

# Whealbi

## Wheat and barley Legacy for Breeding Improvement

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**Collaborative Project  
SEVENTH FRAMEWORK PROGRAMME**

### **Deliverable D6.3**

***Review of selected pre-breeding strategies for efficient utilisation of genetic resources based on practical work and modelling***

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**Actual submission date:** M60

**Project start date:** January 1<sup>st</sup>, 2014    **Duration:** 60 months

**Workpackage concerned:** 6

**Concerned workpackage leader:** KWS

**Dissemination level:** PU

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## Summary

### **Objectives:**

Work Package 6 explored six different approaches to pre-breeding. These exemplify the very wide scope of pre-breeding, demonstrate the time scales involved in pre-breeding, have very different aims and are brought together by the utilisation of valuable genetic variation available in the crop wild relatives and in landrace collections. In October 2018 a workshop session was held to compare and contrast the different approaches. The findings from this exercise are summarised below.

Four projects all worked on developing a broad range of lines with introgressed segments for genetic diversity in barley and wheat, two for each crop. Landrace material, old varieties, outputs from public germplasm development programmes and elite varieties from regions outside Europe were all used as donors of 'novel' genetic diversity currently not present in elite varieties. Different methods for crossing and selection were used, but common for all was to deliver lines that were adapted to European conditions, and which has identifiable genomic sections introgressed.

### **Rationale:**

Selection has proved very efficient for improving traits such as grain yield or grain quality. However yield has reach a plateau in Europe since 1990, as a consequence of climate change and evolution of pests and pathogen, despite continuous effort in breeding programmes. It may be due to an exhaustion of genetic variability in modern breeding lines, or a lack of adaptive alleles to newly encountered biotoc and abiotic environments. Molecular studies show the modern selection has caused a severe bottleneck, and more genetic diversity can be found in genetic resources collection, particularly in old or exotic cultivars. However, the use of such material in breeding programmes in hampered by so-called linkage drag, i.e. the presence of many unfavourable genes in the vicinity of favourable ones. Related species such as wheat genome progenitor or barley vs wheat can even be employed, although with more difficulties in crosses and obtaining recombinations. Different methods for exotic/alien introgression ofuseful variation were employed to address this issue and optimally use old/exotic genetic resources to produce valuable genitors for applied breeding programmes

**Teams involved:** ATK, HU, INRA, CREA, KWS

## Topic 1: What sources of exotic germplasm were used and how were these chosen?

Sub-project: Wheat-barley translocations. Leader: Edina Türkösi (originally led by now-retired Márta Molnár-Láng), Martonvasar, Hungary

- Chromosome substitution lines of barley into wheat have been developed. Technical difficulties with the fertility limitations of making wide crosses were dominated in the early stages of the project. The resulting three wheat barley addition lines therefore trace to a single 6 row barley cultivar (Manas). In this type of exercise almost all the novelty lies in the interspecific contrast of the substituted chromosome thus any barley source would be adequate. The research team now has more control over the target introgressions and therefore in new combinations chosen for new substitution events the target chromosomes and source genotypes are being selected with regard to best knowledge of associated key traits.

Sub-project: Introgression of genomic regions with high protein potential into wheat varieties. Leader: Tzion Fahima, presented by Tamar Krugman, Haifa University, Israel

- The foundations of this work trace back 15 years and depend upon basic research that observed high protein content in wild *T.dicocoides* accessions. Mapping in this wild genepool enabled the approximate location of the most important determinants of high protein to be established. In the current project these wild targets have been introgressed into modern 6x bread wheat. Having specific target fragments enables marker assisted selection to be employed, greatly increasing the efficiency with which the difficult interspecific crossing and subsequent introgression can be done. Recent trial results are very promising confirming that the concept is sound and that novel genetic variation can be introduced from wild relatives in this way. This remains a long process involving many careful steps.

Sub-project: NAM Wheat population. Leader: Gilles Charmet, INRA, France

- The NAM population studied partly depended upon previous work. The structure of the population is based upon a recurrent modern hexaploid wheat cultivar crossed with several older cultivars and landraces. The population has proven very useful for identification of quantitative trait variation with particular regard to genetic factors not seen in the modern cultivars. This approach is valuable for the identification of genetic variation that may have been 'left behind' during recent years of breeding for modern varieties. Any NAM population is limited by the range of variation that is incorporated into the population. Further populations would utilise more detailed marker data and preliminary phenotype data to make more informative crosses.

Sub-project: MAGIC Barley population. Leader: Alessandro Tondelli, CREA, Italy

- This population was based on eight founder genotypes crossed using a multiple array scheme prior to fixing recombinant lines by selfing. The genotypes were selected using diverse barley types. Although the crossing scheme is more complex than for NAM a smaller number of recombinant genotypes is required for the phenotyping phase, making it more efficient at the field stage. A large array marker was successfully used to map the progenies giving 18K informative SNPs. Although a very valuable population was developed the use

of different row types in the founders leads to complications in the assessment of the progenies for quantitative traits owing to segregation of the major gene combinations. It is recommended that future studies should minimise the segregation of unwanted major genes.

Sub-project: Pre-breeding population in wheat. Leader: Jacob Lage, KWS  
Geographically distant elite varieties and outputs from public pre-breeding programmes (CIMMYT and NIAB) of bread wheat were chosen for their diversity with regard to target traits indicated from existing published papers, reports and records. A single backcross to an elite cultivar were developed leading to segregating F<sub>2</sub>, F<sub>3</sub> and further selfed generations. Field selection for diversity in the target traits under a pedigree selection regime was followed by trial assessment. Marker evaluation of the 'diverse' selections at the early trialling stage enabled promising selections with 'exotic' genetic signatures to be identified and passed to the line breeding team for inclusion in new line development.

Sub-project: Barley landrace introgressions. Leader: Peter Werner, KWS  
A collection of diverse 2 row spring barley landraces were crossed to an elite European cultivar. Marker data was used to identify pericentric haplotypes not represented in any current European spring barley cultivars. Following selection of the most diverse landrace sources these target regions were introgressed into the recurrent elite parent. At early generations the phenotypic effect of the introgressed regions was estimated from yield trial and yield component analysis. Selected 'exotic' introgression targets are passed to the line breeder for crossing and subsequent inclusion in new lines.

## **Topic 2: Is the approach used ideal for pre-breeding? What germplasm may result?**

Sub-project: Wheat-barley translocations. Leader: Edina Türkösi (originally led by now-retired Márta Molnár-Láng), Martonvasar, Hungary

This is a very 'macro' level type of pre-breeding, essentially if a chromosome is successfully substituted we expect a large effect on the phenotype. While the effect of substituting each chromosome may be very different there will probably be little difference depending upon the source of the donor chromosome. Certainly, there is a proven track record for the value of 'macro' whole or part chromosome substitutions in wheat breeding. The difficulties of carrying out the interspecific crossing and establishing a stable chromosome addition or substitution line is the biggest problem. Further study is needed to characterise the properties of the substituted chromosome. Potentially the novel germplasm can be crossed with a range of wheat lines to develop novel lines for commercial use.

Sub-project: Introgression of genomic regions with high protein potential into wheat varieties. Leader: Tzion Fahima, presented by Tamar Krugman, Haifa University, Israel  
This is perhaps the ideal strategy for exploitation of novel genetic variation in the crop wild species. The crucial and most difficult problem is to be able to identify the novel target while it is in the wild species. This project has shown that natural variation for the target trait can enable QTL mapping in the wild species. This 'handle' is then

invaluable for the focussed introgression process. If more than one trait can be identified then the whole process is more efficient. Further testing of the resulting lines is required to characterise and evaluate the enhanced protein levels in the novel material.

Sub-project: NAM Wheat population. Leader: Gilles Charmet, INRA, France  
The NAM population is valuable for QTL discovery. This is one of the key tools that can be used to help to categorise and evaluate exotic germplasm prior to introgression. More specifically from each NAM population it is possible to identify QTL effects that could improve the performance of known elite material. One of the sources of knowledge to be used by breeders for marker assisted introgression. The data will be prepared for publication. The NAM population is available to partners for crossing subject to a MTA.

Sub-project: MAGIC Barley population. Leader: Alessandro Tondelli, CREA, Italy  
As with NAM the MAGIC population analysis provides detailed information on the architecture of quantitative traits. This can be used to inform the selection of exotic sources and more usefully provide candidate targets for introgression into the elite germplasm. The population will be kept in the public domain and will be available after publication. CREA will select some of the recombinant lines for local breeding objectives. CREA has a policy that material will be progressed on a one to one basis with breeding companies.

Sub-project: Pre-breeding population in wheat. Leader: Jacob Lage, KWS  
This approach fits alongside established marker assisted introgression schemes for known single gene targets. The more that is known of the potential value of the 'exotic' source the better. A key advantage to this method is that it can become a continuous process with new crosses, based on new information, being initiated each year. Material can be available to WHEALBI partners subject to a MTA together with associated 35k data. Selections will be kept for ongoing internal breeding purposes but the rejected germplasm will usually be discarded.

Sub-project: Barley landrace introgressions. Leader: Peter Werner, KWS  
The principle of screening elite and exotic material using genomic marker data has proved useful in this study for barley. However, barley has a particularly severe problem with the lack of diversity in the pericentric region of the chromosomes which means this approach may not work well for other species. Nevertheless, most species will show some (perhaps small) regions of the elite genepool that are very low in diversity. Identification of these offers the breeder and additional choice of target for focussed introgression. Material can be made available subject to a MTA for academic purposes, not expected to be publicly released for availability to third party commercial organisations.

## Conclusion

Different approaches have been used to introgress exotic or alien (related species) variation into wheat and barley modern germplasm, with the aim of delivering lines which can be use directly in breeder's crosses. This was of course easier for old/exotic parents within a species, and took longer for introgressing alien variation. However all tasks were successful in delivering valuable genitors to breeders.