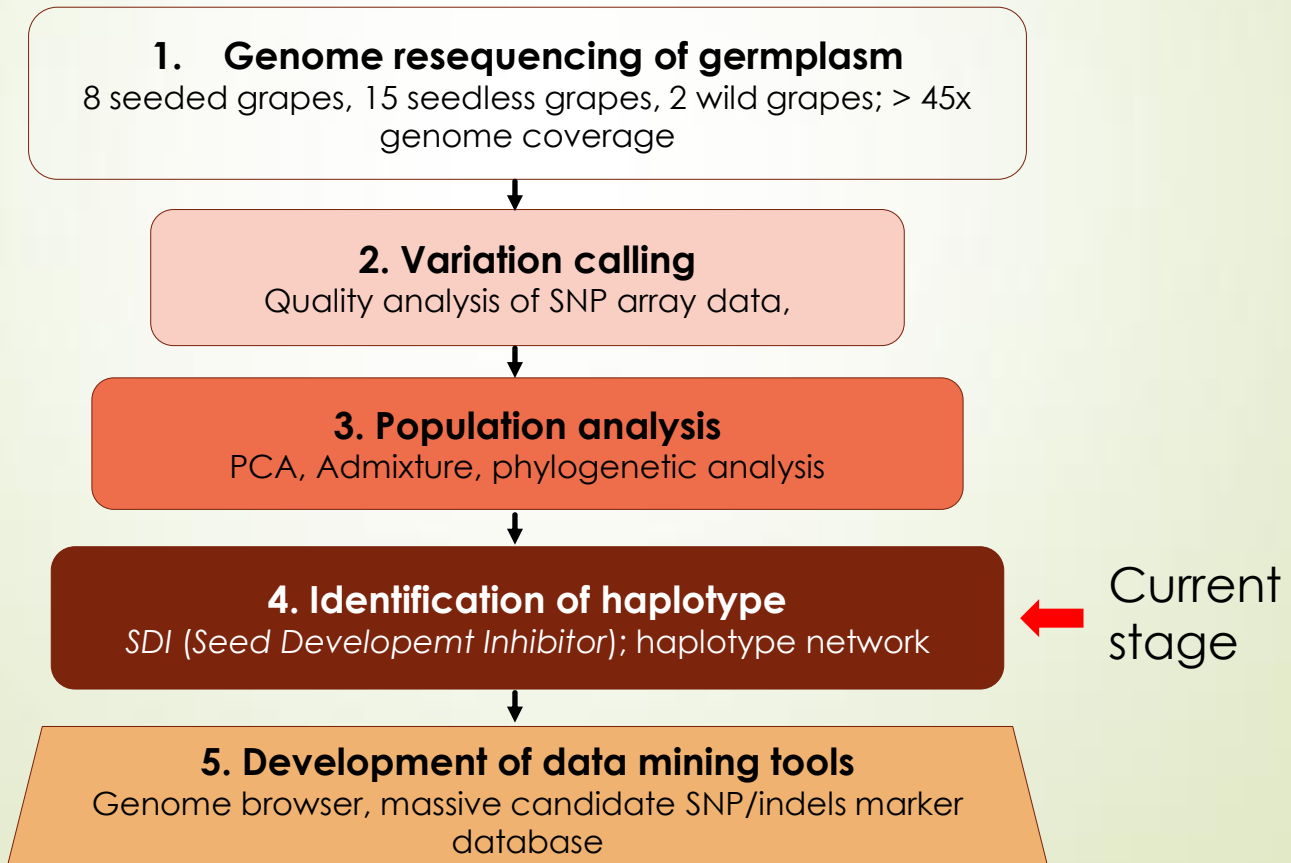
What we know about genetics of stenospermocarpy in grape?

- The most accepted model:
 - ✓ Three independent recessive genes under the control of a dominant regulator gene named *SDI* (*Seed Development Inhibitor*)
- *SDI*
 - ✓ Confirmed by numerous studies
 - ✓ Localized on Linkage group 18
 - ✓ Explain 50% to 70% of the phenotypic variation of the stenospermocarpy
- *VvAGL11* is the causal gene for *SDI*
 - ✓ Expression in mature carpels, developing seeds and pre-and post versison fruits
 - ✓ In silico mapping to the same contig that contains the *SDI* locus and the closest marker to a seedlessness QTL (Costatini et al. BMC Plant Biology 2008, 8:38)
 - ✓ Genetic, physical, and transcriptional evidence (Mejia et al/ BMC Plant Biology 2011, 11:57)
 - ✓ Ectopic expression in the Arabidopsis SEEDSTICK mutant (Malabarba et al. J Exp Bot 2017, 68:1493)
- The three recessive genes has not been identified at the molecular level

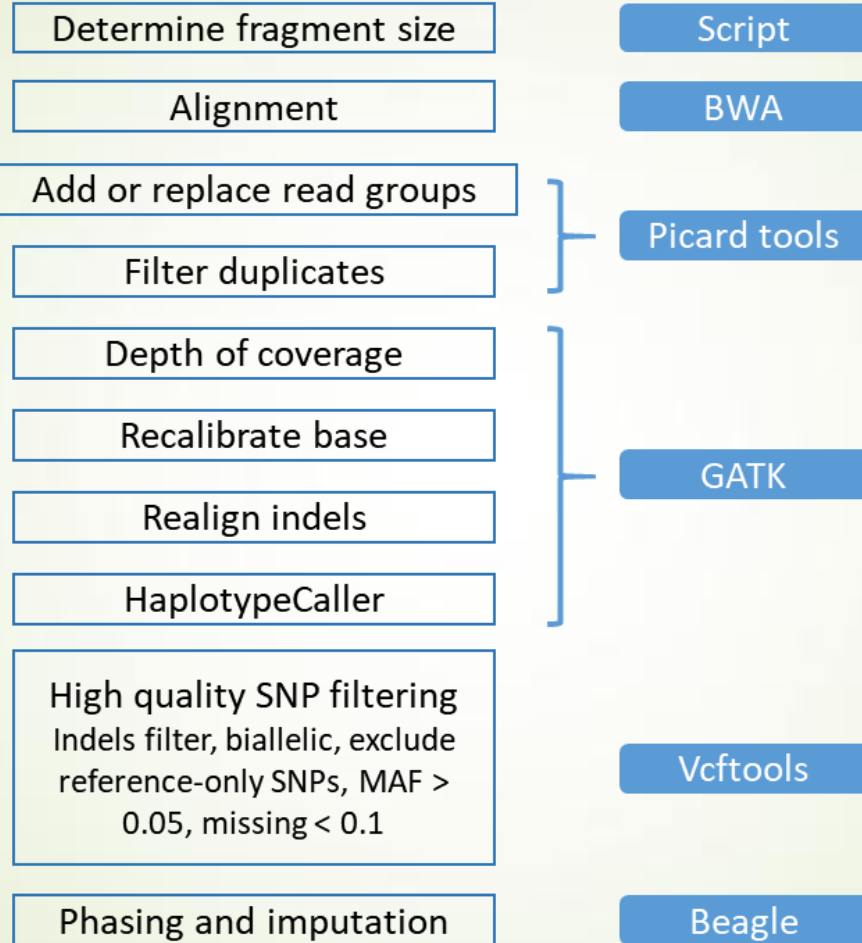
Objectives of This Study

- Identification of seedless-controlling haplotypes by genome resequencing of grape
- We have sequenced nine seeded and 16 seedless grape accessions and downloaded sequencing results of two seeded and one seedless grape accessions

Flowchart of Grape genome analysis



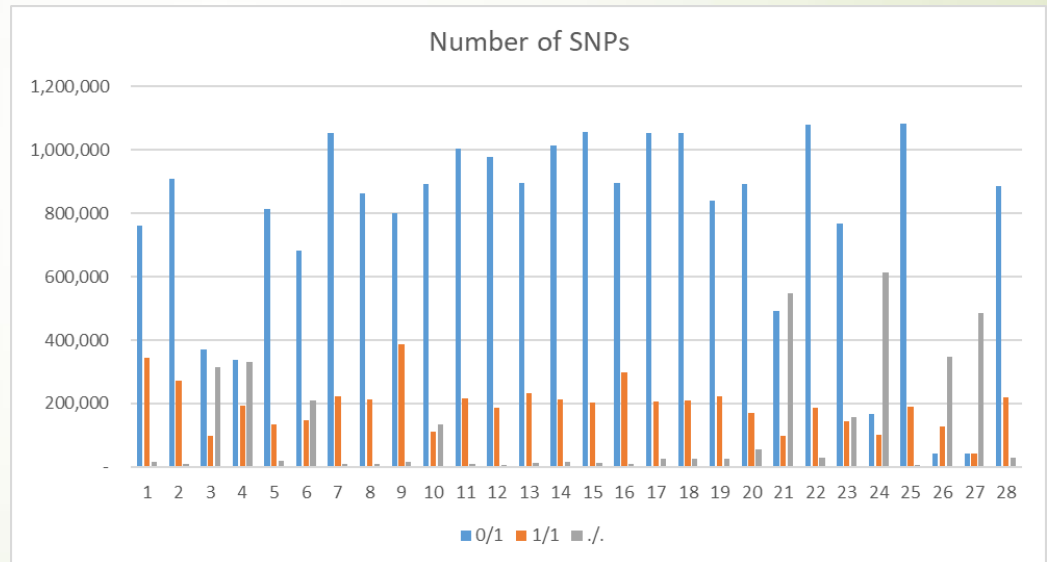
Grape variation calling pipeline



Variation calling results

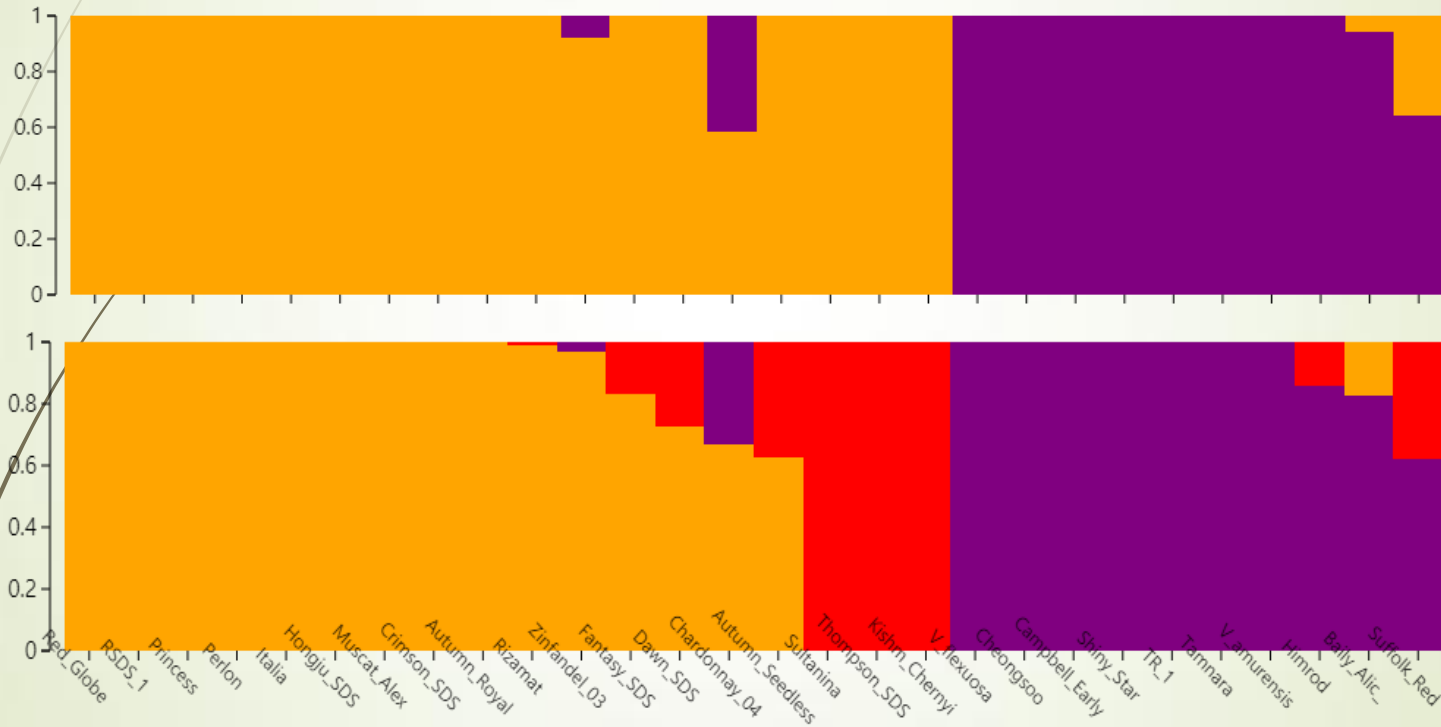
- A total of 3,459,679 high quality SNPs were obtained from the sequencing data after filtration of $> 5\%$ MAF and $> 10\%$ missing rate

Name	0/1	1/1	./.
Autumn_Royal	760,823	343,351	16,583
Autumn_Seedless	909,474	271,196	10,451
Baily_Alic_	369,733	99,201	312,934
Campbell_Early	337,221	192,400	332,142
Chardonnay_04	812,962	135,115	20,612
Cheongsoo	682,218	148,100	209,077
Crimson_SDS	1,051,043	222,627	10,362
Dawn_SDS	860,819	214,337	8,697
Fantasy_SDS	799,559	385,707	16,198
Himrod	890,334	111,590	134,321
Hongju_SDS	1,003,460	216,688	10,606
Italia	977,802	187,910	7,473
Kishm_Chernyi	895,976	233,290	13,529
Muscat_Alex	1,013,100	211,875	14,907
Perlon	1,057,453	204,043	11,726
Princess	894,136	296,969	8,967
RSDS_1	1,052,193	207,783	27,037
Red_Globe	1,052,793	208,076	26,799
Rizamat	841,037	222,048	25,717
Shiny_Star	891,726	168,600	56,274
Suffolk_Red	491,798	96,782	545,998
Sultanina	1,078,809	188,145	30,612
TR_1	768,515	142,841	158,203
Tamnara	166,899	102,340	612,310
Thompson_SDS	1,083,049	189,216	6,315
V_amurensis	43,452	127,916	346,529
V_flexuosa	41,594	41,093	484,314
Zinfandel_03	886,439	219,337	28,112



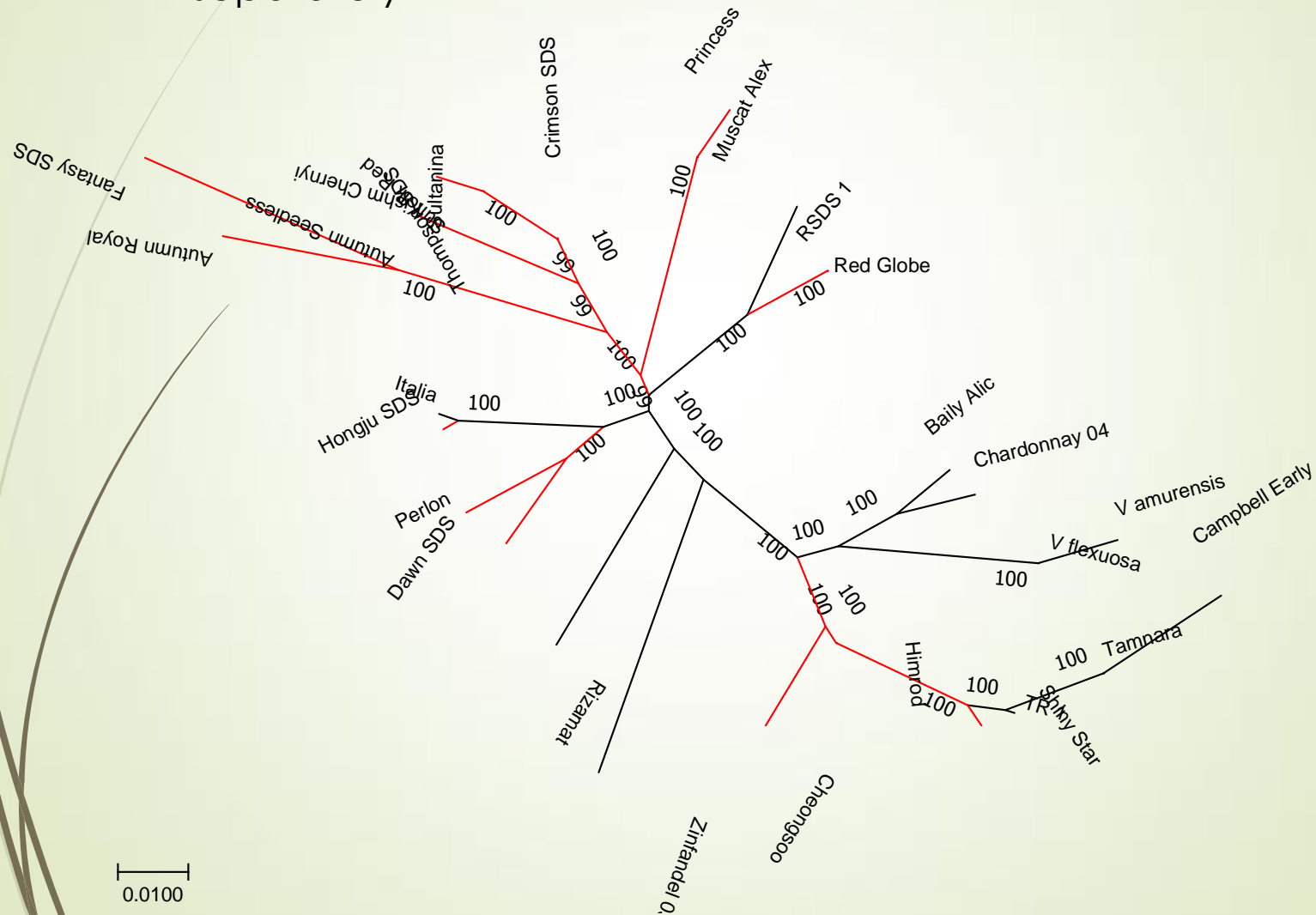
Population structure

- This population was divided into two or three subpopulations by the fastSTRUCTURE analysis



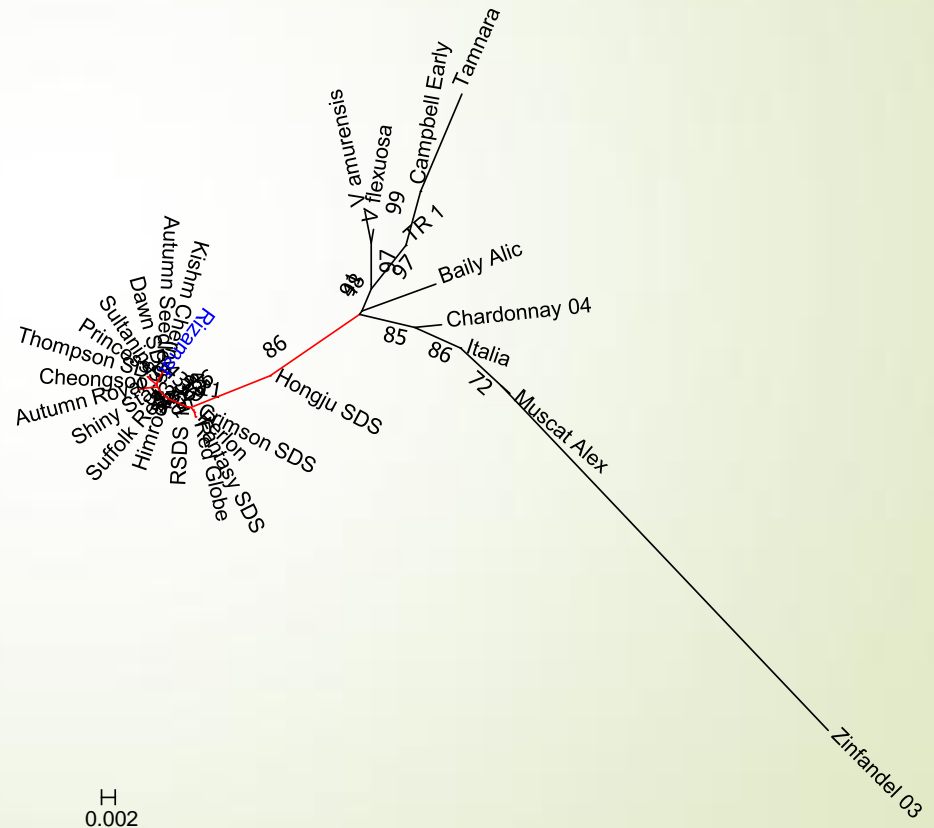
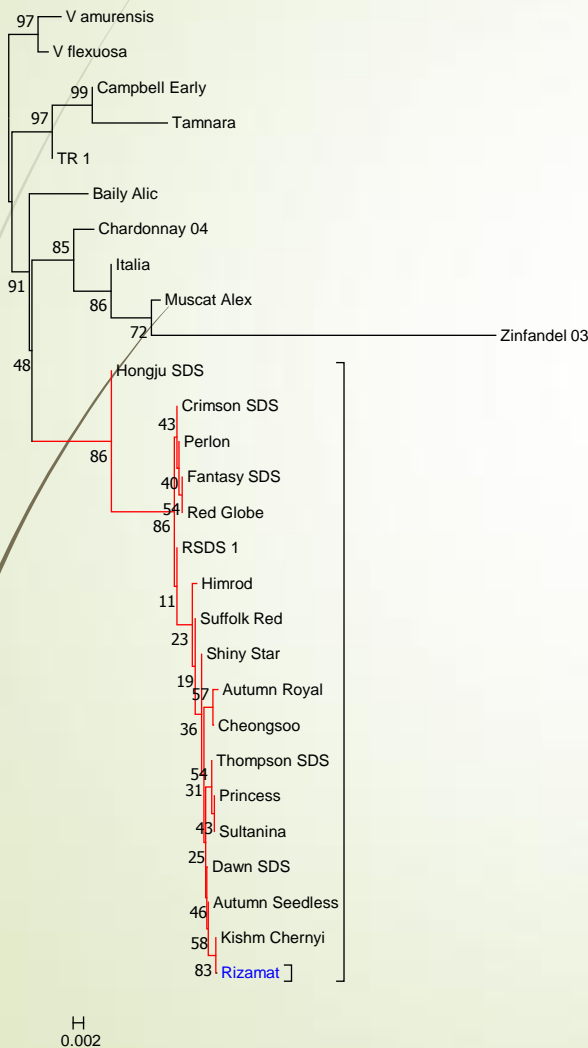
Phylogenetic tree construction

- Phylogenetic analysis supported two or 3 subpopulations
- Seeded and seedless grape accessions were not grouped separately



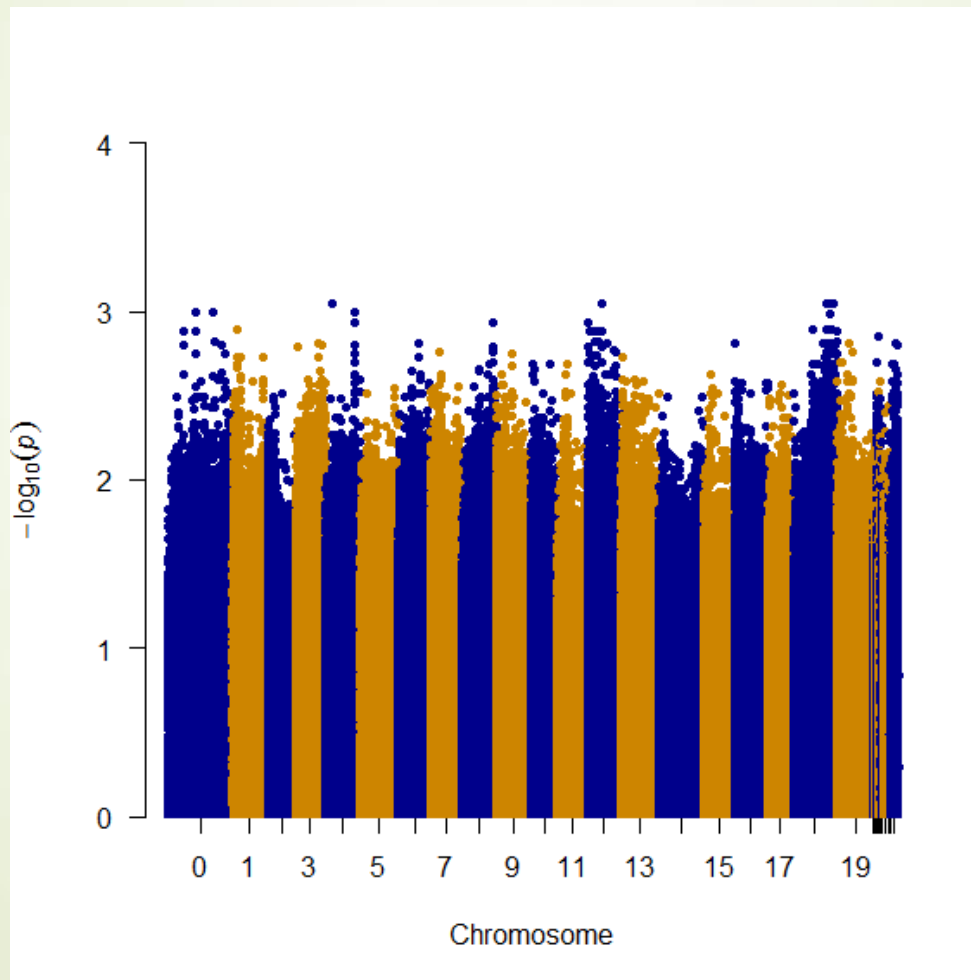
Phylogenetic tree construction

- Interestingly, in a tree that was constructed using SNPs from the 200-kb that contains the *SDI* locus in the middle of it, seeded and seedless grape accessions were grouped separately with an exception of Rizamat
- Whether Rizamat is mislabeled will be examined.



Genome-wide association study

- We are working on GWAS, however, need to find an appropriate GWAS method





Conclusion and future works

- Diversity patterns of seeded and seedless grapes are consistent with the previous findings that the SDI locus is a major seedless-controlling locus
- Our future work will be directed to identify the three recessive genes, which are likely minor QTLs, using GWAS as well as diversity pattern analyses
- We will also catalogue the SNP and indel variation called from our resequencing data for use in grape breeding programs.



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Thank you for your attention

