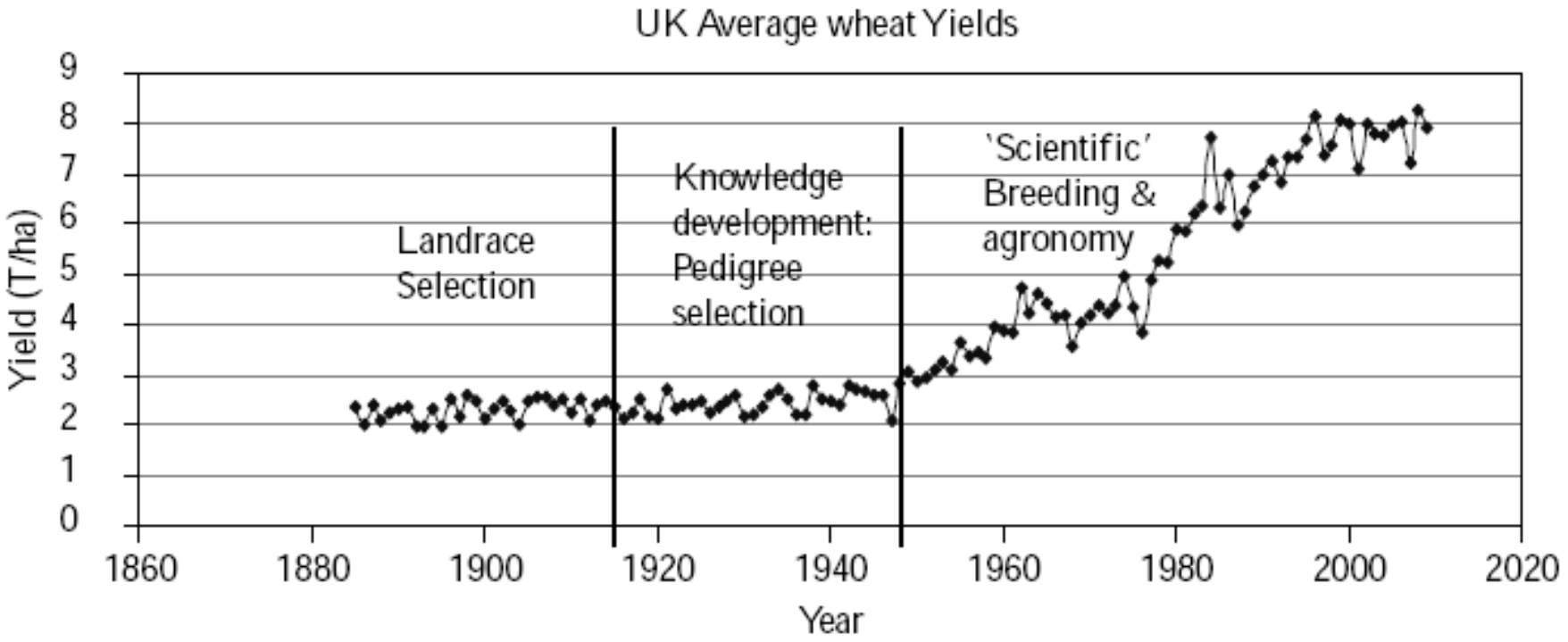
WGIN resource development for UK wheat breeding

Simon Griffiths

John Innes Centre

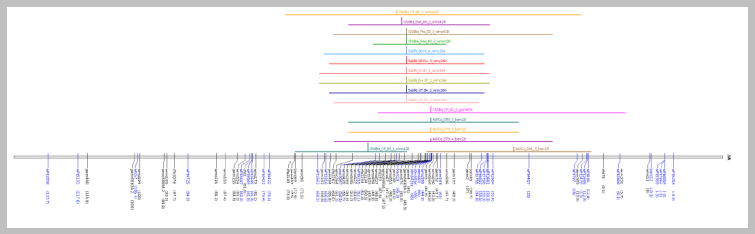
WGIN supports gene discovery and deployment for UK agriculture

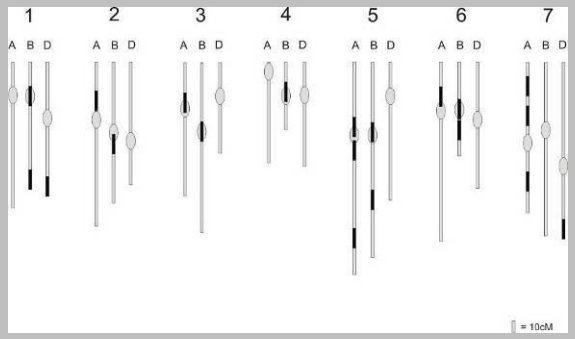


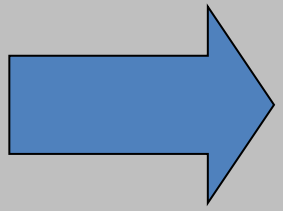
WGIN gene discovery strategy:

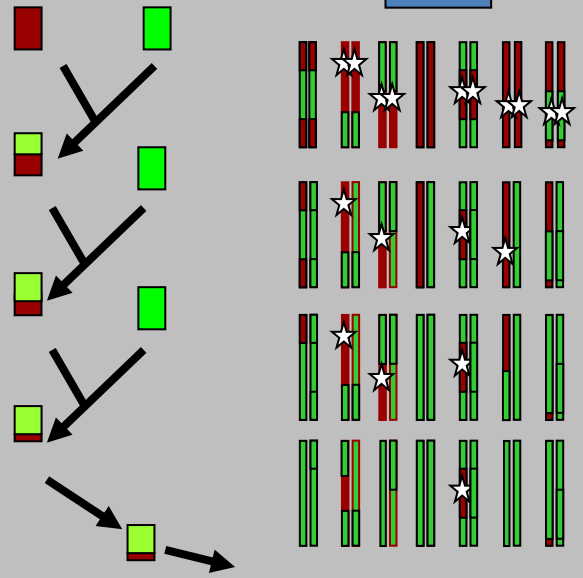
- Spark x Rialto
- Avalon x Cadenza
- Buster x Charger
- Charger x Badger
- Savannah x Rialto
- Shango x Shamrock

- Malacca x Charger
- Savannah x Renesansa
- Lynx x Cadenza
- Beaver x Soissons
- Weebil x Bacanora
- Milan x Catbird



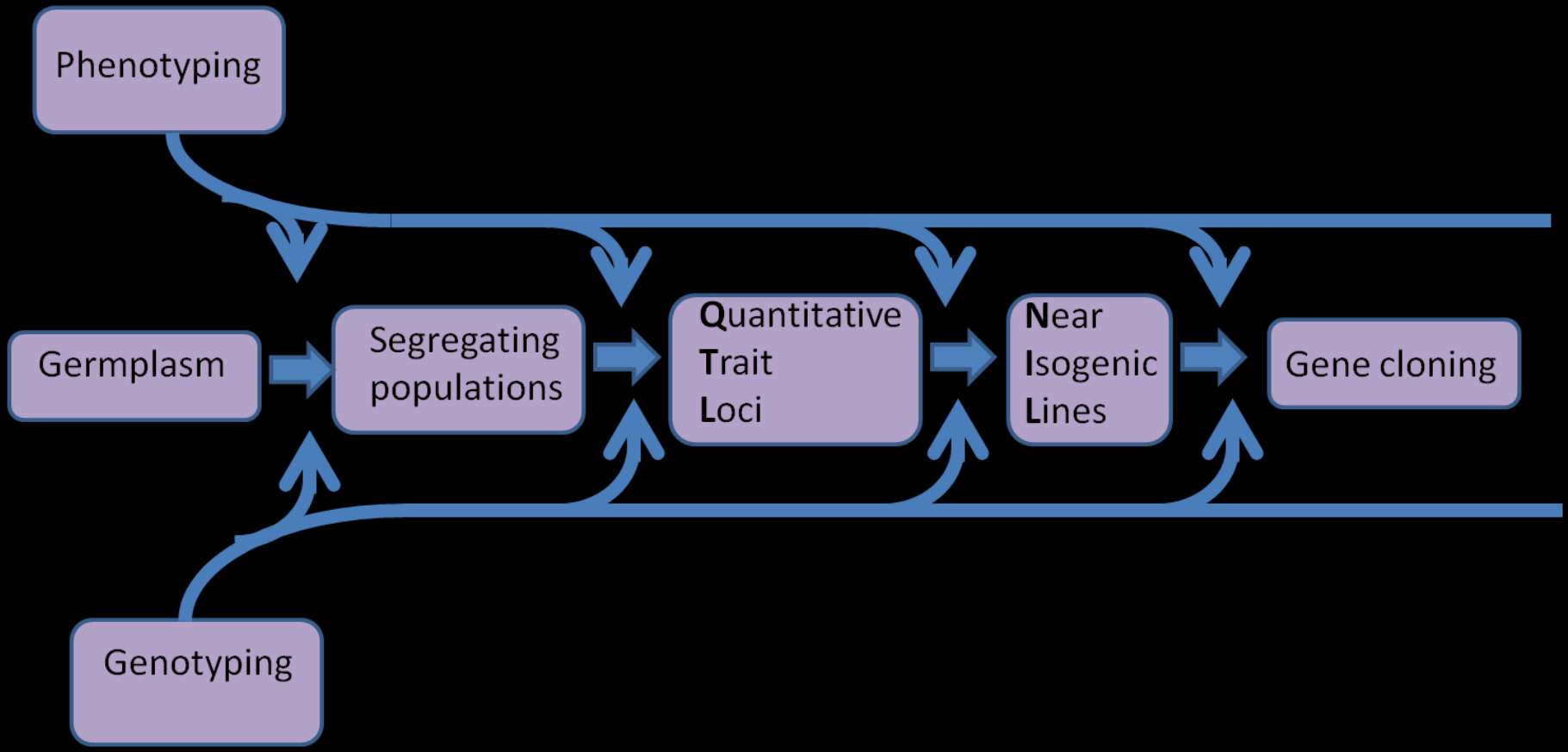






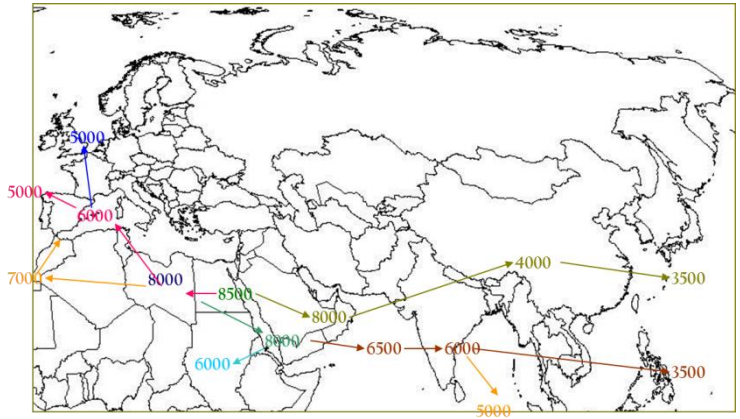
Assess impact of genes

It all starts with germplasm

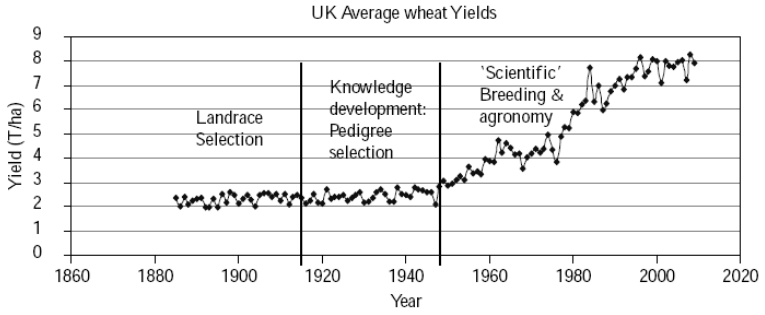


WGIN germplasm panels- AE Watkins and Gediflux

- Watkins (1200 landrace cultivars)-



- Gediflux- NW European winter wheat-



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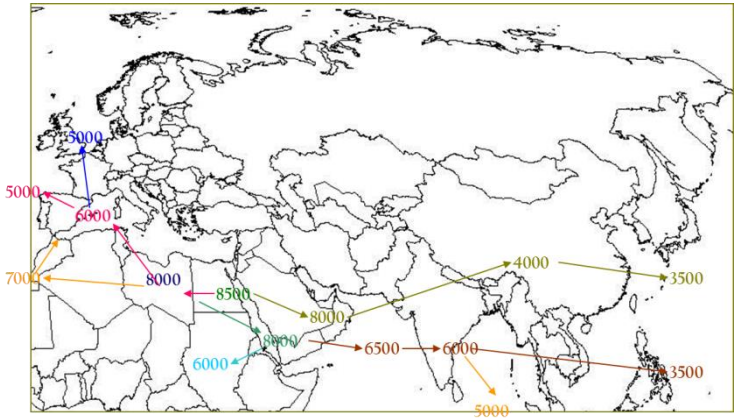

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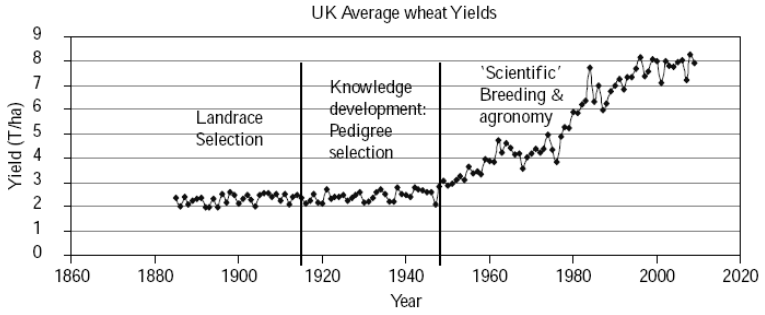

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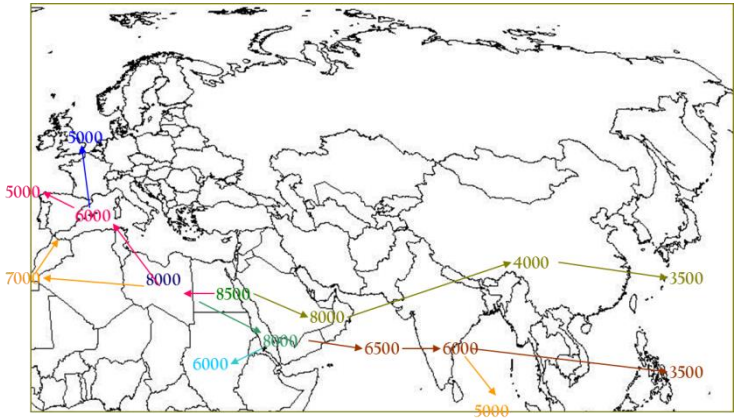

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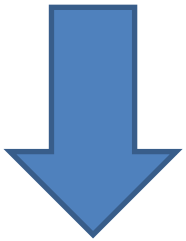
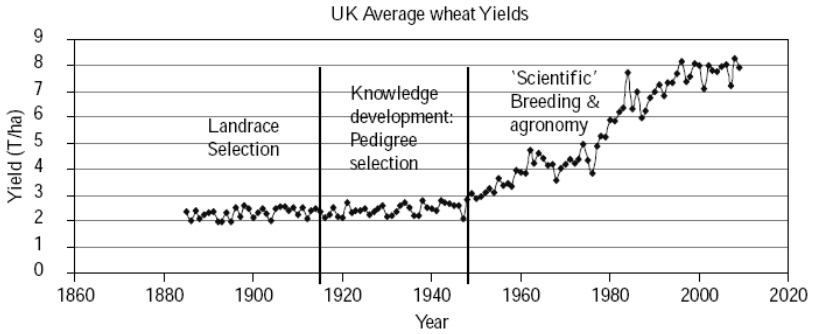
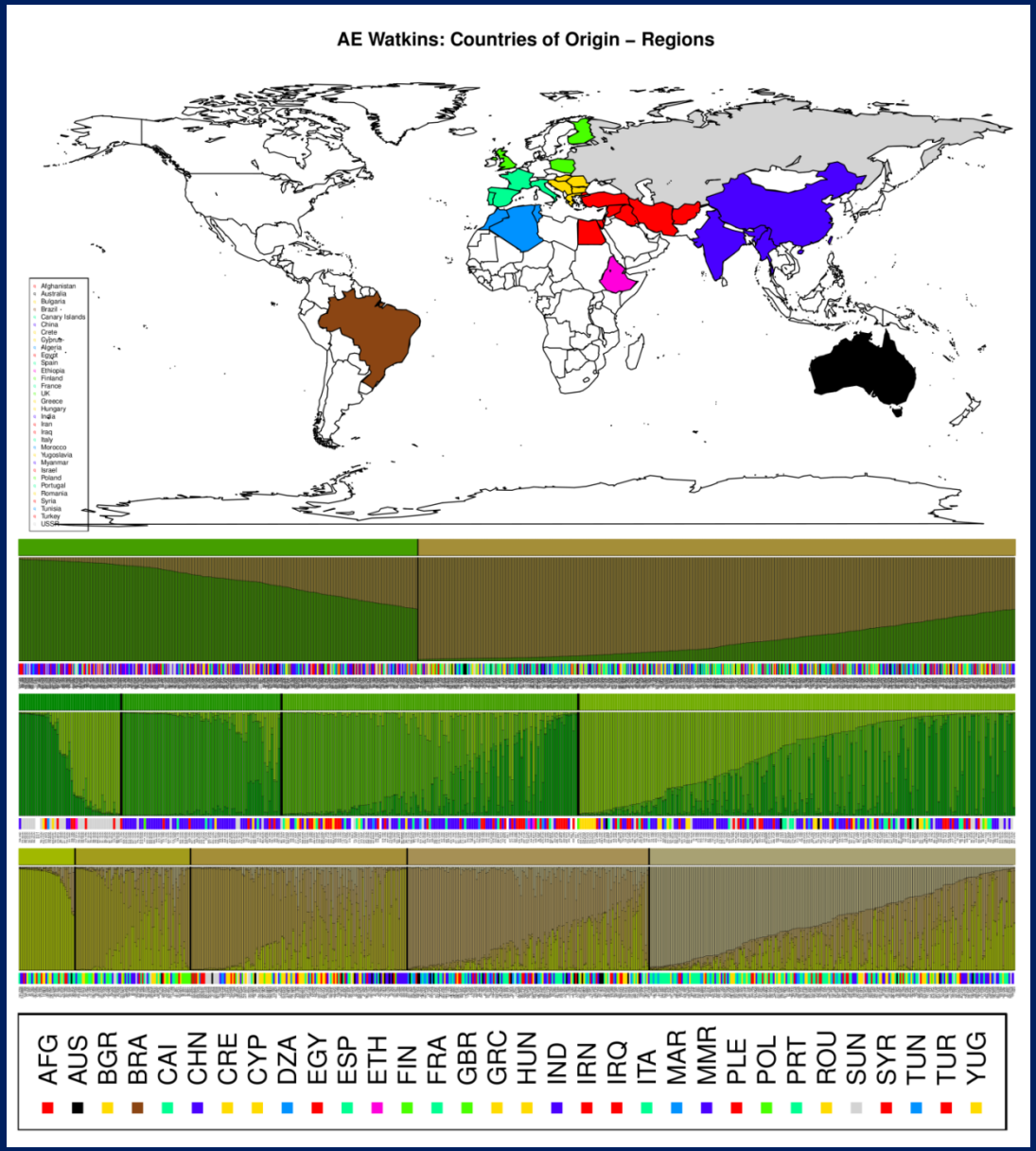


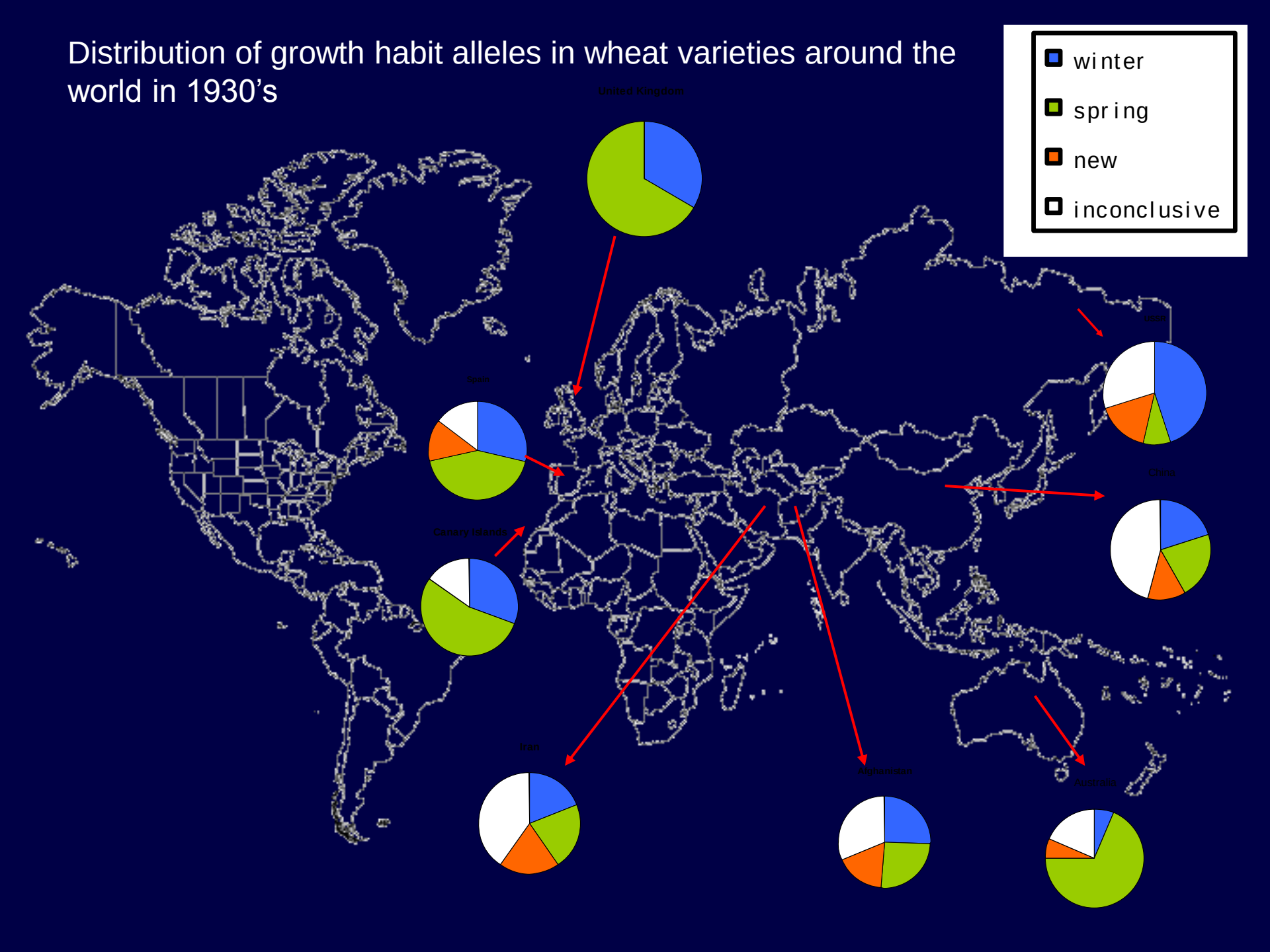
- Current UK commercial varieties



Molecular and Geographic description of Watkins Collection



Distribution of growth habit alleles in wheat varieties around the world in 1930's



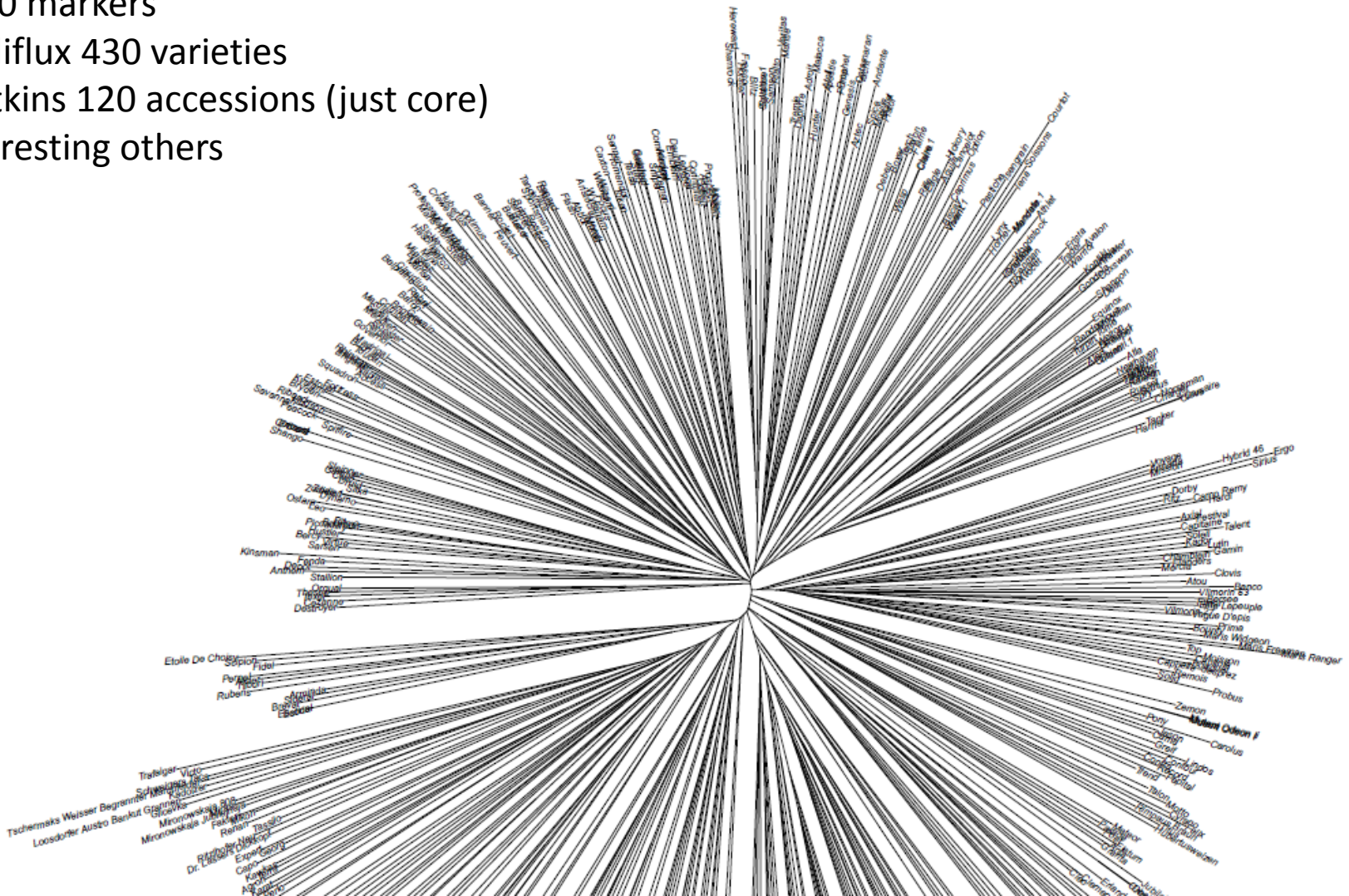
Gediflux captures Western European winter wheat diversity

Country	Varieties	Years of release	examples
Austria	40	40-90	Tassilo (50s) Hubertos (90s)
Belgium	24	50-90	Norda (60s) Escorial (80s)
Germany	18	80-90	Calif (80s) Pegassos (90s)
E Germany	30	40-80	Mahndorf (50s) Kanzler (80s)
W Germany	19	50-90	Muck (50s) Borenos (90s)
Denmark	5	80-90	Anja (80s) Pepital (90s)
France	34	40-90	Vague d'epis (40s) Isengrain (90s)
UK	66	40-90	Holdfast (40s) Equinox (90s)
Netherlands	19	40-80	Lovink (40s) Nautica (80s)
Sweden	26	25-90	Jarl (20s) Meridien (90s)
UK NL	229		

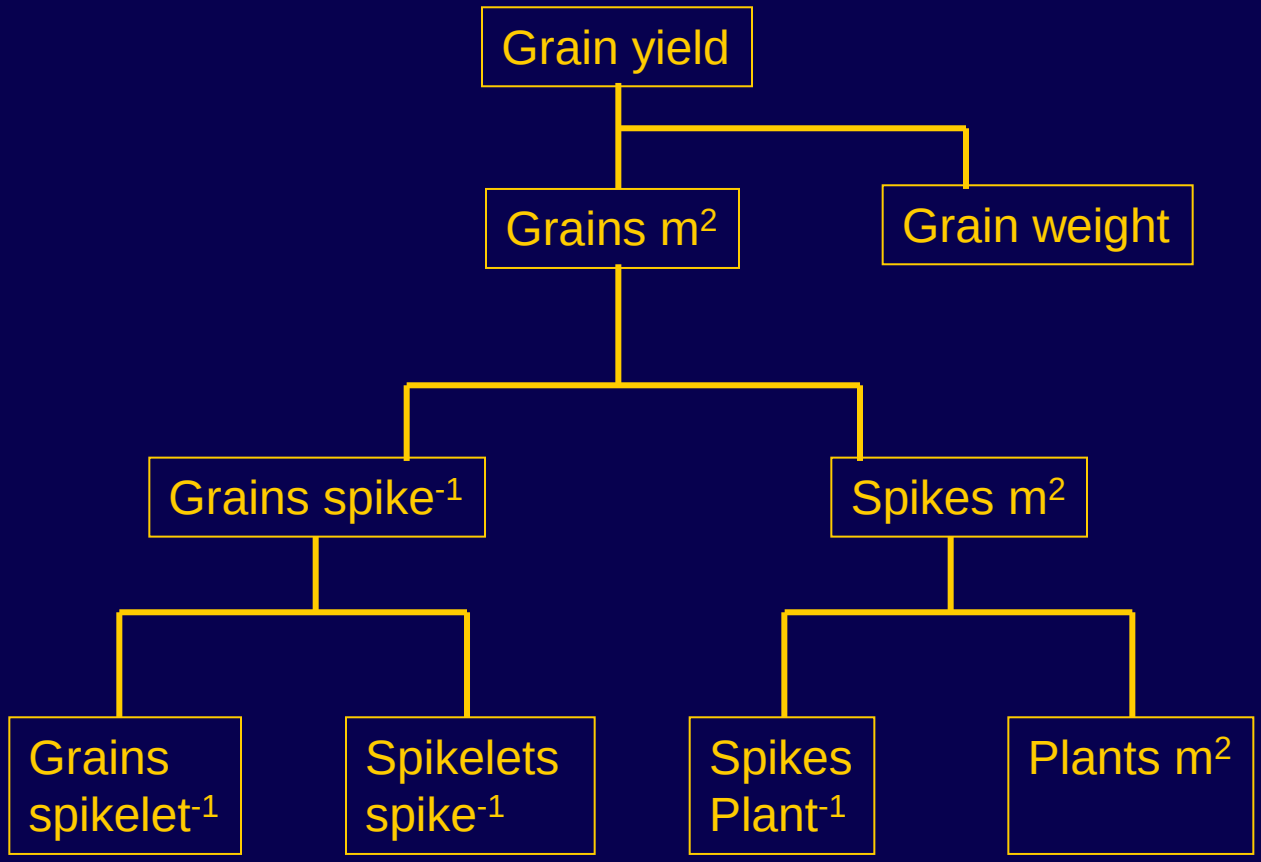
KASP genotyping of Gediflux

The aim is to identify polymorphisms for genetic mapping and MAS

- ~400 markers
- Gediflux 430 varieties
- Watkins 120 accessions (just core)
- Interesting others



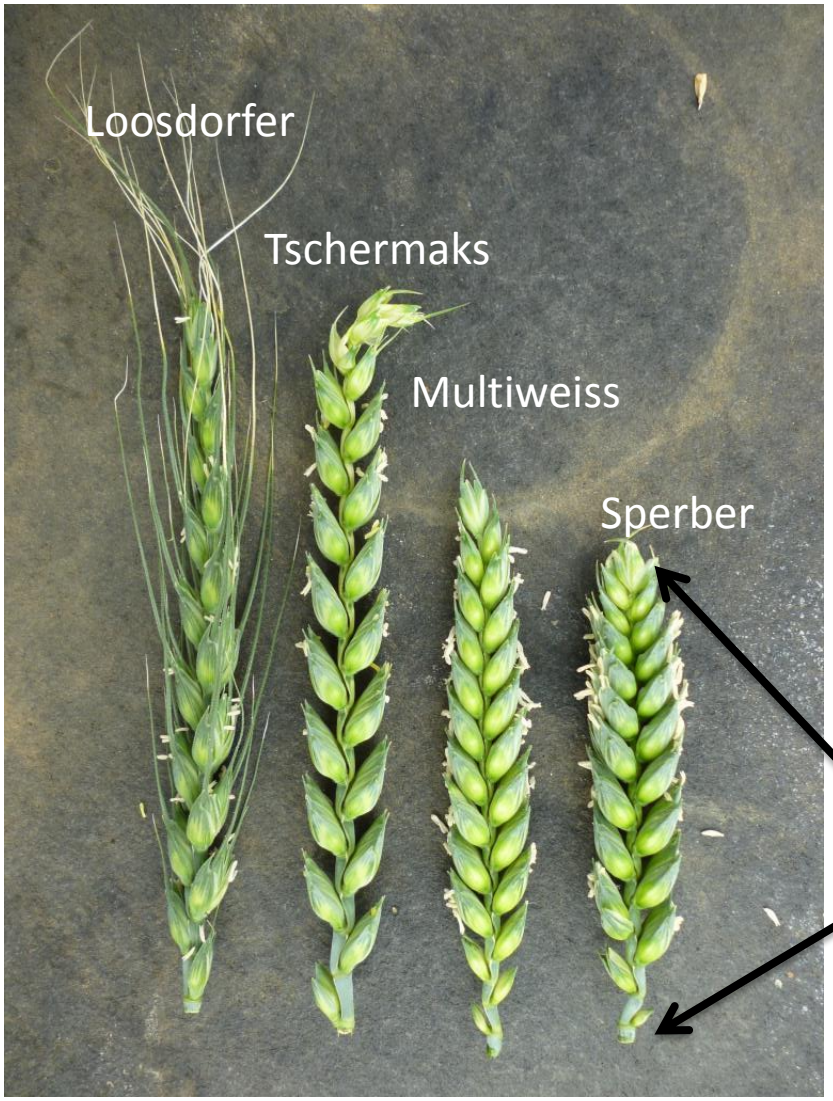
Identification of genetic variation for grain yield potential deployed by NW European wheat breeders



Components of grain yield in Gediflux

<u>Traits recorded for ten tiller samples</u>

ear length
fertile spikelets
infertile spikelets
grain area / TGW
grain length
grain width
grain number / wt



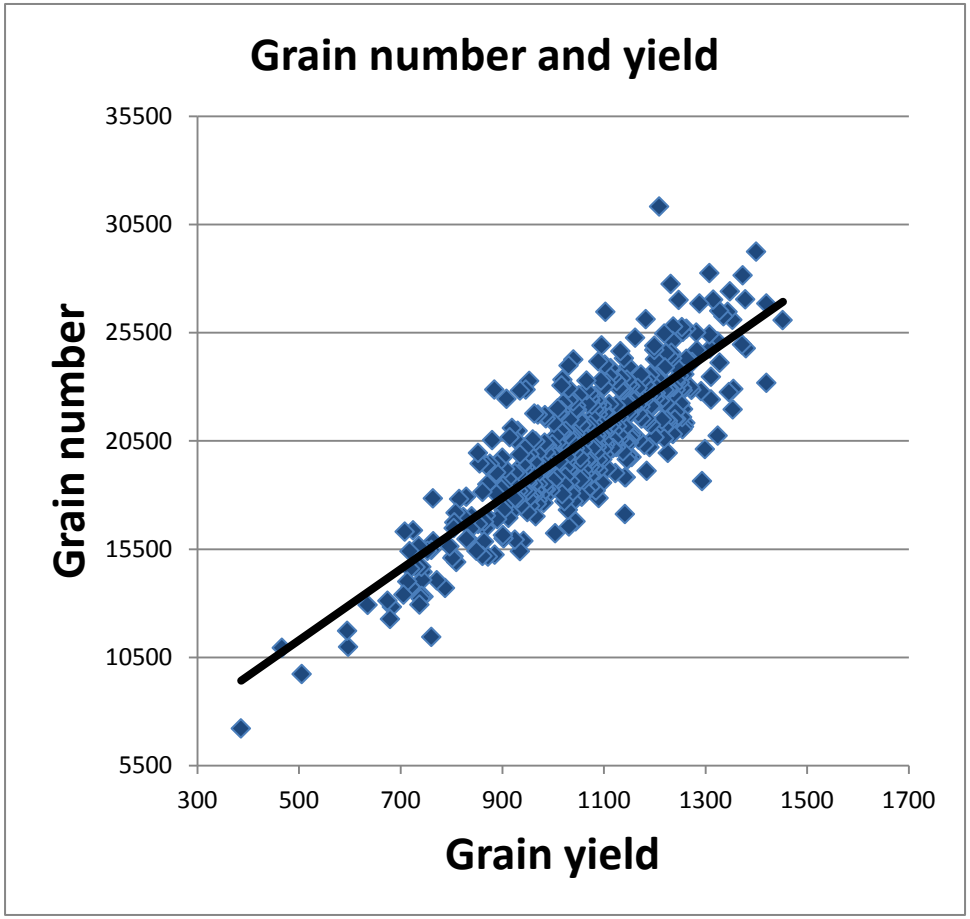
Components of stature in Gediflux

<u>Ten tillers samples</u>

Measurements taken for internode number and lengths.

Presence of coleoptile internodes

Phenotypic outliers might represent underexploited genetic variation



- Deviations from correlation can provide a first indication that rare genetic variation is present
- Genetic gain for grain yield has been driven by grain number
- In this example one variety, Thor, deviates significantly from this trend

WGIN has contributed four new high resolution genetic maps freely accessible to the wheat community

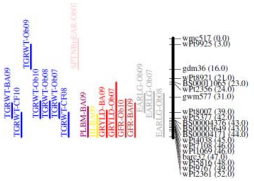
Avalon x Cadenza
Paragon x Synthetic
Paragon x Chinese Spring
Paragon x Garcia

anchoring
BBSRC-WISP
85 Paragon x Landrace

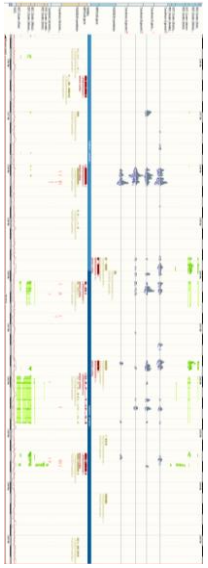
Bi-parental maps

Consensus genetic maps

QTL analysis and NAM



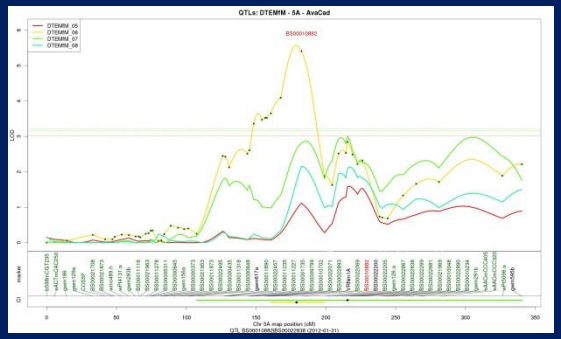
Wheat genome and varietal SNPs



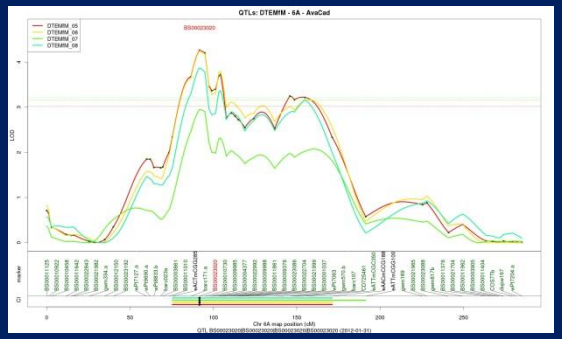
Gene content & haplotypes for WISP QTL intervals

- Markers for MAS
- New genes/alleles
- Targets for cloning
- Parent building
- Understanding mechanisms

Ear emergence QTL in Avalon x Cadenza



5A



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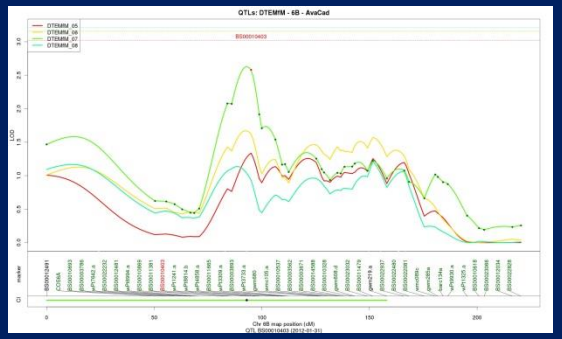

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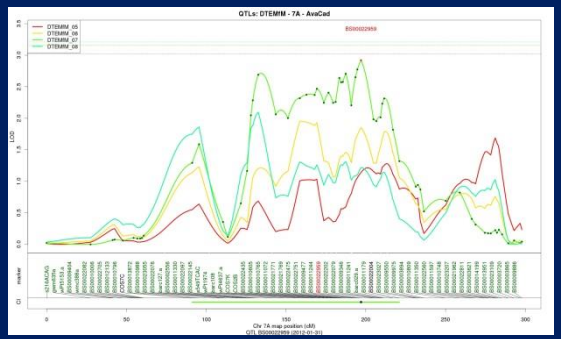

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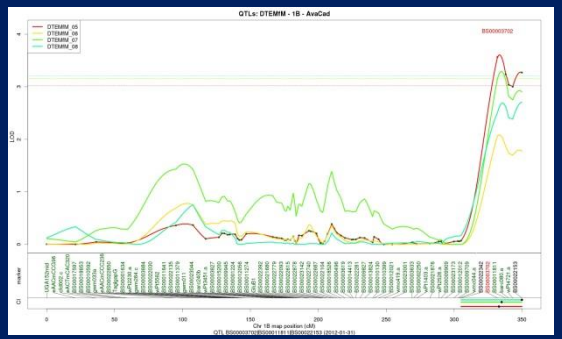

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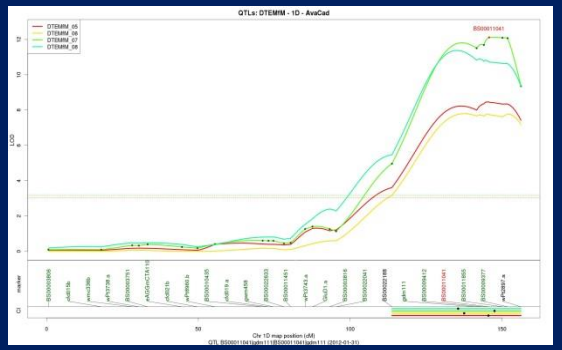
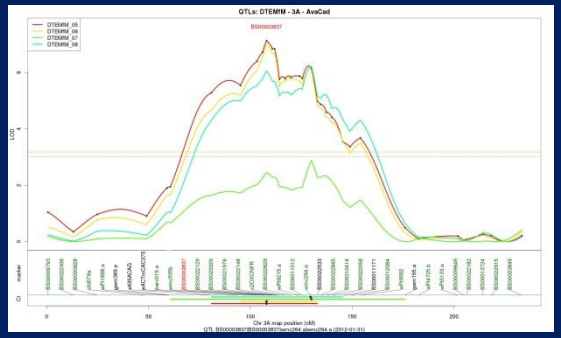
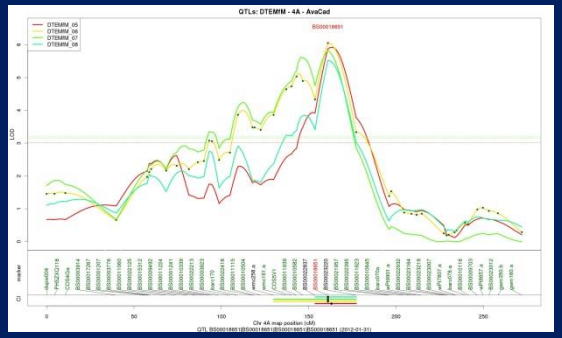


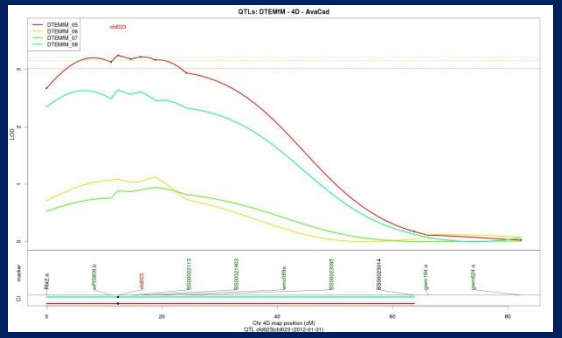
1D



3A



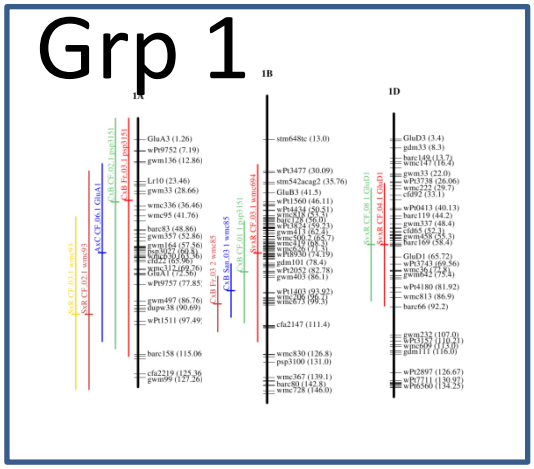
4A

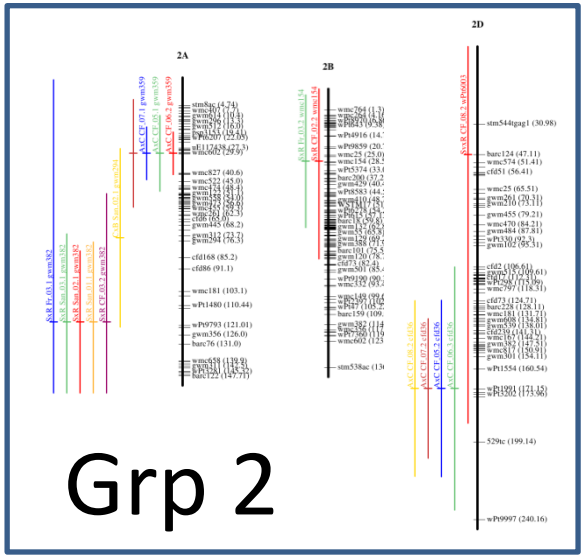


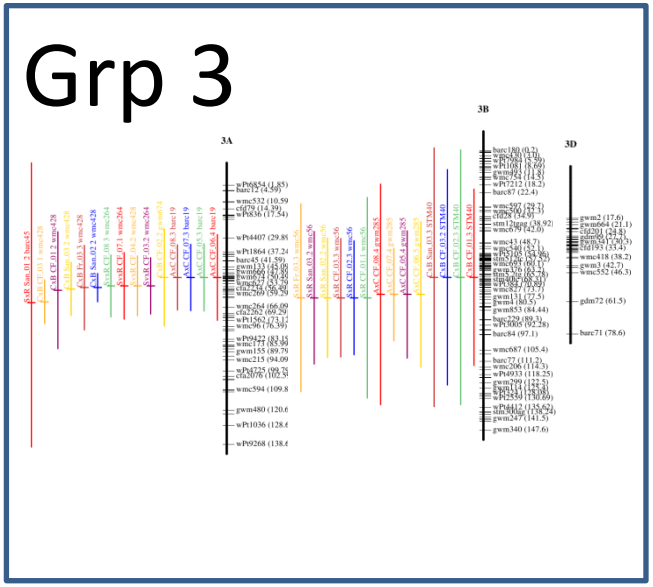
4D

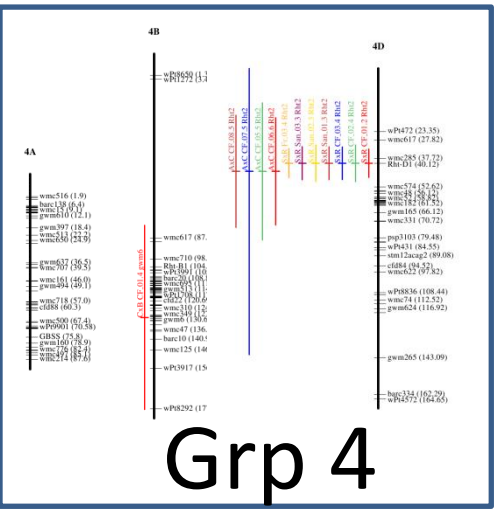
Griffiths et al TAG 2009

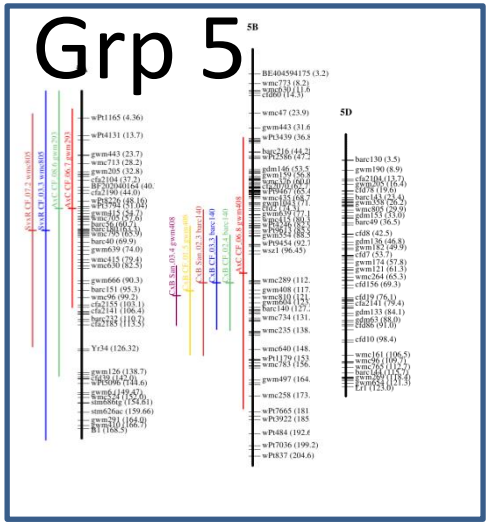
Identifying the genes currently deployed by UK breeders through QTL meta analysis- crop height

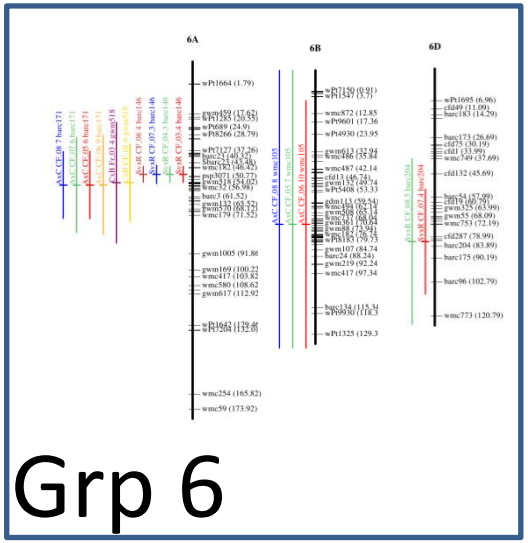


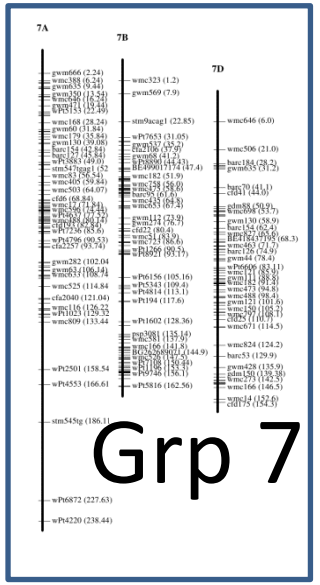




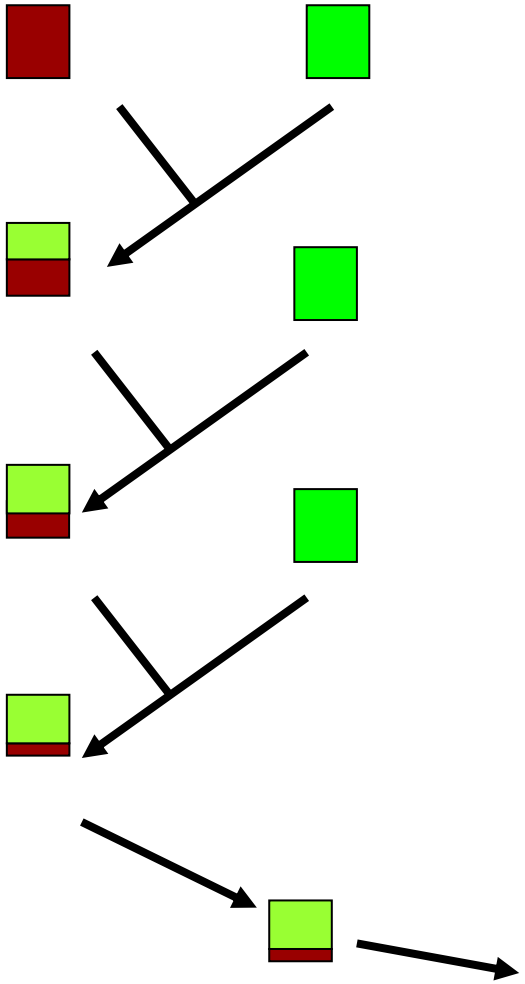


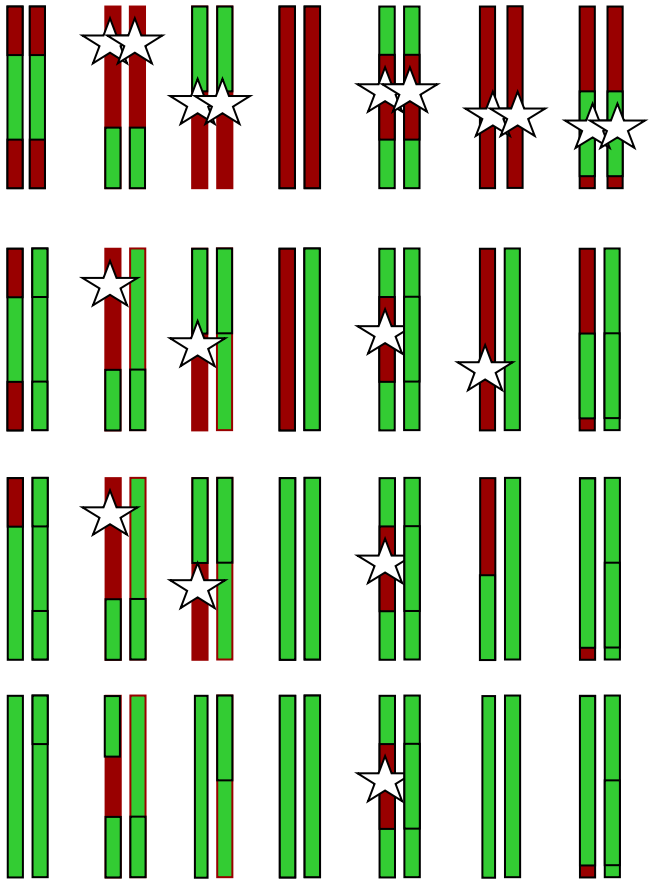






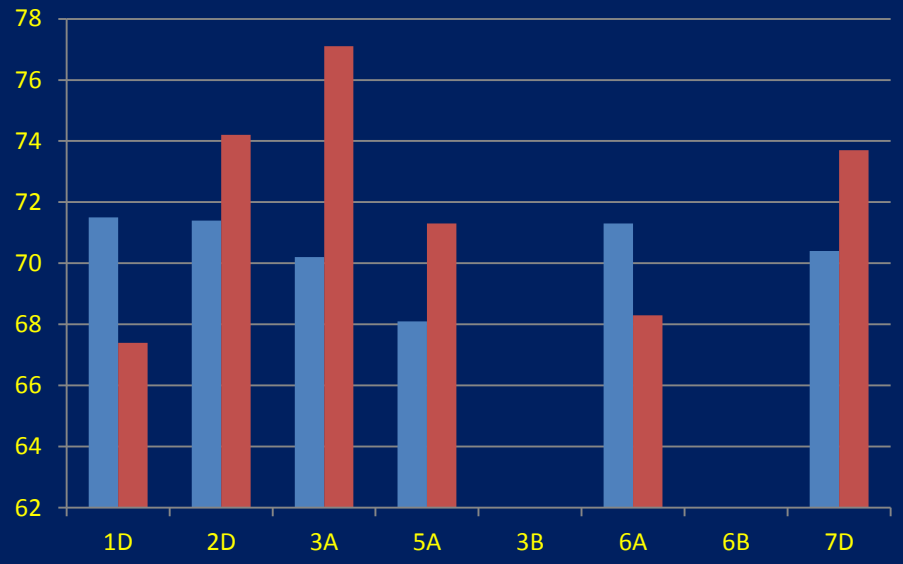
WGIN has used backcrossing to 'Mendelise' QTL

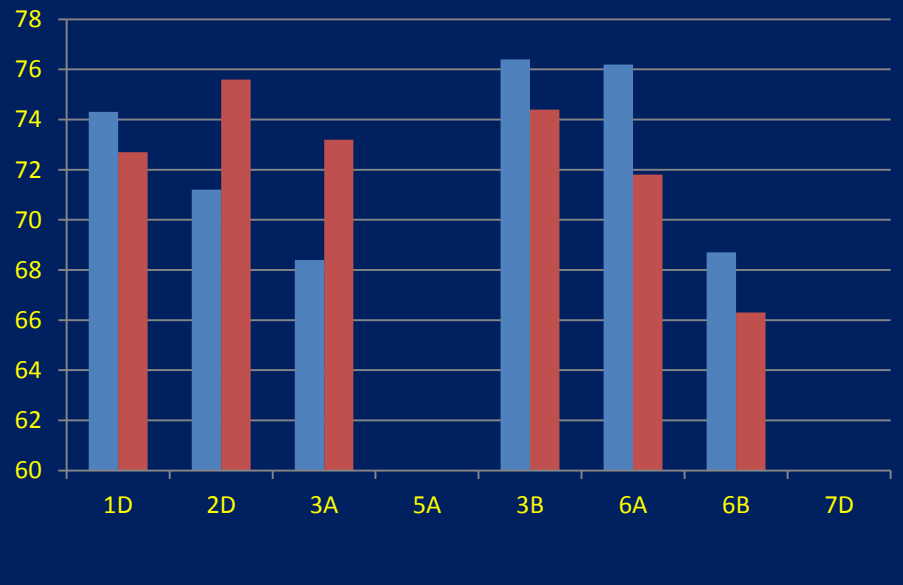




WGIN QTL validation using Near Isogenic Lines

- Shows us if QTL are ‘real’
- Gives an indication of utility in marker assisted selection
- First indication of interactions with other alleles
- Great resource for genetic and physiological dissection of each locus
- Tens of loci for: height, heading date, grain yield, grain shape, bread making quality developed and analysed in the same way





Where next?

- WGIN resource development has opened up new opportunities to enable:
  - Understanding of how genes interact with each other and the environment.
  - Marker assisted selection to help us to build well adapted, high yielding, and stable wheat varieties.
  - Access to fundamental understanding of mechanisms underlying important traits.

Acknowledgements