Natural Variation in Wheat

In this document we will highlight the availability of various mapping populations, based on elite and landrace cultivars.

WISP landrace collection

As part of the Wheat Institute Strategic Programme, a set of resources derived from natural variation in landraces was developed. Access to these lines, and the genotypic and phenotypic data associated with them, is through the WISP landrace website (http://wisplandracepillar.jic.ac.uk/results_resources.htm)
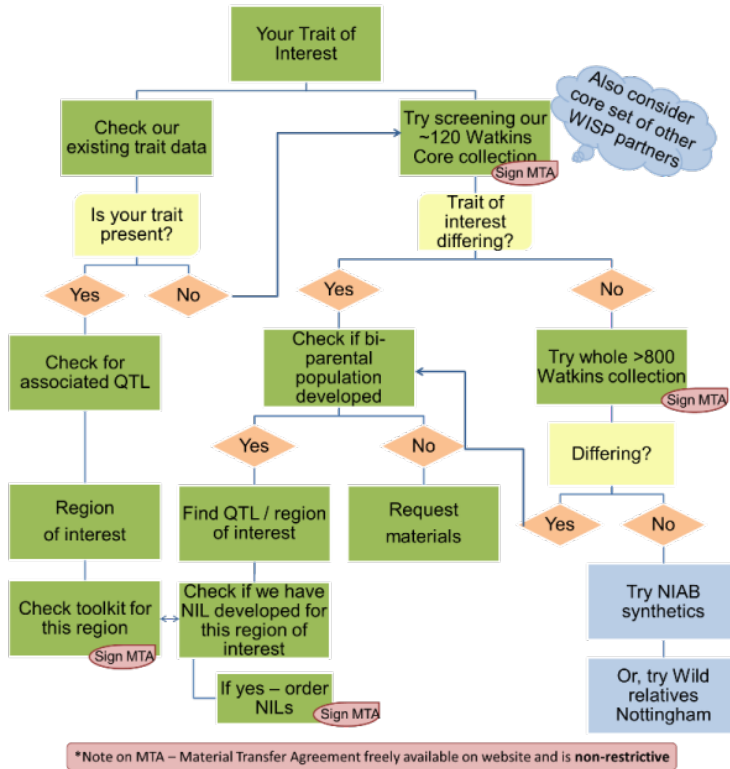
Watkins Collection

This population was developed from over 1,000 landraces collected in the early 20th century mainly from European, Asian, and North African countries. Based on genetic variation data, a core set of 119 lines was selected for more in-depth studies (see Wingen *et al.,* 2014 for details). This collection comprises the bulk of the materials and resources available through the WISP collection.

Gediflux Materials

This is a collection of wheat modern elite cultivars from Europe that have been sown between 1945 and 2000 across "major acreages."

The flowchart below highlights the options available for investigating your trait of interest in the Watkins collection, and other WISP landrace resources. A clickable flowchart is available at http://wisplandracepillar.jic.ac.uk/index.htm.

To access the Watkins data, navigate to http://wisplandracepillar.jic.ac.uk/results_resources.htm

In the first section, "**The AE Watkins bread wheat landrace collection and the diverse Core Set**", each list of lines can be downloaded as an Excel file by clicking on the respective links (**A** for the full

Watkins collection and **B** for the 119 core set). Lines can be ordered by clicking on the link to the SeedStor (**C**).

Accessing the Watkins Collections on the DFW website. The Results and Resources tab contains all the data discussed below, unless otherwise stated. The list of the full Watkins collection can be found in A, or the core set in B. All Watkins accessions can be directly ordered from the SeedStor (C).

The 119 core lines as well as the Gediflux panel have been genotyped using the Axiom 35K SNP array, and this data can be accessed through the CerealsDB portal, by navigating to the Axiom SNP section (http://www.cerealsdb.uk.net/cerealgenomics/CerealsDB/axiom_download.php). The list of lines available can be downloaded, as can the genotyping data, array probes used, and mapping data from five populations. This SNP data has also been incorporated into *Ensembl*Plants and can be visualised in the same manner as the TILLING SNPs, described here.

Details on the NAM populations for the Watkins lines crossed to Paragon and other wheat varieties are in the next section under the heading "**Population development - The Bread Wheat Landrace NAM Panel**", again an excel spreadsheet that can be downloaded (see below). This spreadsheet lists each Watkins accession for which a mapping population has been developed, and the stage the mapping population had reached as of January 2016. It's very possible that the population you're interested in has progressed past the stage listed in the file, so we would recommend getting in touch with Simon Orford at the Germplasm Resource Unit to verify the stage that is available.

	A	B	C	D	E	F	G	I	J	K	L	M	N
1	WISP population development at Jan 2016					x = developed							
2	WATKINS CORE COLLECTION												
3		Population developed with Paragon								with Robigus			
4	Watkins ACC	F1	F2	F3	F4	F5	F6 Stored	F6 Partners and Further	Breeders Toolkit Set1 donors	F1	F2	F3	F4
5	1190004					x							
6	1190007						x				x		
7	1190023				x								
8	1190032						x						
9	1190034							x	x				
10	1190042						x						
11	1190044					x							x
12	1190045						x						
13	1190079					x							x
14	1190081					x							x
15	1190092					x							x
16	1190103					x							

Watkins Accession Numbers

Paragon Population Stage   Other Populations ->

Watkins NAM Populations. The spreadsheet, as shown, lists the stage of each cross between a Watkins accession (yellow) and Paragon (green) or other elite UK wheat varieties (such as Robigus, shown in blue).

For the various NAM populations, SNP genotyping data can also be downloaded from the same site, under the heading "**NAM panel: SNP genotyping and genetic mapping**". The spreadsheet contains genotyping data from SSR (simple sequence repeat) markers for 87 of the Paragon x Watkins F_4 mapping populations. In addition to the SSR markers, KASP genotyping has also been used to extend the genotyping. Of these 87 populations, 3 have also been sequenced using the Axiom SNP arrays. This data is available as an Excel spreadsheet at the second link. Of the three populations, two (PxW49 and PxW94) each have data for over 4000 SNPs, while the third population, PxW705, has data for just under 1,500 SNPs. These genotyping data can be used to facilitate mapping of traits identified within the pre-genotyped populations.
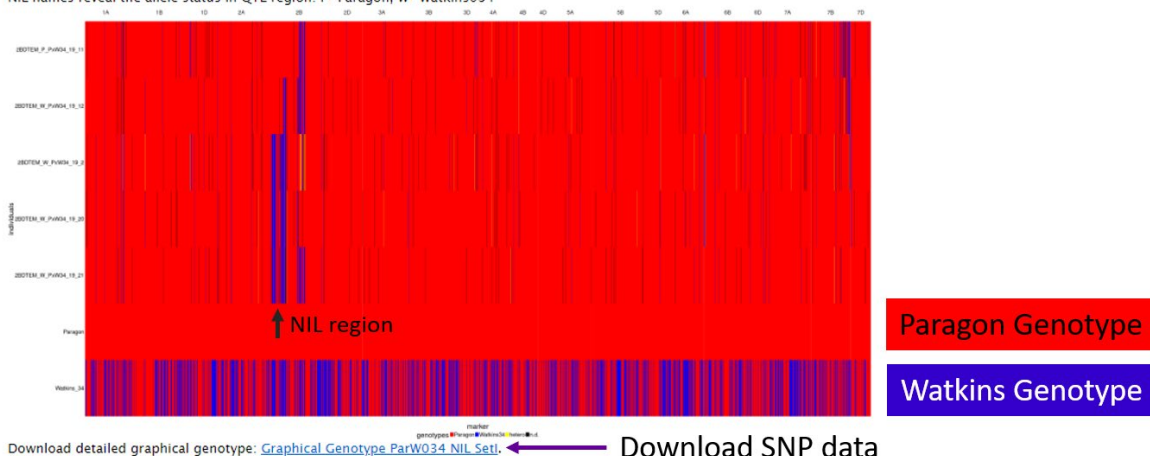
This genotyping data can be correlated with phenotypic data available for the Watkins collection itself and for subsets of the NAM mapping populations, under the heading "**NAM panel: Trait Data**". All phenotyping data can be downloaded as an Excel file. Three years of phenotyping data is available for the Watkins collection, two years for the full set of 912 lines, and one further year of phenotyping for the core set. The traits phenotyped include yield and grain size traits, stem morphology traits, and heading date.

Phenotyping was also carried out for particular NAM populations each year from 2011-2017. The phenotyping data is available to download, along with the QTL mapping analysis that was carried out for each year (found under "**NAM panel: QTL mapping**"). Of the QTLs identified, a subset were then introgressed into Paragon using Marker Assisted Selection, to the final BC_2F_2 stage. NILs with Paragon vs Watkins alleles across the QTLs of interested have been tested in field trials at the BC_2F_2 stage, though the data is not yet available. Genotypes of each NIL set derived from the Axiom SNP array can be viewed by clicking on the links for each set (I or II) and can be downloaded as Excel files. An example of a "graphical genotype" can be seen below, from http://wisplandracepillar.jic.ac.uk/graphical_genotypes_nil_setI.htm. Some of these NIL pairs have been tested in multi-envorinment trials, as part of the Breeder's toolkit, and can be found here: http://wisplandracepillar.jic.ac.uk/toolkit.htm.

Paragon X Watkins034 QTL

2B–days to ear emergence (DTEM)
NIL names reveal the allele status in QTL region: P=Paragon, W=Watkins034

↑ NIL region

Paragon Genotype

Watkins Genotype

Download detailed graphical genotype: Graphical Genotype ParW034 NIL SetI. ← Download SNP data

Genotyping Image of NIL Paragon x Watkins034. Red SNPs correspond to Paragon genotype, blue correspond to Watkins. The NIL has been defined in the 2B chromosome; see "NIL region" arrow. The top five rows correspond to NIL lines; the top line has the Paragon genotype across the NIL, while the lower four lines have the Watkins genotype. The genotypes of Paragon (second from bottom) and Watkins034 (bottom) are also shown. You can see that the Watkins parent line is a mix of Paragon and non-Paragon genotypes.

References:

Wingen, L. U., et al., (2014). "Establishing the A. E. Watkins landrace cultivar collection as a resource for systematic gene discovery in bread wheat." Theoretical and Applied Genetics 127(8): 1831-1842.

Wingen, L. U., et al., (2017). "Wheat Landrace Genome Diversity." Genetics 205: 1657-1676.

NIAB MAGIC Populations

A MAGIC (Multiparent Advanced Generation Inter-Cross) population derived from 8 parents has been developed at NIAB in the UK. The eight founding parents derive from UK and North European winter wheat genotypes- Soissons, Alchemy, Brompton, Claire, Hereward, Rialto, Robigus, and Xi19. The genomes of Robigus and Claire have been sequenced by the Earlham Institute, and the remaining six parents are currently being sequenced. The population was initially used to map the *B1* awning locus as a proof-of-concept, highlighting the utility of these populations for use in mapping traits.

Particular benefits of the MAGIC population include multiple generations of inter-crossing and the large allelic variation within the population derived from the 8 founding parents. Currently the population consists of more than 700 genotyped F_7 lines; the generations of inter-crossing mean that the chromosomes are highly re-combined, facilitating trait mapping via GWAS.

Data pertaining to the MAGIC populations can be obtained from the NIAB website: http://www.niab.com/pages/id/402/NIAB_MAGIC_population_resources. All of the 1,091 recombinant-inbred lines (RILs) can be ordered by contacting James Cockram, as detailed on the website. Details on the pedigrees of the various RILs can be downloaded as an Excel file, "MAGIC_pedigree_tables.xlsx" (A). 720 RILs (at F_5) were genotyped using the iSelect SNP array, which can be downloaded from the website (B). From this data, 643 lines were used to develop a genetic map of the MAGIC population, as detailed in Gardner *et al.,* 2016 (C). Alongside the genetic data, a selection of phenotypic data from previous publications is also available on the website (D). This phenotypic data includes traits such as flowering time, yield, various disease scores, awns, and

Seed availability

We cannot maintain large stocks of all the lines. We can supply ten seeds each of the 1091 RILs, currently at F7, subject to the cost of shipping (including any phytosanitary and other import charges) and a small charge for the cost of seed replacement. Contact James Cockram for further information. We also ask that you download our Material Transfer Agreement, sign and date it, and return it to James Cockram at NIAB, either by fax (+44 (0)1223 277602), post or by email as a scanned document.

Files for downloading:

All Phenotype and marker data analysed in:

Scutari Marco, et al. (2014) Multiple quantitative trait analysis using bayesian networks. *Genetics* 198:129-137

Scutari_et_al_2014.zip ← **D**

All marker data:

MAGICeliteSNPs.zip ← **B**

Line means for awns, analysed in:

Mackay et al (2014) An eight-parent multiparent advanced generation inter-cross population for winter-sown wheat: creation, properties, and validation. *G3: Genes| Genomes| Genetics* 4:1603-1610.

awns.csv ← **D**

Pedigree information on the MAGIC elite population:

MAGIC pedigree tables.xlsx ← **A**

MAGIC genetic map published in:

Gardner, K.A., Wittern, L.M., Mackay, I.J. (2015) A highly recombined, high-density, eight-founder wheat MAGIC map reveals extensive segregation distortion and genomic locations of introgression segments. Plant Biotechnol. J., *doi*: 10.1111/pbi.12504

MAGIC_genetic_map_PBJ2015.xlsx ← **C**

Accessing the NIAB MAGIC population. As discussed above, details on the MAGIC pedigree (A), marker data (B), genetic map (C), and phenotypic data (D) can be downloaded from the NIAB website. This is a screenshot of the body of the webpage accessed at http://www.niab.com/pages/id/402/NIAB_MAGIC_population_resources.

References:

Mackay, I. J., et al. (2014). "An Eight-Parent Multiparent Advanced Generation Inter-Cross Population for Winter-Sown Wheat: Creation, Properties, and Validation." G3: Genes|Genomes|Genetics 4(9): 1603.

CSIRO MAGIC populations

Two separate MAGIC populations have been developed from Australian wheat cultivars by CSIRO. There is a 4-way MAGIC population, derived from four Australian spring wheat varieties, Yipti, Chara, Baxter, and Westonia (Huang *et al.,* 2012).

A second, 8-way MAGIC population was also developed, derived from three of the same cultivars alongside five other parents obtained from Canada, Israel, China, Mexico, and the USA.

Data for the 8-way MAGIC population can be downloaded from the following website: https://data.csiro.au/dap/landingpage?pid=csiro%3A37477 or from the CSIRO Data Access Portal: https://data.csiro.au/collections/#/collection/CI37780. Requests for access to the populations can be made to Bill Bovill at CSIRO (Bill.Bovill@csiro.au).