**Tracing the ancestry of modern bread wheats**

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**For more than 10,000 years, the selection of plant and animal traits that are better tailored for human use has shaped the development of civilizations. During this period, bread wheat (Triticum aestivum) emerged as one of the world’s most important crops. We used exome sequencing of a world-wide panel of almost 500 genotypes selected from across the geographical range of the wheat species complex to explore how 10,000 years of hybridization, selection, adaptation and plant breeding shaped the genetic makeup of modern bread wheats. We observed considerable genetic variation at the genic, chromosomal and subgenomic levels deciphering the likely origins of modern day wheats, the consequences of range expansion and allelic variants selected since its domestication. Our data supports a reconciled model of wheat evolution and provides novel avenues for future breeding improvement.**

Bread wheat has an allo-hexaploid genome consisting of three closely related subgenomes (AABBDD). It is proposed to have originated from two polyploidization events, (*i*) a tetraploidization some 0.5 million years before present (ybp) from the hybridization between wild Triticum urartu Tumanian ex Gandilyan (AA) and an undiscovered species of the Aegilops speltoides Tausch lineage (BB), followed by (*ii*) a hexaploidization some 10,000 ybp as a result of hybridization between a descendant of this original tetraploid hybrid (AABB) and the wild diploid Aegilops tauschii (Coss) (DD)**1**. Archaeobotanical evidence suggests that the resulting allo-hexaploid wheats were domesticated in the Fertile Crescent, a region extending from Israel, Jordan, Lebanon, Syria to South-East Turkey, to northern Iraq and western Iran **2-5**. Modern cultivated bread wheats are therefore the product of at least 10,000 years of human selection during domestication and cultivation (improvement and breeding). Today they comprise high-yielding varieties adapted to a wide range of environments ranging from low humidity regions in Nigeria, Australia, India, and Egypt to high humidity regions like South America**6***.*

**results**

**Wheat genomic diversity** - In order to explore the origins and patterns of genetic diversity that exist within the currently accessible wheat gene pool, we assembled a worldwide panel of 487 genotypes that included wild diploid and tetraploid relatives, domesticated tetraploid and hexaploid landraces, old cultivars and modern elite cultivars (Supplementary Table 1). Mapping exome capture sequence data**7** from these lines onto the ‘Chinese Spring’ reference genome sequence (IWGSC**8**) revealed 620,158 high confidence genetic variants (including 595,939 SNPs and InDels between hexaploid genotypes) distributed across 41,032 physically ordered wheat genes (Supplementary Table 2). Equivalent sequence coverage at the chromosome and homoeologous gene/region levels (medians within one standard deviation) excluded bias in the detection and calling of structural variants (Supplementary Figure 1). Furthermore, correlation between gene and structural variant distribution (r>82%) across the three subgenomes, expected from exome capture experiment, supports the lack of bias in genic variant detection at the chromosome level with a visible gradient from distal gene-rich regions to pericentromeric gene-poor regions (Supplementary Figure 2). Both individual subgenomes (with a B>A>>D gradient) and chromosome compartments (with a telomere>core>>centromere gradient) exhibited differences in structural variant enrichment (Supplementary Figure 3). In summary, our variant dataset provides a comprehensive overview of wheat genomic diversity at various scales (gene, region, chromosome and genome), and represent a rich source of genetic information for exploitation by both the academic and agricultural research communities (Figure 1, circles #1 to #3).

Phylogenetic and principle component analyses revealed three major factors driving the partitioning of diversity within our panel (Figure 2): vernalization requirement (winter *vs* spring), historical groups (groups I to IV, oldest to newest: old landraces to modern elite lines) and geographical origin (Europe, Asia, Oceania, Africa and America), Figure 2a and Supplementary Figure 4. Among the 11 major tree clades chosen on the criteria of size, representativeness and statistical support, permutation tests for the conservation of clade monophyly confirmed a strong grouping for all three factors (p-value<10e-6). However, the deep structure of the phylogeny is centered around continental difference, and subsequently more recent shifts in growth habit traits (such as vernalization requirement) resulting from intense selection for yield in modern wheat breeding practices. Superimposing both country and continent of origin onto the phylogenetic clusters suggests that the observed genetic diversity is mainly structured along an east-west axis consistent with established routes of human migration out of the Fertile Crescent. Two paths to Western Europe follow an inland (*via* Anatolia and the Balkans to Central Europe) and a coastal (*via* Egypt to the Maghreb and Iberian Peninsula) route, complemented by two additional paths north-east and along the Inner Asian Mountain Corridor, followed by further colonization events in American, Oceanian, African territories (Figure 2b, Supplementary Figure 5) **9**.

**Wheat selection footprints** - We next explored selection footprints resulting from domestication (comparing wild and domesticated wheats) and breeding (comparing historical bread wheat groups I to IV) using a sliding-window (as opposed to variant- or gene-centric) approach to deciphering local reduction in diversity and taking into account the geographical structuring of the wheat panel (Figure 1 circles #4 and #5). For the detection of domestication signals, we computed the nucleotide diversity per site (π) over non-overlapping 1 Mb sliding windows for wild diploid (*T. urartu*, *A. speltoides*, *A. tauschii*), wild tetraploid (*T. dicoccoides*) and the domesticated hexaploid (*T. aestivum*) wheats from Asia, where the previous diploid and tetraploid progenitors in our panel originated. Contrasts between wild wheat ancestors and hexaploid landraces support considerable heterogeneity in the reduction of diversity (RoD) during the domestication process along the wheat genome (Supplementary Figure 6). Strongly affected genomic regions (1,221), showing a loss of at least four-fifths of the diversity (RoD>0.8, red dots in Figure 1 circle #5), cover 9% of the wheat genome (1.2 Gb). Known domestication genes conferring brittle rachis *(Brt)*, tenacious glume *(Tg)*, homoeologous pairing (*Ph*) and non-free-threshing character *(Q)* were identified in close (<5 Mb distance) proximity to these regions. Interestingly, known domestication genes only account for a minority of the observed peaks, suggesting that further domestication genes still need to be discovered (Supplementary Table 3) **10-11**, as reported for other grass species such as maize12.

To unravel genomic regions targeted by breeders during the last two centuries (since 1830) of wheat improvement, we compared the RoD statistics in the European panel within historical groups II, III and IV (*i.e.* those subject to breeding) to those of Group I (landraces), Figure 3a. Our results are consistent with two main rounds of diversity reduction, an initial wave between Groups I and II (11.7% of RoD), reflecting early breeding improvement, and a second wave between groups III and IV (13.3% of RoD) that followed the green revolution (*i.e*. renovation of agricultural practices starting between 1950 and the late 1960s). Modern wheat varieties showed an average loss of nucleotide diversity of 21.8% compared to those of Group I, with strong variation within and between chromosomes (Figure 3b). This appeared to be more intense on the A (median RoD =33.2%) and B (median RoD =28.0%) subgenomes compared to the D subgenome (median RoD =5.8%), which may reflect their different contributions to wheat improvement (Figure 3a). To identify genetic markers/regions selected by wheat breeders, we performed a genome-wide scan across all samples using the individual-centric method PCAdapt**13** to take into account the graduated population structure within and between groups, and at a higher granularity among European and Asian samples separately (Supplementary Figure 7). We identified 5,089 polymorphic sites exhibiting improvement signals (p-values < 0.0001, red dots in Figure 1 circle #4). Known genes including *Ppd* and *VRN* genes forphotoperiod sensitivity andvernalization, *Rht* for reduced height, *Glutenin* (Glu) and *Gliadin* (Gli) genes involved in seed storage protein accumulation, *FZP* for Frizzy panicle, *GNS* for grain number, *Wx* for waxy as well as the *CUL* (uniCULm) gene driving plant architecture, were located close (<5 Mb distance) to these improvement signals (Supplementary Table 3)**14-17**. Large genomic regions (>10 Mb) where selection appears to have occurred during the last two centuries (between historical groups I and IV) and eventually become fixed, were observed especially on chromosome 1A and the two most structurally re-arranged chromosomes 4A and 7B of the wheat genome (Figure 3b)**18**. Extending the 8,308 and 9,948 polymorphic sites associated to improvement footprints observed in the European and Asian genotypes over 2 Mb overlapping windows, defined a cumulative genomic space of 950 Mb (7% of the genome) and 1.3 Gb (9% of the genome) with selection signatures for the two geographical areas respectively. Interestingly, only 168 Mb (13 to 18% of the previous genomic space under selection) of the genomic regions harboring selection signatures are identical between the European and Asian germplasm, suggesting independent improvement targets from the two geographic origins (Supplementary Figure 7).

We then tested whether the observed allelic variation could be linked to two key life-history traits, heading date (HD) and plant height (PH) by conducting multi-environment genome-wide association studies (GWAS), Figure 1 circles #6 and #7. We grew and evaluated 435 hexaploid bread wheat genotypes for heading date and plant height in four common garden experiments (partially replicated design) in France (INRA, Clermont-Ferrand), Hungary (ATK, Martonvasar), Turkey (University of Çukurova, Adana) and United Kingdom (KWS, Cambridge). A sub-set of 390,657 SNPs, stringently filtered for call rate (<0.80) and Minor Allele Frequency (MAF, >0.05) was used for GWAS. We identified 48 and 40 genomic sites significantly associated (p-values of 0.01 FDR significance thresholds) with variation in HD (Supplementary Figure 8, Supplementary Table 4) and PH (Supplementary Figure 9, Supplementary Table 5) respectively, including regions (<15 Mb) containing known (*Ppd*, *VRN, FDL* for Flowering Locus D like, *WPCL* for Phytoclock for HD and *Rht* for PH)**19** and unknown genes. The current data provide the basis for identifying relevant candidate genes in the previously detected, but currently unknown, loci for functional validation, as exemplified for the major HD association detected on the chromosome 2A where *Cry* (Cryptochrome) is a putative driver (Supplementary Figure 8). Notably, diversity, selection footprint and GWAS analyses clearly showed that only a small fraction of homoeologous loci harbour coincident signals, supporting the view that modern hexaploid bread wheats behave genetically as diploids, as previously suggested from the convergent pattern of (also referenced as parallel advantageous) selection shown to be rare between homoeologous regions 14.

**Wheat origins** - Finally, we implemented a network-based phylogenetic approach**20-21** involving the inference of 1,000 trees from repeated random haplotype samples (RRHS) with maximum likelihood, subsequent graph reconstruction analysis and community clustering to reconstruct the reticulated evolutionary history of modern hexaploid bread wheats from their diploid and tetraploid progenitors. The resulting clustered consensus network (Figure 4a) comprises signals of vertical (species relationships) and horizontal (reticulation) events within the *Triticum*-*Aegilops* species complex. The intermediate positioning in network of synthetic polyploid wheats (*i.e* synthetic *T. turgidum* deriving from *T. durum* x *T. dicoccoides* and synthetic *T. aestivum* deriving from. *T. durum* x *A.* *tauschii*) between their direct progenitors validate the robustness of our phylogenetic inference of the entire wheat panel (Figure 4a, Supplementary Figure 10). An integrative model of wheat evolution (Figure 4b) was derived from the combined conclusions drawn from the in-depth analysis of the networks’ edges and edge weights**20-21** (Figure 4a, Supplementary Figure 10, Supplementary Table 6), and supported through the evaluation of alternative consensus tree topologies**22** (Supplementary Figure 11) and gene flow tests using Patterson's D statistic**23** (Supplementary Figure 12, Supplementary Table 7). For example, we were able to reconstruct, at the subgenome level, the introgressions at the base of modern synthetic *T. turgidum (*F7 RIL offsprings) polyploids mentioned earlier and detected as hybrids (Supplementary Figures 10-11-12) by all methods with dominant *T. dicoccoides* genotypes and multiple independent *T. durum* introgressions**24**, illustrating the resolution obtained by using a combination of complementary approaches.

Our proposed model (Figure 4b) largely refines the widely accepted evolutionary path leading to modern bread wheat with the hybridization of wild diploid AA and SS (close to BB) genotypes leading to wild tetraploid AABB progenitors, which subsequently hybridized with a wild diploid DD genotype resulting in the hexaploid *T. aestivum* (AADDBB) lineage**24**. In our analysis, the wheat B genome is confirmed to be derived from the *Aegilops* section *Sitopsis* lineage, which gave rise to *A. speltoides* (SS), while the progenitors of *A. tauschii* and *T. urartu* represent the established origins of the D and A genome lineages, respectively**25**. *T. araraticum* (also referenced as *T. araraticum* Jakubz) represents the closest wild descendant of the AAGG tetraploid ancestor. It appears to have been subsequently domesticated to form *T. timopheevii* (Zhuk.) Zhuk while also hybridizing with *T. boeoticum* leading to the hexaploid *T.* zhukovskyi (Menabde & Ericzjan) lineage (AAAAGG)**26,27**. The model confirms wild emmer (*T. dicoccoides*) as the closest descendant of the progenitor of the modern A and B wheat subgenomes of all the modern tetraploid AABB and hexaploid AABBDD genotypes. Our data suggest that during the early phase of domestication and cultivation, a pool of wild emmer wheat *T. dicoccoides* (Körn. ex Asch. & Graebner) Schweinf. gave rise to at least two distinct lineages of domesticated tetraploids, *T. dicoccum* Schrank ex Schübl. (domesticated emmer, also known as *T.* *dicoccon* Schrank) and *T. durum* Desf. (domesticated durum or hard or pasta wheat)**28,29**. Finally, the model supports *T. aestivum* as being most likely derived from an ancestral hybridization event between the previous *T. durum***30** lineage and a D lineage close to wild *A. tauschii***31** (Figure 4b, Supplementary Figure 11). Subsequently, *T. spelta* emerged from the hybridization between the hexaploid *T. aestivum* and the tetraploid *T. dicoccum,* and still harbors evidence of *T. dicoccum* introgressions today (Supplementary Figure 12). Additional putative reticulation events (Supplementary Figure 12), supported only by either of the three analytical approaches (network, tree, Patterson's D) need further investigation and were not integrated in our evolutionary model (Figure 4b).

Such a reticulated evolutionary scenario would first have led to a founder hexaploid bread wheat gene pool (*α* community, Figure 4a) that was established during and following domestication. This would likely have consisted of primitive wheat landraces originating in the Fertile Crescent, leading to two (*β* and γ) derived communities of hexaploids (Figure 4a, Supplementary Figure 13). While the γ cluster is enriched for modern genotypes from Western Europe (*i.e*. lines originating from 1986 or later, mostly comprising wheat cultivars and current varieties), the β cluster is enriched for Eastern Europe countries formerly part of the Warsaw Pact from May 1955, during the Cold War. The clear separation in evolutionary phylogeny between these two modern pools (β and γ) may reflect how human history and resulting socioeconomic consequences have influenced the genetic makeup of modern wheat germplasm, with β genotypes still grown in Hungary and Ukraine today, while γ genotypes still dominate many parts of the European Union.

**discussion**

Bread wheat derives from a reticulated evolution from its di- and tetraploid progenitors involving massive and recurrent hybridization and gene flow events with T. *dicoccoides* beingthe progenitor of the A and B subgenomes of all the modern tetraploid and hexaploid genotypes, and the *T. durum* lineage being the most likely ancestor of today’s bread wheat cultivated germplasm. Such a complex history of hybridizations and gene flows explains the observed partitioning of diversity at the genomic scale (impoverished on the D subgenome) and supports the view that modern hexaploid bread wheats behave genetically as diploids with compartmentalized selective footprints, as well as trait loci, with only a small fraction of homoeologous loci harbouring domestication and/or breeding sweeps or driving phenotypic traits showing coincident signals. Modern bread wheat originated in the Fertile Crescent some 10,000 ybp and the variation observed in the genepool today has been shaped during domestication by human migration, anthropogenic selection and latterly by breeding. Associations identified between diversity and both known and novel genes influencing plant height and flowering time demonstrate the potential value of our panel for both fundamental and applied studies. Importantly, the hallmarks of adaptation to new environments remain highly topical research subjects during a period of accelerated climate change and both our selective sweep analyses and GWAS highlight targets for future gene and/or allele discovery. The combined data and germplasm collection we report here and made available to the broader research community represents a rich source of genetic diversity that should find application in understanding and improving diverse traits, from environmental adaptation to disease resistance and nutrient use efficiency.

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**figure legends**

**Figure 1: Wheat genome diversity map.** Genome histograms illustrating (from outer to inner circles) the density in genes (1), SNPs (2), InDels (3), genome scan for improvement among European genotypes (4), reduction of diversity during the domestication between wild tetraploids *vs* domesticated hexaploids for subgenomes A and B and between wild diploids *vs* domesticated hexaploids for subgenome D (5), as well as GWAS for heading date (HD, 6), plant height (PH, 7) on the 21 chromosomes (from 1A to 7D) illustrated in circles for the three subgenomes (A, B and D). Homoeologous genes are joined with colored lines between chromosomes in the center (8). The three outer circles show centromeres (grey blocks) and telomeres (blue blocks).

**Figure 2: Geographical components of the panel structure. a-** Cartoon illustrating the phylogenetic relatedness among the hexaploid bread wheat genotypes, with a color code (right) in pie charts along the 11 major tree clades illuminating their geographical origins (see the associated world map in panel B), historical groups (I to IV) and growth habit (winter, spring, alternative, and facultative). **b**- Cartoon illustrating the phylogenetic relatedness between wheat accessions of different geographical origins (see color legend in panel A) with colored connecting lines on the world map illustrating phylogenetic tree edges (panel A) associated with a mean of at least 1 transition per simulation and illuminating the known historical routes of wheat migration, out of the Fertile Crescent (green connecting lines), west through inland (1) and coastal (2) paths, and north-east (3) and along the Inner Asian Mountain Corridor (4) followed by further colonization (black connecting lines) of American (5), African (6), Oceanian (7) territories.

**Figure 3: Temporal evolution of wheat diversity**. **a-** Nucleotide diversity (π, y-axis) from the hexaploid wheat genotypes (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). **b**- Chromosomal distribution (x-axis) per subgenomes (A, B and D) of nucleotide diversity (π y-axis) between landraces (group I) and modern wheats (group IV, dots) with bars illustrating the range of variation in diversity between these two groups (colored in red for ROD≥80%). Large regions of reduced diversity are shown in grey boxes.

**Figure 4: Model of reticulated evolution**. **a-** Clustered phylogenetic consensus genotype network of 1000 maximum likelihood tree topologies inferred from repeated random haplotype samples (RRHS). Nodes represent individual genotypes and are color-coded by taxon. Node size is proportional to the number of connections (*i.e*. node degree). Edges represent minimal evolutionary distances in the RRHS trees deduced by the minimal spanning tree (MST) algorithm and are color-coded by the respective subgenome (green: A; purple: B; orange: D). Edge transparency is proportional to the relative number of RRHS trees were the edge was an MST edge (*i.e*. edge weight). **b**- Cartoon, based on the current data, analysis, and prior assumptions illustrating the hexaploid bread wheat evolutionary scenario based on the stronger edges of the subgenomes phylogenetic networks (extracted using a minimum spanning tree available in Figure S11) with green, purple and yellow brown columns illustrating respectively the path from the A, B and D subgenomes with the species-centered color-code used in panel A. Arrow colors illustrate the phylogenetic relatedness between subgenomes (plain arrows are indicative of the main, vertical signal; and dashed arrows show alternative path well supported by the inferred topologies and indicative of introgression or gene flow). Circles illuminate putative extinct ancestor intermediates. Additional *Sitopsis* species (white framed grey boxes) were not part of this study, but are included for completeness.

**methods**

**Plant material -** The wheat panel consists of 487 genotypes comprising 13 diploid, 38 (including 25 AABB) tetraploid and 436 (including 435 AABBDD) hexaploid genotypes including landraces, cultivars and currently grown varieties from 68 countries. For a detailed description of all lines/varieties used in this study see Table S1 and passport information available at https://urgi.versailles.inra.fr/download/iwgsc/IWGSC\_RefSeq\_Annotations/v1.0/iwgsc\_refseqv1.0\_Whealbi\_GWAS.zip. The genotypes were structured into four historical groups: landraces (group I, before 1935), old cultivars (group II from 1936 to 1965), cultivars (group III, from 1966 to 1985) and modern varieties (group IV, after 1986). The genotypes have been grouped according to their country of origins with (in alphabetic order): Af, Afghanistan; Ag, Argentina; Alb, Albania; Alg, Algeria; Ar, Armenia; As, Austria; Au, Australia; Az, Azerbaijan; Be, Belgium; Bu, Bulgaria; Br, Brazil; Ca, Canada; Ch, China; Co, Colombia; Cr, Croatia; Cz, Czech republic; Dn, Denmark; Eg, Egypt; Et, Ethiopia; Fi, Finland; Fr, France; Fyrm, Former Yugoslav Republic of Macedonia; Ge, Germany; Go, Georgia; Gr, Greece; Hu, Hungary; In, India; Ir, Iran; Is, Israel; It, Italy; Ja, Japan; Ke, Kenia; Ko, Korea; La, Latvia; Le, Lebanon; Me, Mexico; Mo, Morocco; Ne, Nepal; Ni, Niger; Nt, Netherlands; Nz, New Zealand; Pa, Pakistan; Po, Poland; Pr, Portugal; Ro, Romania; Ru, Russia; Sa, South Africa; Sp, Spain; Sw, Sweden; Sy, Syria; Sz, Switzerland; Ta, Tajikistan; Tk, Turkmenia; Tn, Tunisia; Tu, Turkey; Uk, United Kingdom; Ukr, Ukraine; Ur, Uruguay; Usa, United States of America; Zi, Zimbabwe. The genotypes have been finally grouped according to regions and continents of origins with Fertile Crescent (Ir, Is, Le, Sy, Tu), Central Asia (Af, Ar, Az, Go, Pa, Ta, Tk), Eastern Asia (Ch, Ja, Ko), Northern Asia (Ru), Central Europe (Alb, Bu, Cr, Cz, Fi, Hu, La, Po, Ro, Ukr, Fyrm**),** Southern Europe (Gr, It, Pr, Sp), Western Europe (As, Be, Dn, Fr, Ge, Sw, Sz, Nt, Uk), Indian Peninsula (In, Ne), Northern Africa (Alg, Eg, Mo, Tn), Sub-Saharan Africa (Et, Ke, Ni, Sa, Zi), South America (Ag, Br, Co, Ur), North America (Ca, Me, Usa), Oceania (Au, Nz).

**Exome sequencing -** As the large wheat genome consists of >80% mobile and repeated elements, whole-genome resequencing is a cost-intensive and likely highly error-prone approach to comprehensively catalogue genetic diversity. To circumvent this limitation, we used a wheat exome-based target enrichment sequencing assay to capture variation in and around the gene-containing regions of 487 wheat genotypes. We selected Roche’s Nimblegen SeqCap EZ wheat exome design (120426\_Wheat\_WEC\_D02), https://sequencing.roche.com/en/products-solutions/by-category/target-enrichment/shareddesigns.html. This is a design comprising 106.9Mb of low copy regions of the wheat genome developed by the Wheat Exome consortium**7,14**. To optimize the cost, we used a multiplex of six individually barcoded accession DNAs, combined prior to capture. Captured DNA were sequenced as paired ends (2x125 bp) on Illumina HiSeq instruments using HiSeq2500 high output mode. Genomic DNA (gDNA) samples were checked using the PerkinElmer DropSense in order to verify gDNA integrity. Samples were quantified by Picogreen assay and normalized to 20 ng/ul in 10 nM Tris-Hcl (pH 8.0) as suggested in the NimbleGen SeCap EZ Library SR protocol. The gDNA was fragmented at the mean fragment size of 350 bp and whole genome libraries were prepared according to the Kapa Library Preparation protocol and quantified by Nanodrop. Six libraries were pooled and used for the hybridization with the SeqCap Ez oligo pool (Design Name: 120426\_Wheat\_WEC\_D02) in a thermocycler at 47°C for 72 h. Capture beads were used to pull down the complex of capture oligos and genomic DNA fragments and unbound fragments were removed by washing. Enriched fragments were amplified by PCR and the final library was quantified by qPCR and visualized on Agilent Bioanalyser. Sequencing libraries were normalized to 2 nM, NaOH denatured and used for cluster amplification on the cBot. The clustered flow cells were sequenced on Illumina HiSeq2500 high output mode with a 6-plex strategy (*i.e.* 6 samples per HiSeq lane) with a 125 bp paired-end run module. Exome capture (Nimblegen) and next generation sequencing (Illumina) delivered on average 34 million read pairs per genotype.

**Variant (SNPs, InDels) calling** – Raw reads were mapped to the hexaploid Chinese Spring reference sequence v1.0 using the 'mem' subcommand of BWA (version 0.7.12, http://bio-bwa.sourceforge.net/). Samtools (version 1.3, http://samtools.sourceforge.net/; http://www.htslib.org/) was used to mark duplicate reads. Variants were called using samtools/bcftools (version 1.3) and filtered for overlap to exonic regions (+/- 1 Kbp) based on the current IWGSC genome annotation v1.0. Genotypes were subsequently filtered for a minimum sequencing depth (DP) of 3 and a genotype quality (GQ) of at least 10. Two sets of genotype calls from experiments with Axiom 35k and iSelect 80k SNP arrays (details from CerealsDB, http://www.cerealsdb.uk.net/) with a total of 38 genotypes in common between either of those sets and the current exome capture were used to approximate optimal filter criteria leading to the lowest false discovery rate (FDR). Variant positions were removed if the total count of samples with defined genotype (e.g. not missing) was below 10 or the minor allele frequency was below 1% to derive the initial set of variants. This set was further subjected to imputation using beagle (default parameters) and the output was again analyzed for false discovery rate by comparison to iSelect genotype information. Based on this evaluation, the optimal trade-off between FDR, number of variants and missing values was considered to be 0.6 for genotype probability (GP, estimated by beagle) and 4% minor allele frequency (MAF, after imputation) and the final imputed variant dataset was generated applying these criteria. We detected 620,158 small-scale variant positions on to the IWGSC Refseqv1.0 wheat genome assembly (targeting 41,032 of the 110,790 high confidence HC genes). The variants comprised 56,163 Indels (9%) and 563,995 SNPs (91%). 595,939 of the variants (96%) were found in the 435 AABBDD hexaploid genotypes (Table S2).

**Phylogenetic analysis - *Hexaploids phylogeny*-** The analysis of phylogeny for the 435 hexaploid bread wheat was inferred on an alignment of 91,554 SNPs (for a total of 65,467 distinct alignment patterns) found on triplets (2,855) of orthologous genes conserved in all three subgenomes A, B and D. The data was analyzed with iqtreeX**20** (GTR+GAMMA(4) model), with 1,000 ultrafast bootstraps**32**. Geographical regions for ancestral nodes were reconstructed using the following protocol: 10,000 simulations were performed using the stochastic mapping algorithm of the R phytools package**33** (using the equal rates model), the region of a node was then chosen as the one with maximum sampled frequency. Eleven major tree clades were identified based on criterion of size, representativeness and statistical support to offer a good coverage of the tree, while taking into account sampling bias for European individuals. World maps used to illustrate the geographical structure of the panel diversity were obtained with R packages (countrycode, geosphere, maps) in Figure 2b, Supplementary Figures 5-13c. ***Di-Tetra-Hexaploids phylogeny*-** To account for ambiguities and possible biases in phylogenetic inference from SNP data arising from varying levels of heterozygosity, linkage disequilibrium (LD), incomplete lineage sorting and reticulate evolution, we implemented a network-based approach to reconstruct the species history and community structure in the sampled *Triticeae* genotypes. To this end, we stringently filtered biallelic, polymorphic SNPs present in >90% of the genotypes from non-imputed data accounting for LD (delivering 15,490 filtered SNPs) and implemented a repeated random haplotype sampling procedure including heterozygous sites (RRHS**21**) to infer 1,000 maximum likelihood tree topologies with the ASC\_GTRGAMMA model and JC69 distances in RAxML (asc-corr=felsenstein). While these RRHS trees were analyzed also in the form of conventional consensus topologies and densitree visualizations, to infer taxonomic clades, we analyzed the evolutionary distances among the tips of the 1,000 trees using the minimum spanning tree (MST) algorithm in Python. The MST graphs were subsequently combined into a weighted, phylogenetic consensus network whose nodes were clustered into clades using the Newman-Girvan Edge-Betweenness algorithm in Cytoscape 3.6**34**. The clustered network topology was plotted considering edge-betweeness in Cytoscape and taxonomic clades were inferred by intersection of community clusters with taxon information which was annotated using the AutoAnnotate plugin**34**. The relative number of RRHS trees where a respective edge was selected by the MST algorithm were used as edge weights and were interpreted similar to bootstrap support values in the consensus tree topologies. The composition, geographical and historical origins of the identified wheat communities were analyzed using χ2tests and barplots in R. Gene flow in subgenomes A and B was investigated with the Patterson's D statistic (or ABBA-BABA statistic) using ANGSD**35** with a threshold of Z statistic > 4**36**. An integrative model (Figure 4b) of wheat evolution was built by manual consolidation of the support values of the edges in the phylogenetic consensus network (Figure S10 and table S7), the various consensus and IUPAC tree topologies (Figure S11), the ABBA-BABA results (Figure S12) as well as the literature. Where species relationships remained ambiguous on the sole basis of the network approach, *i.e.* when similar phylogenetic relatedness between groups of genotypes defines several possible evolutionary paths between putative progenitors and descendants, we then considered the results of the ABBA-BABA statistical test (Figure S12 as well as Table S6), and the existing literature when available. The Figure 4b only reports the reticulation events identified on the basis of phylogenetic consensus networks supported by the ABBA-BABA analysis in both the A and B subgenomes.

**Diversity analysis & selection footprints** – ***Improvement***- Genome scans breeding signatures among the hexaploid samples were performed under PCAdapt**13**, an individual-based method of genome scan able to handle massive NGS data. Given that PCAdapt is based on principal components, this method does not require any partitioning of the dataset in different groups and can therefore be applied on continuous pattern of population structure. This method is therefore conceptually robust to any source of errors associated with the boundaries of these groups and can take into account the gradual variation among all individuals of the improvement continuum (*i.e.* time series-like data). For each dataset, selection of the best number of principal components (K) was performed after a first assessment of the percentage of variance explained by 20 principal components. Analyses were performed assuming K=4 for the whole dataset and K=3 for both European and Asian datasets. Computations were run under R version 3.4.3. Candidate genes for improvement are either associated with highly significant p-values or considered in close vicinity (0 to 5 Mb) to loci with breeding signatures (Table S3). π and Tajima’s D was computed over 1 Mb non-overlapping sliding windows on European genotypes to take into account the strong signal of intercontinental genetic signatures. To perform this analysis, we took into account the number of sites covered by reads aligned to the reference. All sites with a total depth of coverage greater than 1,461 (*i.e.* at least 3 reads per individual on average) were considered as covered. A ROD (reduction of diversity) index was then estimated for each 1 Mb window by comparing diversity of each group (II, III or IV) to “Landraces” (Group I) as following: 1 – (π Group / π Landraces). To further explore population structure, principal Component Analysis (PCA) was performed with the R package FactoMineR**37**. Signatures of improvement were detected for loci associated with a p-value < 0.0001*, i.e.* a -log10-transformed p-value >4. ***Domestication***- Similarly, genomic regions with domestication signatures were identified using differences in diversity (π) between diploid, tetraploid and hexaploid genotypes by computing the ROD index over 1Mb windows. Signatures of domestication were detected for regions associated with ROD >0.8. Candidate genes for domestication were considered in close vicinity (0 to 5 Mb) to loci with domestication signature (Table S3). Visualization were performed with R**38** packages such as graphics, stats, circlize and dendextend**39-42**.

**Field experiments and GWAS** - These analyses focused on 435 hexaploid wheat genotypes evaluated for heading date and plant height in four common garden experiments in France (INRA, Clermont-Ferrand), Hungary (ATK, Martonvasar), Turkey (University of Çukurova, Adana) and United Kingdom (KWS, Cambridge). Trials were grown under an augmented partially-replicated design with 20% of the genotypes replicated twice and two check cultivars assigned uniformly to eight plots. Raw data were corrected for spatial heterogeneity using replicated controls and the SpATS package in R**43**. After filtering out SNPs with Call Rate <0.80 and Minor Allele Frequency (MAF) <0.05, a final set of 390,657 SNPs were used for subsequent analysis. Finally, circular genome maps were drawn under the R package circlize**44**.A chromosome-specific kinship matrix was calculated using 1,000 SNPs sampled at random from each chromosome. In this chromosome-specific kinship, , is the realized additive genetic relationship matrix calculated from all molecular markers along the whole genome, except those in the chromosome being tested**45**. For example, to test SNPs in chromosome 1A, was calculated with SNPs sampled from all chromosomes, except those from 1A. was calculated following the equation proposed by Astle and Balding**46**, with as typical entry for the relationship between genotypes *i* and *j*:

(1)

where is a marker score indicating the allele count for least frequent allele (2, 1, 0) for genotype *i* at marker *k*, and is the corresponding allele frequency. The matrix above was calculated using the “realizedAB” option in the “kin” function of the Synbreed package**47**.

A multi-environment mixed model GWAS analysis was performed analogous to the method described by Millet et al.**48** and Thoen et al.**49**. Correction for population structure and kinship was done on the basis of eigen vectors (“principal components”) extracted from the chromosome specific Astle and Balding kinship matrices, . The number of significant principal components was calculated following Patterson et al.**50**. We scanned the genome with the following single locus model:

(2)

In Equation (2), is an intercept term, the fixed environmental main effect stands for the genotype specific scores on the *p*-th kinship principal component, with *p=1...P*, and and are the corresponding fixed regression coefficients for these principal components correcting for population structure with respect to the genotype main effect and the GxE interaction, respectively. is a term for the fixed SNP effect, while contains the marker information. This means that fitted QTLs are allowed to have an environment specific effect, or, that at each marker position, QTLs model main effect and a QTLxE term simultaneously. The test for being zero in all environments or being non zero in at least one environment was a Wald test**51,52**. is a random genotypic main effect, is a random genotype by environment interaction. The random terms for and have variances and , that were restricted to be positive. The error term is environment-specific and was confounded with the term. The model was fitted in ASREML-R (VSN-International, 2016). Genomic control was applied a posteriori to correct for inflation**53**.

The genome-wide significance threshold with multiple testing correction was calculated following the method proposed by Li and Ji **54**. For each chromosome, the correlation matrix for the SNPs was calculated. Then, the effective number of independent tests per chromosome was estimated from the eigenvalues of the correlation matrix. The effective number of independent tests was summed across chromosomes (and the significance threshold for individual markers was calculated as , where the genome wide test level was .

**Software**. The relevant source codes and analysis workflows used to generate the results presented in the different sections of the manuscript, figures and tables, were deposited in a public github repository, accessible at https://github.com/dandaman/whealbiCode and comprise the following analysis steps: 1. Raw data processing and variant calling, 2. Genome-wide association study (Figure 1), 3. Geographical component of the panel structure (Figure 2a) 4. Components of the panel structure (Figure 2b) 5. Computation of nucleotide diversity (Figure 3) 6. Studying the phylogeny and reticulate evolution of the wheat species complex using repeated random haplotype sampling (RRHS; Figure 4) 7. Inference of hybridization and introgression events using ABBA-BABA (Figure 4b).

**Data availability.** All data analyzed and generated during this study are included in this published article and its supplementary information files (6 tables and 13 figures) and are available online at https://urgi.versailles.inra.fr/download/iwgsc/IWGSC\_RefSeq\_Annotations/v1.0/iwgsc\_refseqv1.0\_Whealbi\_GWAS.zip (Catalog of imputed and non-imputed variants as vcf file and passport information for the 487 genotypes as .xls file). The Whealbi SNPs data can be displayed in open access on the IWGSC reference genome browser55 at <https://urgi.versailles.inra.fr/jbrowseiwgsc/gmod_jbrowse/?data=myData%2FIWGSC_RefSeq_v1.0>. The sequence data are available at NCBI under the accession number PRJNA524104.

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**Editorial Summary:**

Exome sequencing of a worldwide panel of 487 wheat genotypes including landraces, cultivars and modern varieties sheds light on wheat genomic diversity and the evolution of modern bread wheat.