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Table 2: Natural variation resources available in wheat.

Collection	Short description
Wild wheat relatives and progenitor species	
Seeds of Discovery	Wheat and wild relative accessions held by ICARDA and CIMMYT
Open Wild Wheat	Accessions of *Aegilops tauschii* (D genome progenitor)
Wild wheat introgression lines	Introgression lines from *Aegilops caudata, Aegilops speltoides, Amblyopyrum muticum, Thinopyrum bessarabicum, Thinopyrum elongatum, Thinopyrum intermedium, Thinopyrum ponticum, Triticum timopheevii, Triticum urartu*, rye and wheat cultivars (Chinese Spring, Higbury, Paragon, Pavon 76)
Synthetic hexaploid wheat	
Synthetic hexaploid wheat	Sythetic hexaploid wheats generated using *Aegilops tauschii* (DD) + European tetraploid (AABB) wheat
Wheat diversity panels	
Watkins historic collection of landrace wheats	World collection of wheat landraces grown as farmer saved seed before the 1930s. Genetically stable collection developed by two generations of single seed descent
GEDIFLUX (Genetic Diversity Flux) collection	Western European winter wheat varieties that individually occupied over 5% of national acreage from 1945 to 2000. Bi-parental populations with Paragon (ongoing)
NIAB wheat association mapping panel	Bread wheat varieties released between 1916-2007. Predominantly UK varieties (68%), also other North Western European countries e.g. France (10%) and Germany (8%)
OzWheat diversity panel	Genetic diversity in Australian wheat breeding (colonial landraces 1860s, first Australian-bred cultivars 1890s, CIMMYT-derived semi dwarfs 1960s, post 2000 wheat)
Vavilov wheat collection	Hexaploid wheat accessions including landraces, historic breeding lines and cultivars. Pure lines generated by single seed descent

WHEALBI wheat panel	Worldwide wheat accessions including diploid and tetraploid wild relatives, old hexaploid landraces and modern elite cultivars
Global Durum Wheat (GDP) panel	Diveristy used in durum wheat breeding programs globally, including landraces and modern varieties
Tetraploid wheat Global Collection (TGC)	Wild emmer wheat, domesticated emmer, durum wheat landraces and other tetraploid wheat sub-species (*Triticum aethiopicum, Triticum carthlicum, Triticum polonicum, Triticum turanicum, Triticum turgidum, Triticum karamyschevii* and *Triticum petropavlovsky*)
MAGIC populations	
CSIRO, Aus	4-way (parents Baxter, Chara, Westonia, Yitpi); 8-way (parents Baxter, Westonia, Yitpi, AC Barrie (Canada), Xiaoya54 (China), Volcani (Israel), Pastor (Mexico), Alsen (USA))
NIAB , UK	8-way (parents Alchemy, Brompton, Claire, Hereward, Rialto, Robigus, Xi19, Soissions); 16-way (Banco, Bersee, Brigadier, Copain, Cordiale, Flamingo, Gladiator, Holdfast, Kloka, Maris Fundin, Robigus, Slejpner, Soissons, Spark, Steadfast, Stetson)
Germany	8-way (Event, Format, BAYP4535, Potenzial, Ambition, Bussard, Firl3565, Julius)
Durum	4-way (Claudio (Italy), Colosseo (Italy), Neodur (France), Rascon/2*Tarro (advanced CIMMYT line))

Number of accessions
80,000 accessions: 56,342 domesticated hexaploid (8 taxa); 18,946 domesticated tetraploid (8 taxa); 3,903 crop wild relatives included all known 27 wild species from *Aegilops–Triticum* species complex and 11 genomic constitutions.
265 accessions
153 stable homozygous introgression lines available
50 synthetic hexaploid wheats + pre-breeding accessions; backcross populations with Robigus and Paragon also available
829 accessions (core set of 119 represent majority of assayed genotypic variation). $F_{4:5}$ mapping populations against Paragon, mainly for the core set.
479 accessions
480 accessions
285 accessions
295 accessions

487 accessions

1,056 accessions

1,856

1,500 (4-way) and 3,000 (8-way) RILs

NIAB 8-way MAGIC: >1,000 RILs; NIAB 16-way MAGIC: ~600 RILs

394 $F_{6:8}$ RILs

334 $F_{7:8}$ RILs

Genotyping
DArT-seq
Whole genome shotgun sequenced (10-30x)
35K Axiom Wheat Relative Genotyping array + 710 KASP markers (Grewal *et al.,* 2019)
35K Axiom breeders array
35K Axiom breeders array (Allen *et al.,* 2017); subset exome sequenced (Gardiner *et al.,* 2018)
35K Axiom breeders array
90k SNP array
90k SNP array + additional 26K SNPs from transcriptome data
DArtT-seq (34,311 polymorphic markers)

Exome capture (~600,000 genetic variants in ~40,000 genes; 12,000 genes identified as putative presence/absence variation compared to RefSeqv1.0)
90k SNP array
90k SNP array
90k SNP array, microsatellite and DArT markers > 20,000 SNPs mapped in each population
35K breeders array. Genome sequence (Claire, Robigus, others underway). Exome capture sequence of 16-way parents. Skim-seq of all RILs underway.
5,435 SNPs from SNP array
90k SNP array

Data/seed availability
CIMMYT Dataverse (http://hdl.handle.net/11529/10548030), **Germinate data warehouse** (http://germinate.cimmyt.org/wheat/). Records for all germplasm accessions can also be accessed at https://ssl.fao.org/glis/
Sequencing: https://opendata.earlham.ac.uk/wheat/under_license/toronto/; **Seed**: https://www.seedstor.ac.uk/search-browseaccessions.php?idCollection=38)
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Seed: https://www.niab.com/pages/id/326/Resources; **Genotype**: https://www.niab.com/pages/id/491/Wheat_90k_SNP_dataset; **Pedigree information**: https://www.niab.com/pages/id/501/UK_Wheat_varieties_Pedigree
Seed and Genotype: contact Shannon Dillon from CSIRO (Shannon.Dillon@csiro.au)
Genotype: Dr Lee Hickey at The University of Queensland (l.hickey@uq.edu.au); **Seed**: Australian Grains Genebank (sally.norton@ecodev.vic.gov.au)

Genotype: https://urgi.versailles.inra.fr/download/iwgsc/IWGSC_RefSeq_Annotations/v1.0/iwgsc_refseqv1.0_Whealbi_GWAS.zip; **Seed**: https://www.gbif.org/dataset/a52ca10a-136a-4072-a6de-3ec6e7852365

Genotype: ms in preparation; **Seed**: ICARDA genebank http://indms.icarda.org (Filippo Bassi, F.Bassi@cgiar.org)

Genotype: GrainGenes; **Seed:** on request for non-commercial use from University of Bologna (marco.maccaferri@unibo.it and roberto.tuberosa@unibo.it)

Seed and Genotype: on request from CSIRO (Bill.Bovill@csiro.au)

Claire and Robigus genomes: https://opendata.earlham.ac.uk/opendata/data/Triticum_aestivum/EI/v1.1/; **Genotyping and Seed**: http://www.niab.com/pages/id/402/NIAB_MAGIC_population_resources

Genotype and pedigree: http://doi.org/10.14459/2018mp1435172 (click the "open attachment browser" link); **Seed**: Bavarian State Research Centre for Agriculture (Freising, Germany)

Genotype and pedigree: https://onlinelibrary.wiley.com/doi/full/10.1111/pbi.12424; **Seed:** on request for non-commercial use from University of Bologna (marco.maccaferri@unibo.it and roberto.tuberosa@unibo.it)

More information/Reference
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