

Identification of Candidate Abiotic Stress Tolerance Loci in Wild Cranberry Using Environmental Association



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Takeaways

- Environmental association may help identify abiotic stress-adaptive genetic variation in wild cranberry
- We detected 143 associations between marker loci and environmental variables
- Potential heat, cold, and soil pH stress tolerance loci were identified at low frequency and are targets for selection

Introduction

Abiotic stresses such as heat and frost threaten production of quality cranberry (*Vaccinium macrocarpon* Aiton.) fruit.

Wild cranberry germplasm may contain genetic variation for tolerance to these abiotic stresses.

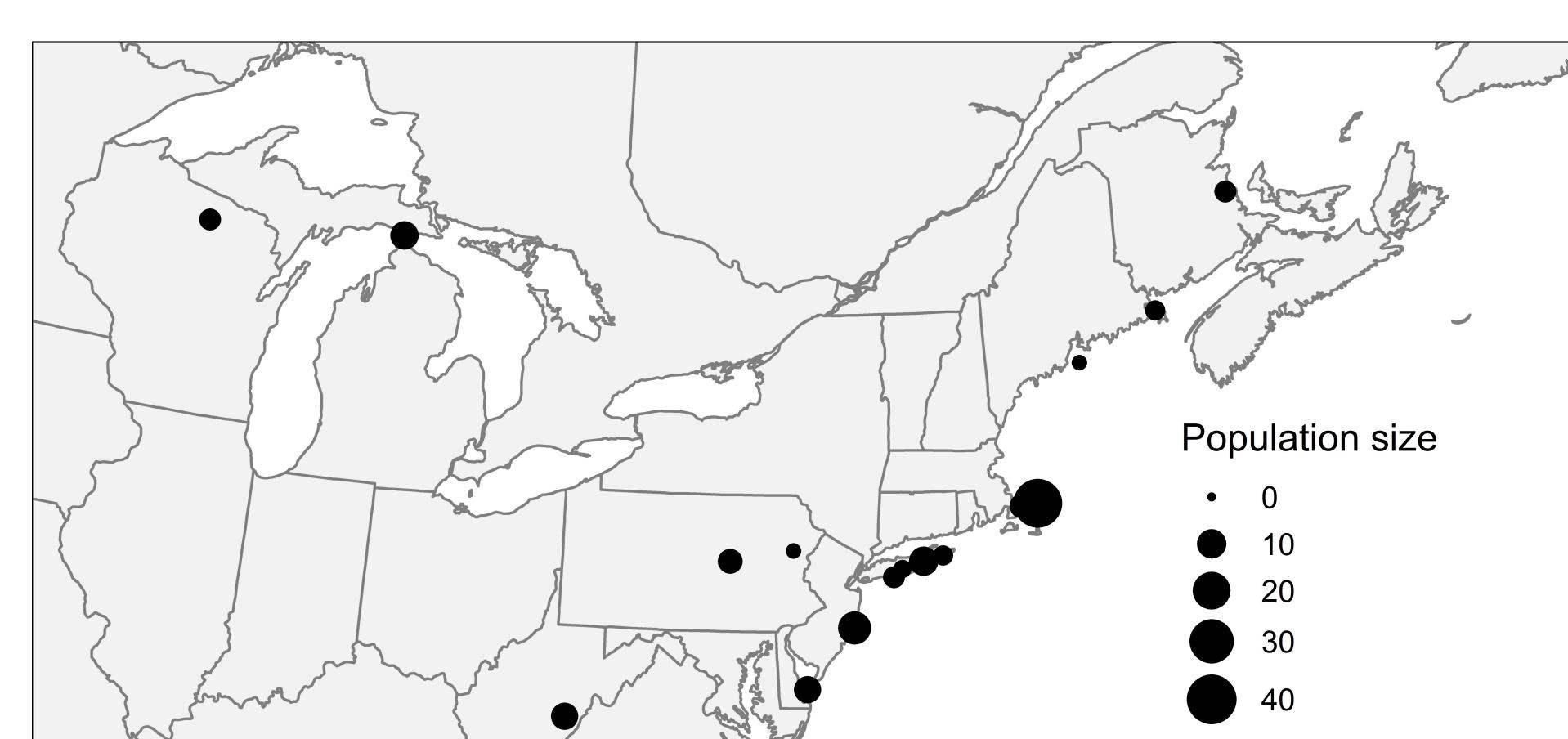
Identifying genomic regions associated with adaptation to environments would facilitate the targeted use of wild germplasm in breeding programs.

Environmental association analysis correlates allele frequencies in natural populations with environmental factors¹. This can help identify genomic regions potentially underlying adaptive variation to abiotic stresses^{2,3,4}.

Objective: Use environmental association to identify genomic regions associated with local environmental factors in wild cranberry populations.

Materials and Methods

We used a collection of 111 wild cranberry individuals sampled from 17 locations (populations) between 1991 and 2000.



4,582 SNP marker genotypes were obtained using genotyping-by-sequencing⁵.

We obtained bioclimatic data (19 WorldClim⁶ variables) and soil data (20 SoilGrids⁷ variables) for each cranberry population.

Category	N _{Variable}	Example Variables
Geography	3	Elevation, Latitude, Longitude
Temperature	11	Annual Mean Temperature, Mean Diurnal Range
Precipitation	8	Annual Precipitation, Precipitation of Wettest Month
Soil	20	Bulk Density Subsoil, pH Topsoil, % Sand topsoil

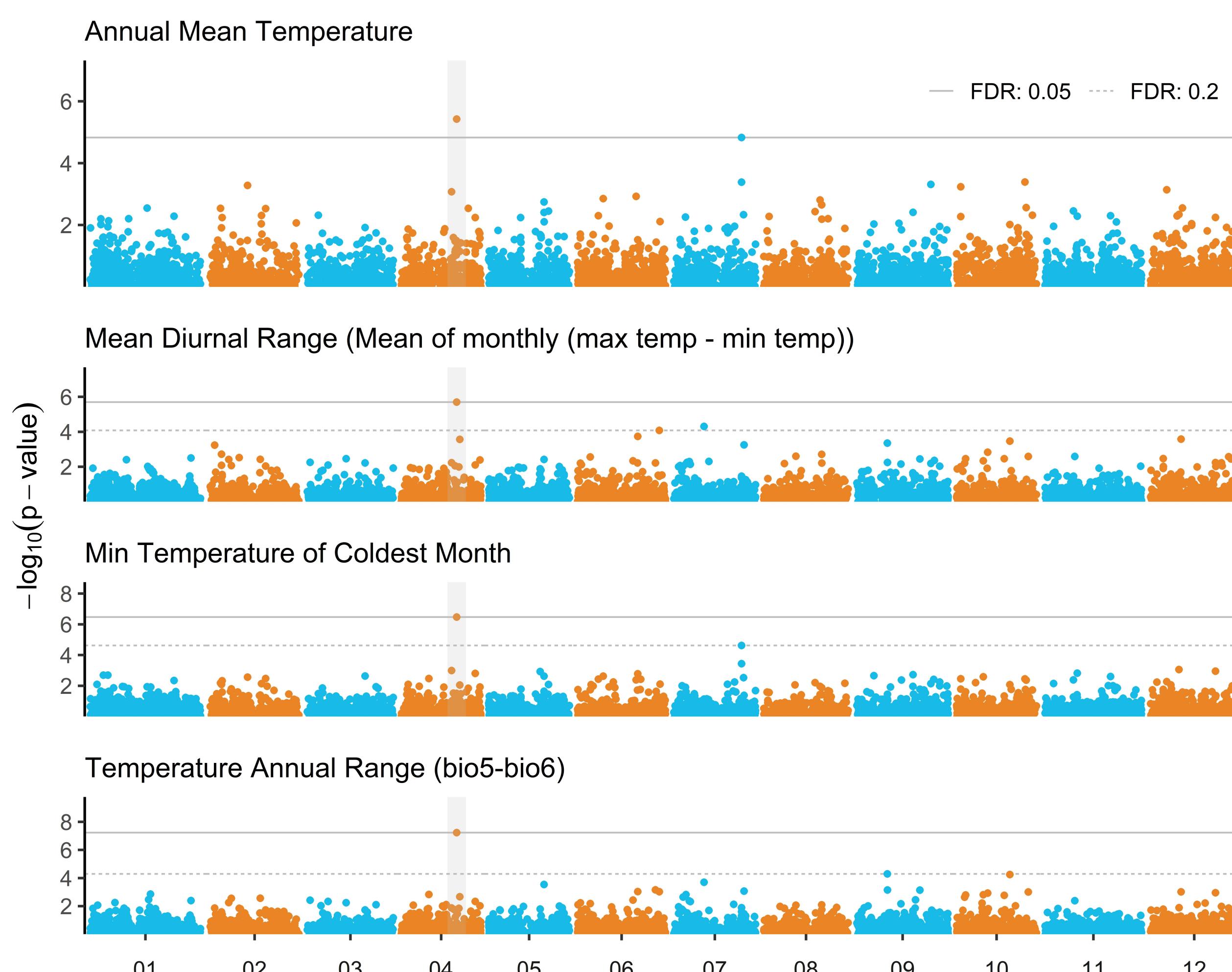
We conducted an environmental association using a mixed-model framework (similar to traditional genomewide association studies):

$$\text{Continuous environmental variable} \rightarrow \mathbf{y} = \mathbf{S}\mathbf{a} + \mathbf{X}\mathbf{b} + \mathbf{Z}\mathbf{u} + \mathbf{e} \leftarrow \text{Residual}$$

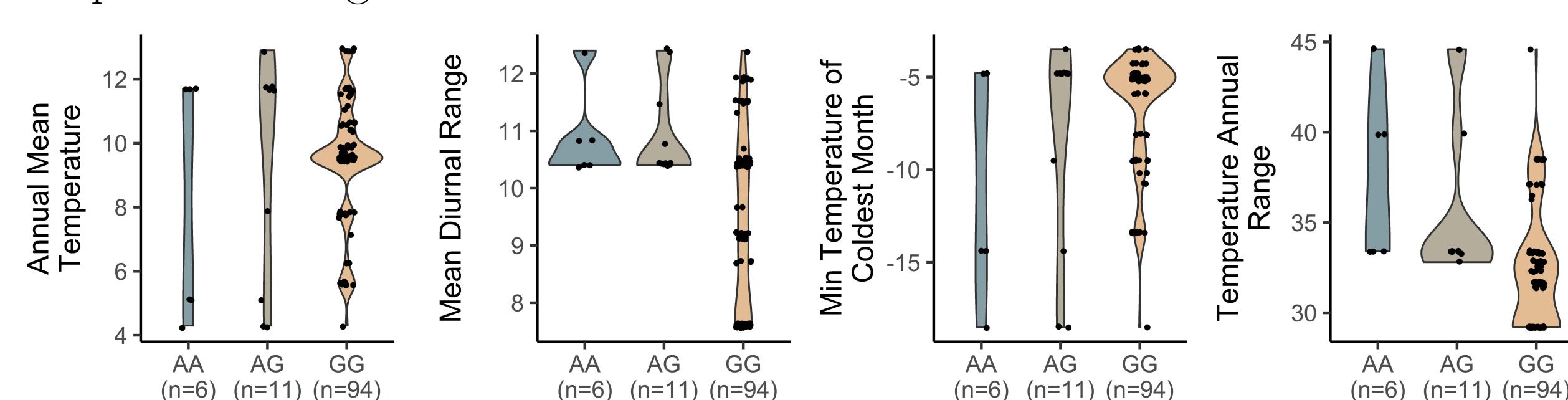
SNP effect ↑ Population structure ↑ Background SNPs

Results

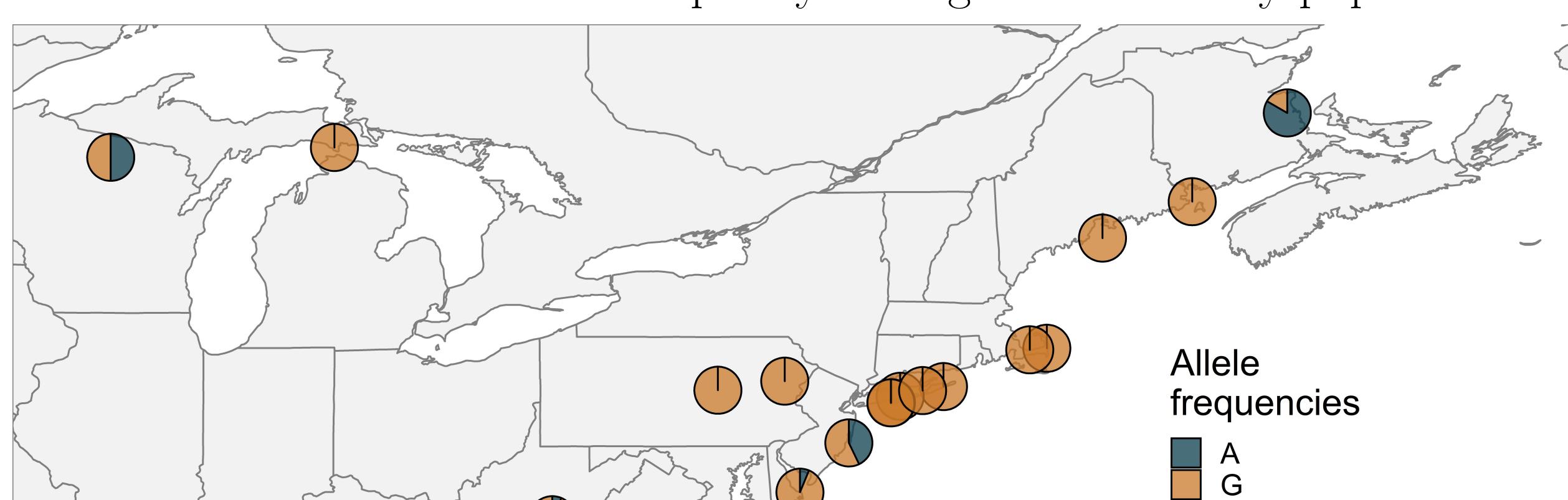
Example 1: chromosome 4 region associated with multiple temperature variables



The **A** marker allele is associated with colder temperatures and wider temperature ranges.

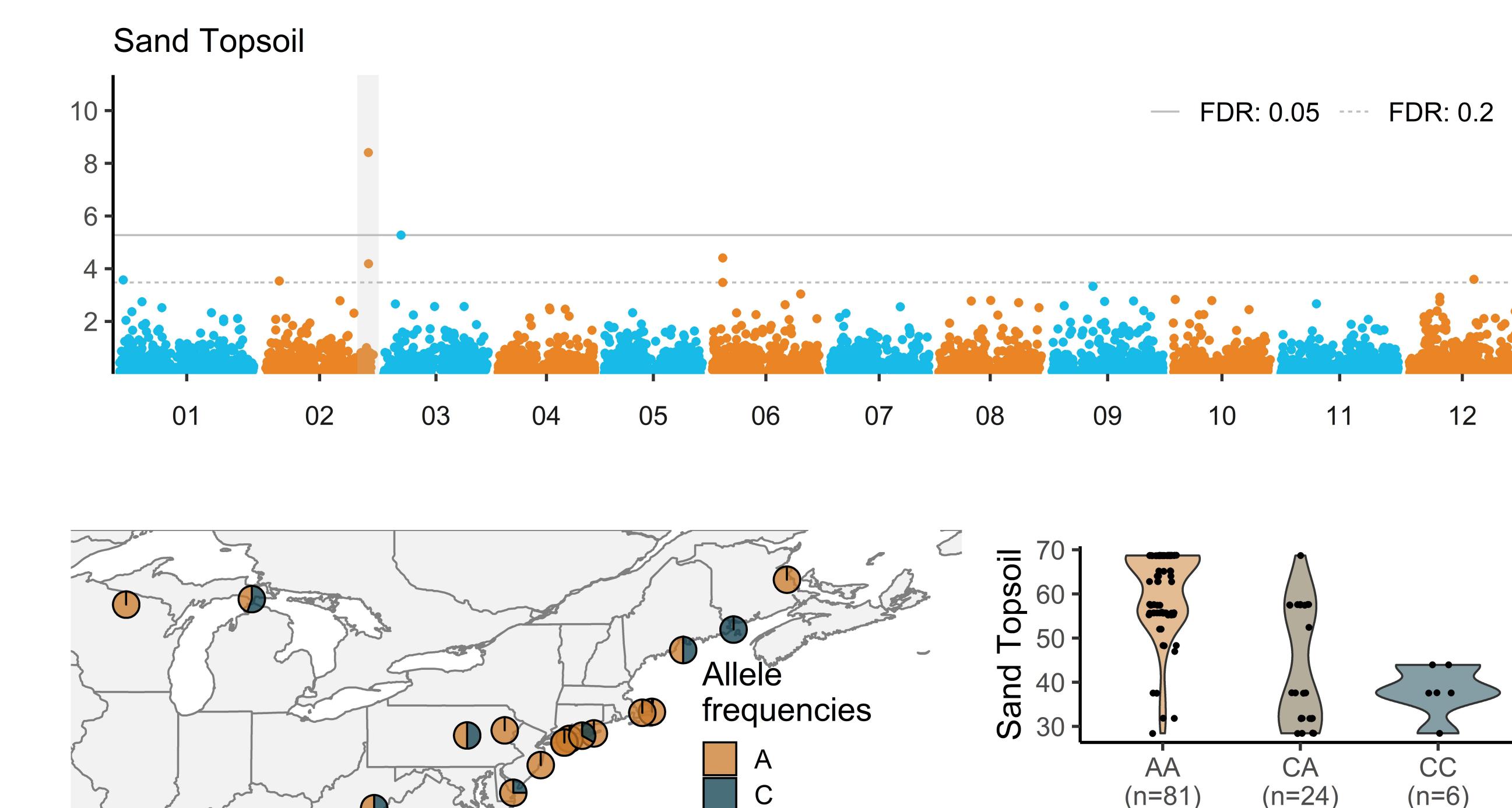


This favorable allele is at low frequency among wild cranberry populations.

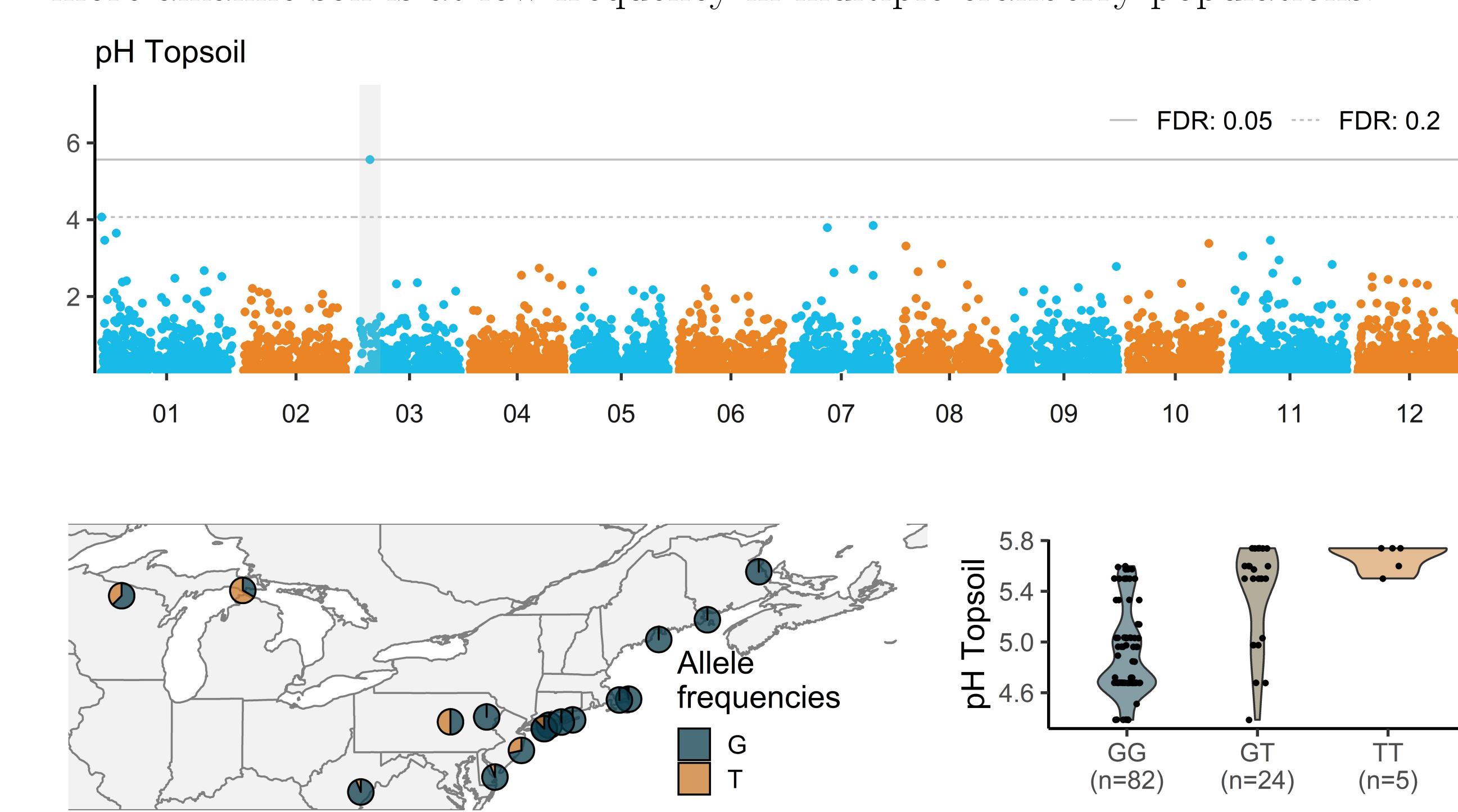


Example 2: genomic regions associated with soil characteristics

A low-frequency allele on chromosome 2 is associated with reduced topsoil sand content.



A chromosome 3 locus is associated with soil pH; the allele associated with more alkaline soil is at low frequency in multiple cranberry populations.



Summary of environmental associations

- 143 marker associations were detected for 36 environmental variables
- 74 unique markers across all 12 chromosomes were associated with bioclimatic variables
- 5 markers were associated with ≥ 5 variables

Acknowledgements

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References

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Implications for cranberry improvement

- We identified genomic regions associated with environmental factors related to important cranberry abiotic stresses.
- Low-frequency alleles favorably associated with abiotic stresses are ideal targets for selection.
- Individuals possessing these alleles are candidates for pre-breeding germplasm.