Linkage Disequilibrium at different scales on 3B chromosome of bread wheat

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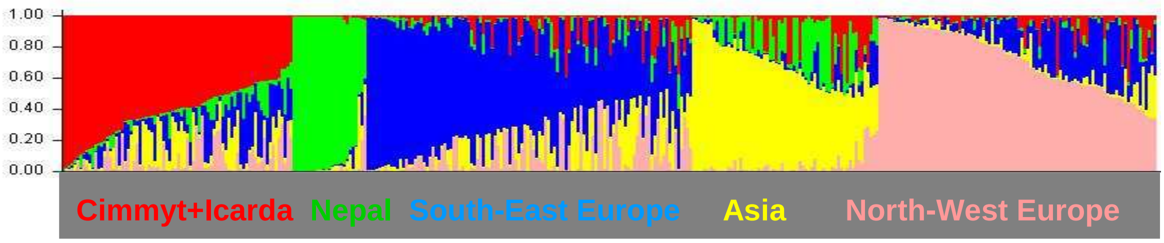
Linkage disequilibrium (LD) is the non-random association of alleles at linked or unlinked loci throughout the genome within a population. It may be estimated using squared allele-frequency correlations, r^2 for pairs of polymorphic sites . Association mapping studies, based on LD, present a considerable interest for crop genetic improvement. But the resolution of association mapping depends on the structure of LD in the collection studied.

A highly polymorphic worldwide core collection of 372 bread wheat lines (Balfourier et al., 2007) was used to analyse LD at three scales along the chromosome 3B. Five ancestral gene pools have be identified within this core collection, indicating a strong geographical structure (Horvath et al, 2009), as illustrated below in the barplot figure from STRUCURE software.

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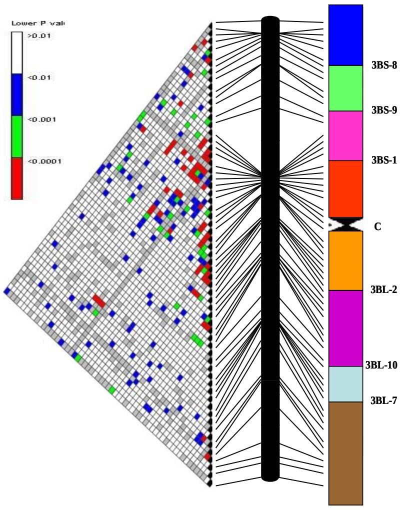
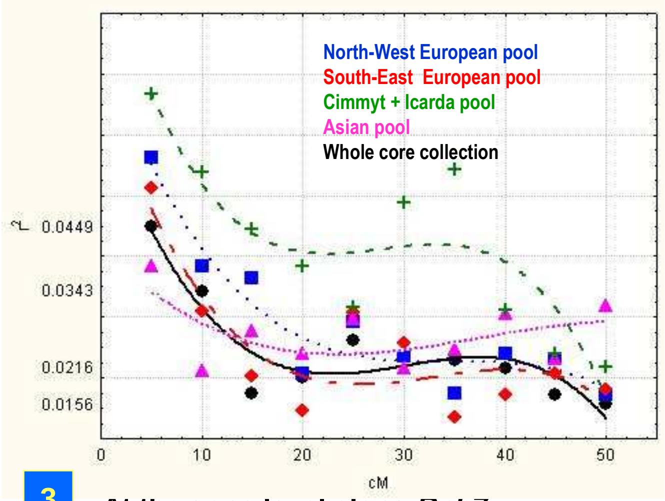
At the 3B chromosome scale: 107 microsatellites (SSRs) and Diversity Arrays Technology (DArTs)

1

- ✓ Significant LD in centromeric region and in the telomeric region of the short arm
- ✓ Global tendency was a decrease of r^2 around 20 cM. Variations were observed between the five gene pools: the CIMMYT-ICARDA pool presented the longest range of LD on the whole chromosome, spreading out to 30 cM contrary to Asian pool whose LD decreased at 20 cM

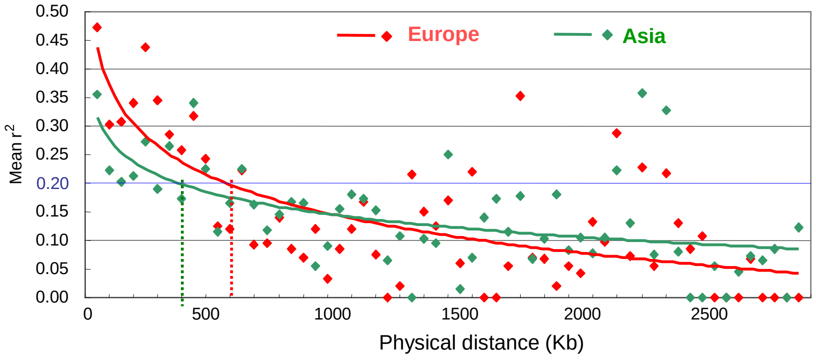




At the R locus (*Rph7-Fhb1*) scale - 3.2 Mb on 3BS8 deletion bin: 42 SSRs and SNPs (single nucleotide polymorphisms)

2

- ✓ r^2 values were higher than 0.20 until 600 kb
- ✓ Differences between geographical origins: 600 in Europe - 400 kb in Asia.

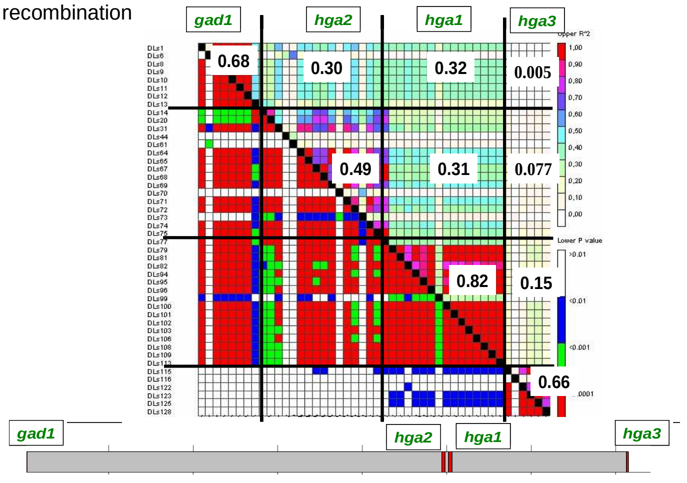


To conclude, in the region under study, LD dissipates over distances of 600-700 kb. This was unexpected from the evolutionary history of *Triticum aestivum* and would be favourable for association studies in this core collection.

At the gene level along *Rph7:* 46 SNPs in 4 genes

3

- ✓ Intra-gene mean r^2 values from 0.49 to 0.81.
- ✓ Low mean r^2 value of LD between *gad1* and *hga3 (*separated by 725 kb) confirming the decay of LD within 600-700 kb in this region
- ✓ Heterogeneity: No LD between *hga2* and *hga3*, separated by 218 kb. Despite the larger distance between *gad1* and *hga2* (500 kb), higher level of LD suggesting difference of recombination



References : Balfourier et al, (TAG, 2007); Horvath et al, (TAG 2009)

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