

Whealbi

Wheat and barley Legacy for Breeding Improvement

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Collaborative Project
SEVENTH FRAMEWORK PROGRAMME

Deliverable D2.3

Manuscript(s) describing species and genome wide molecular variation, and linking the observed variation to eco-geographic and adaptive variables

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Project start date: January 1st, 2014 **Duration:** 60 months

Workpackage concerned: 2

Concerned workpackage leader: JHI

Dissemination level: PU

Table of contents

TABLE OF CONTENTS	1
SUMMARY	3
1 MANUSCRIPTS	4
1.1.Wheat :Tracing the ancestry of modern bread wheats	4
1.2 Barley :Exome sequences and multi-environment field trials elucidate the genetic basis of adaptation in barley	5
CONCLUSION	5
APPENDIX I	6
APPENDIX II	7

Summary

The objective of this deliverable was to address a broad range of biological questions using the diversity data present in the wheat and barley collections generated from WP2. These include categorising mutation types, identifying useful variation based on joint analysis with eco-geographical and common garden (WP3); prioritising certain geographical regions for further exploration of diversity, identifying selective sweeps and evolutionary and cultivation history. To achieve this, we have developed specific pipelines using the most recent and complete wheat and barley genome assemblies together with available variant callers and a range of custom filters. Two high impact manuscripts have been written by teams from work packages 1 to 5, with INRA leading the wheat paper and Biometris and JHI the barley paper.

1. Manuscripts

1.1 Wheat manuscript 'Tracing the ancestry of modern bread wheats'

This manuscript was prepared by Jerome Salse and colleagues from across the WHEALBI consortium and has been submitted to Nature Genetics (authors and affiliations listed in Appendix I)

The manuscript describes the exome capture data of 500 carefully selected lines representing a worldwide collection of di- and tetraploid wild relatives as well as old hexaploid landraces up to modern elite cultivars. The exome capture data covers genetic variation at ~1/2 of all wheat genes. Together these provide a comprehensive overview of wheat genetic diversity at a range of scales (gene, region, chromosome, genome), delivering a rich resource for future exploitation by both the academic and agricultural research communities (Figure 1).

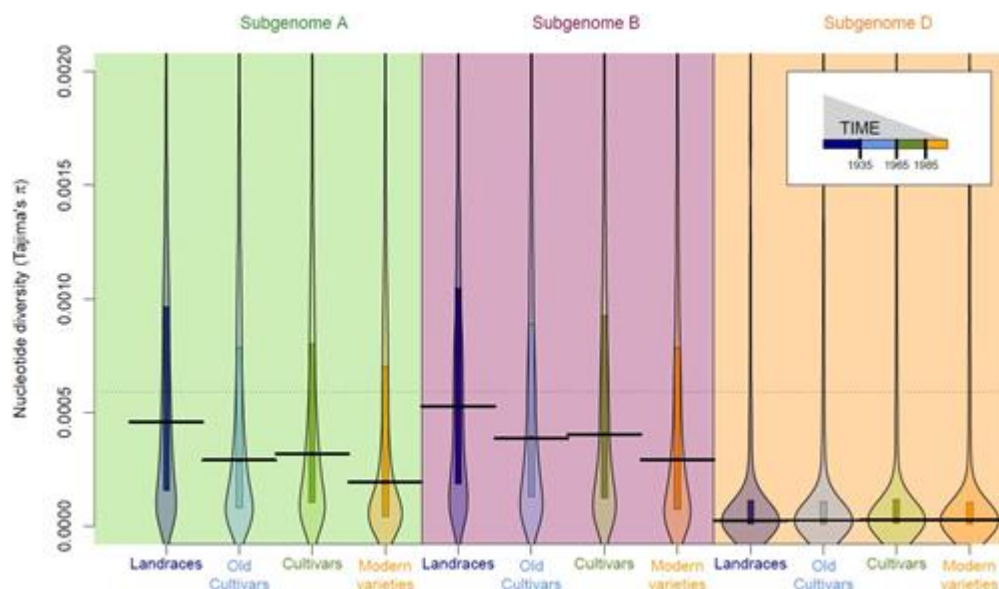


Figure 1. Temporal evolution of wheat diversity. A- Nucleotide diversity (y-axis) from the hexaploid wheat accessions (x-axis) between subgenomes (A, B and D) and historical groups (landraces, old cultivars, cultivars and modern varieties) covering the last centuries of breeding (*cf* timescale legend in the white box)(From Pont et al., 2019)

The manuscript provides clear novel insights into wheat ancestry in (i) unveiling genomic signatures of domestication and breeding at the chromosome and gene scales supporting independent targets of breeding in Asia and Europe following the east-west expansion from the center of origin, (ii) delivering genomic drivers of key traits (heading date and photoperiod) related to wheat adaptation during the green revolution, (iii) proposing that modern cultivated bread wheat are the result of recurrent hybridization and gene flow between diploid, tetraploid and hexaploid progenitors with *T. durum* lineage being the most likely ancestor of today's bread wheat cultivated germplasm. The current manuscript supports a reconciled model of wheat evolution, expansion and associated selected genes since its domestication and provides novel avenues for future breeding improvement.

1.2 Barley manuscript ‘Exome sequences and multi-environment field trials elucidate the genetic basis of adaptation in barley’ (authors and affiliations listed in Appendix II)

This manuscript was prepared jointly by Daniela Bustos-Korts and Ian Dawson with colleagues from across the WHEALBI consortium and has been submitted to New Phytologist.

In this manuscript, genetic diversity is being made accessible to breeders through the adoption of exome sequencing for genotypic characterisation of a barley collection that was carefully chosen to represent an important range of world-wide genetic diversity, including landraces and cultivars, with measurements of a range of phenotypic traits across multi-environment field trials. Exome sequences were successfully obtained and validated for 403 WHEALBI barley accessions and the adaptation patterns was analysed for 371 cultivated accessions (Figure 2).

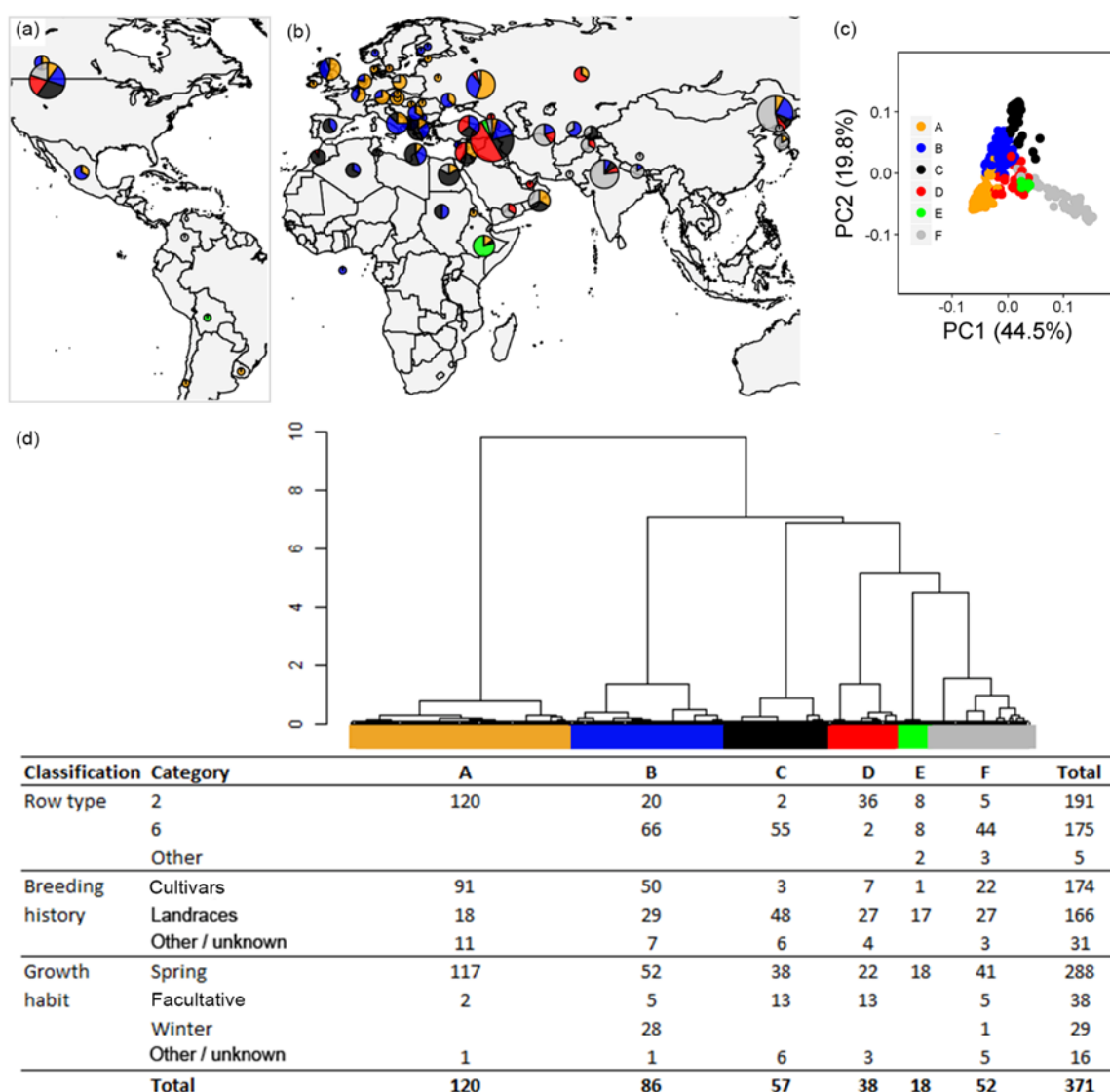


Figure 2 (a) and (b) Geographic distribution of six sub-populations of genotypes identified through cluster analysis of significant kinship principal components. Pie chart size reflects the number of genotypes collected from a particular

geographical region, while slice size shows the proportion of genotypes belonging to a particular sub-population. (c) Principal components biplot of the kinship matrix, showing the classification of genotypes into the six sub-populations. (d) Hierarchical clustering based on Ward distances, and composition of each of the six subpopulations, considering their row type, breeding history and growth habit classifications (From Bustos-Korts et al., 2019)

The analysis of exome sequences allowed to identify six sub-populations coinciding approximately with geographical origins, breeding histories and growth habits of accessions. These sub-populations explained an important proportion of the phenotypic variance across environments, showing how molecular variation is useful to identify sub-populations for that are suitable for further allele exploration. Multi-environment GWAS showed a range of QTLs close to known trait-related genes, indicating that WHEALBI accession panel and field trials provide a powerful platform for genetic analysis. The identification of contrasting alleles in our study provides insights into which geographical regions are promising sources of alleles useful for European crop breeding programmes.

Conclusion

Although there has been delays in the analysis and subsequent writing of both manuscripts, the resulting papers are to date the most comprehensive diversity studies to be published for both cereals. Both papers will be published in high impact journals reaching the target audiences. Both are the first to use high throughput genomics and informatics technologies to generate over half a million gene-based DNA polymorphisms, representing a global resource for both crops. Providing the basis for deciphering the evolutionary and adaptive history of these crops, as well as providing a foundation for future crop improvement and exploitation.

Appendix I

Tracing the ancestry of modern bread wheats.

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Appendix II

Exome sequences and multi-environment field trials elucidate the genetic basis of adaptation in a diverse barley collection

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