Genetic analysis of phenotypic variation measured in the Oregon Wolfe Barley collection

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QBio305: Population and Quantitative Genetics

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1   Introduction

Task definition: Paper about the phenotypic variation measured in the Oregon Wolfe Barley collection. This paper has to follow the structure of a scientific journal paper and should include the following analyses:

- ANOVA of plant height You find the data in

```
dta---ANOVA_QTLanalysis.csv
```

, which includes the measurements of all groups. The group is actually not a replicate, because you just measured the same plant several times. However, for the purpose of this exercise pretend that the group is a valid replicate, and do not include it in your model.

- Genetic linkage mapping of the qualitative trait your group has scored (which marker is in closest linkage?)

- QTL analysis of plant height You find the data in

```
dta---ANOVA_QTLanalysis.csv
```

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Submit your paper as a pdf to agatha.walla@hhu.de and timo.hellwig@hhu.de. Deadline: December 22, 2023

Introduction: The Oregon Wolfe Barley collection. Text of 500 words describing the OWB population. See https://barleyworld.org/owb and (Costa et al., 2001).

Linkage maps and mapping qualitative traits: Text of 200 words.

Quantitative traits and QTL mapping Text of 200 words.

2   Materials and methods

Plant population and phenotyping: How large was your population? Which traits did we score, and how did we score them in detail?

Side note: the plants were 2 month old.

Statistics: Which statistical methods did we use and how did we implement them? Which are potential problems with these approaches? Which software/packages and versions did we use?

3   Results

Show the ANOVA table and an overview of the linkage and QTL plots you have generated in this course with the code you have used.

What are your major findings?

Are your traits in proximity to any of the following known genes and if so, can they explain your trait?

Locus Chromosome References:

VRS1 2H https://doi.org/10.3390/ijms23042276

ZEO1 2H https://doi.org/10.1242/dev.170373

Kap 4H https://doi.org/10.1038/374727a0

LKS2 7H https://doi.org/10.1093/jxb/ers182

Gpa1 2H https://doi.org/10.1186/s12870-021-02915-9

Nud 7H https://doi.org/10.1073/pnas.0711034105

Blp1 1H https://doi.org/10.3389/fpls.2017.01414

4   Discussion

TODO...

References

Costa, J. M., Corey, A., Hayes, P. M., Jobet, C., Kleinhofs, A., Kopisch-Obusch, A., Kramer, S. F., Kudrna, D., Li, M., Riera-Lizarazu, O., Sato, K., Szucs, P., Toojinda, T., Vales, M. I., & Wolfe, R. I. (2001). Molecular mapping of the oregon wolfe barleys: A phenotypically polymorphic doubled-haploid population. *Theoretical and Applied Genetics*, *103*(2-3), 415–424. https://doi.org/10.1007/s001220100622

A Appendix A

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