

Characterization of the hexaploid sweetpotato inheritance using ultra-dense multilocus genetic map.

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Context

The hexaploid sweetpotato (*Ipomoea batatas* (L.) Lam., $2n = 6x = 90$) is an important staple food crop worldwide. Despite its undeniable social and economic importance, genetic studies in sweetpotato significantly lag behind major diploid crops due to its complex hexaploid genome. To fully characterize the inheritance pattern in sweetpotato, we built an ultra-dense multilocus integrated genetic map of a full-sib population derived from a cross between the cultivars 'Beauregard' and 'Tanzania' (BT population) using our newly implemented software, MAPpoly¹. Using the genotypic probabilities computed across all linkage groups, we inferred the complete hexaploid haplotypes for all individuals in the offspring and evaluated the levels of preferential pairing and multivalent formation.

Mapping population and genotype calling

- Biparental cross: 'Beauregard' × 'Tanzania', 315 full-sib progeny.
- Genotyping: modified GBS protocol optimized for polyploids (GBSpoly)² using the genome of two diploid sweetpotatoes, *I. trifida* and *I. triloba*³, as reference.
- SNP calling using SuperMASSA⁴.
- After filtering, a total of 38,701 high confidence SNPs were used to build the map.
- The probability distribution of the genotypes was incorporated in a HMM to model the genotyping errors⁵.

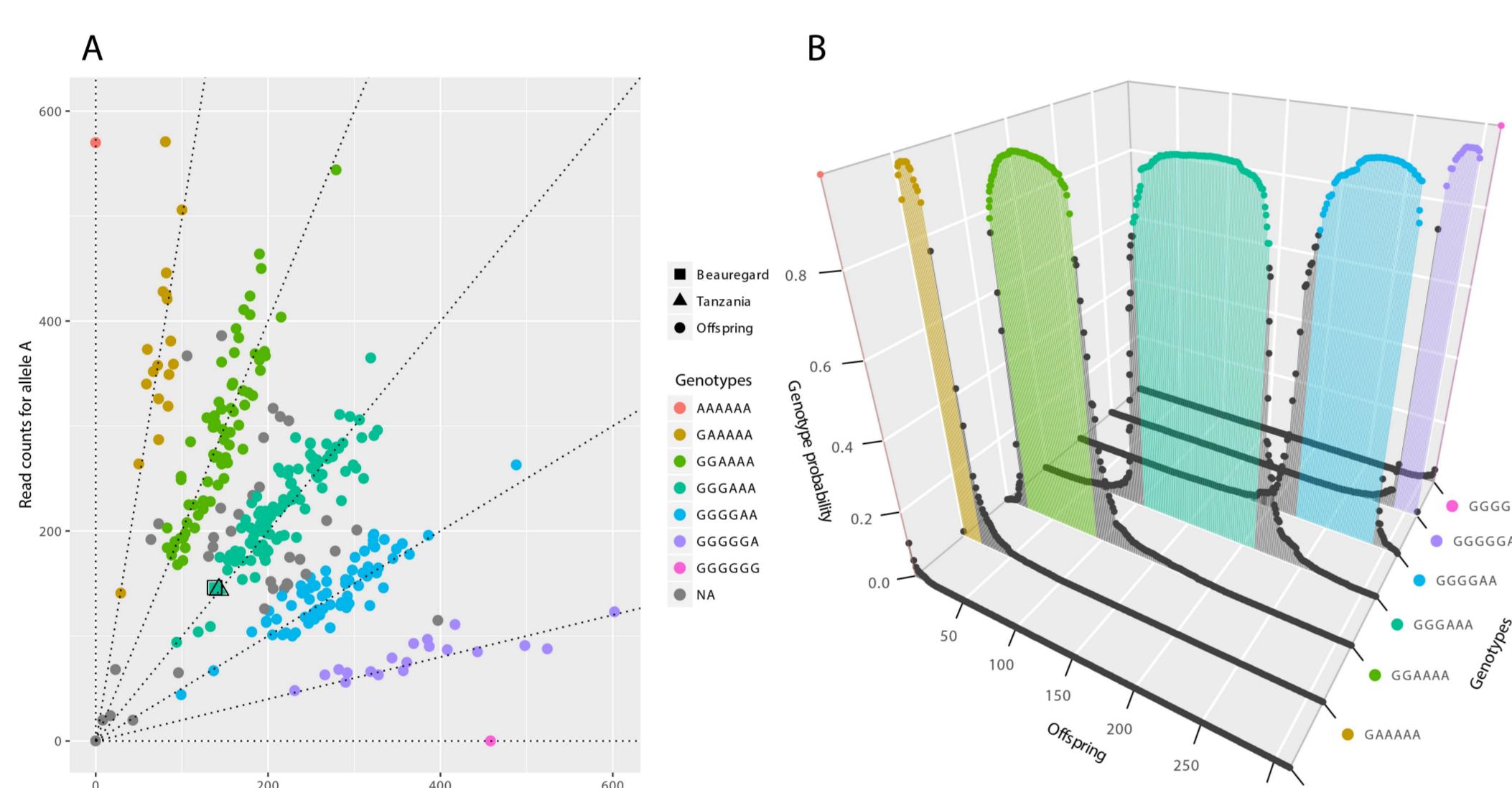


Figure 1: Example of genotype call of SNP TFS1_30010438. (A) Scatter plot of the read counts for the two allelic variants A and G. (B) Inferred probability distribution of genotypes for each individual in the offspring. Loci where the highest posterior probability was smaller than 0.8 were assigned as missing data (gray dots).

Sweetpotato phased genetic map

- 15 linkage groups consistent with the chromosomes of the diploid reference genomes
- Multidimensional Scaling Algorithm (MDS)⁶ was used to order SNPs. *I. trifida* reference genome was used to propose alternative SNP orders within collinearity blocks and evaluated the likelihood of the resulting maps.
- Multilocus fully phased map containing 30,684 SNPs (60.7% simplex and double-simplex, and 39.3% multiplex markers) spanning 2,708.4 cM.
- 81.9% of all map positions in 'Beauregard' and 77.2% in 'Tanzania' had a GIC > 80%

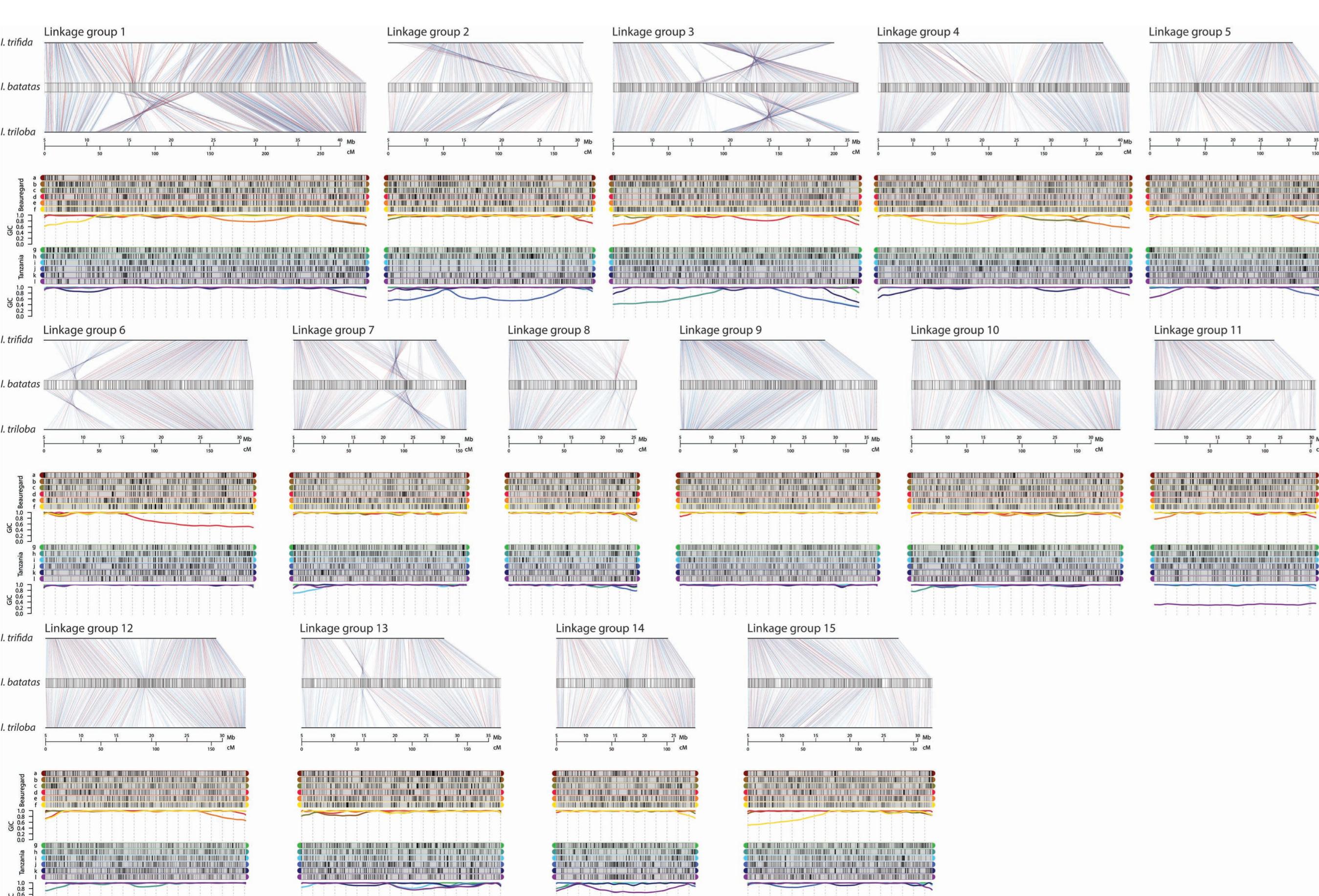


Figure 2: Sweetpotato genetic map⁷. Blue lines connecting the map and reference genomes indicate SNPs shared between *I. trifida* and *I. triloba* reference genomes and red lines indicate private SNPs. Above each map, we present a graphical representation of the parental linkage phase configuration of the homology groups for parents 'Beauregard' and 'Tanzania'. The Genotypic Information Content (GIC), is presented below each homology group.

Haplotype reconstruction and multivalent formation

- Most of the meiotic configurations (73.3%) were resolved in bivalents, although a small portion of multivalent signatures (15.7%), and inconclusive configurations (11.0%) were also observed.

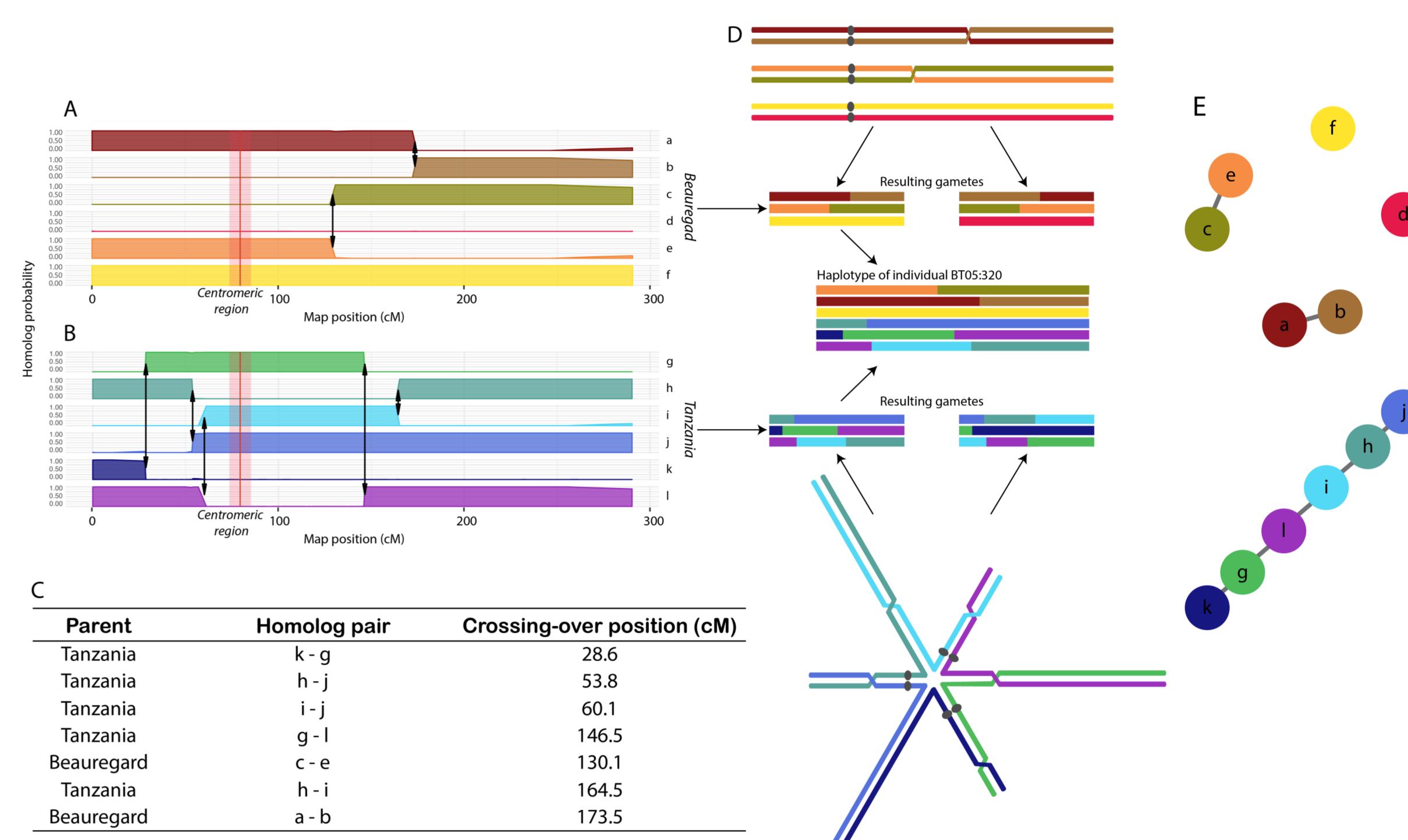


Figure 3: Example of haplotype reconstruction and distribution of meiotic configurations for individual BT05.320, linkage group 1. (A) and (B) Probability profiles for 12 homologs indicating the segments inherited from parents 'Beauregard' and 'Tanzania', respectively. The arrows indicate recombination points; (C) Recombination signature table; (D) Possible meiotic configuration that originated gametes for individual BT05.320 in 'Beauregard' and 'Tanzania' and resulting gamete. E) Representation of the meiotic results as a graph where nodes represent the homologs and the edges represent recombination events.

Preferential Pairing

- Except for low levels of preferential pairing in linkage group 2, we observed a hexasomic inheritance mechanism in all linkage groups.

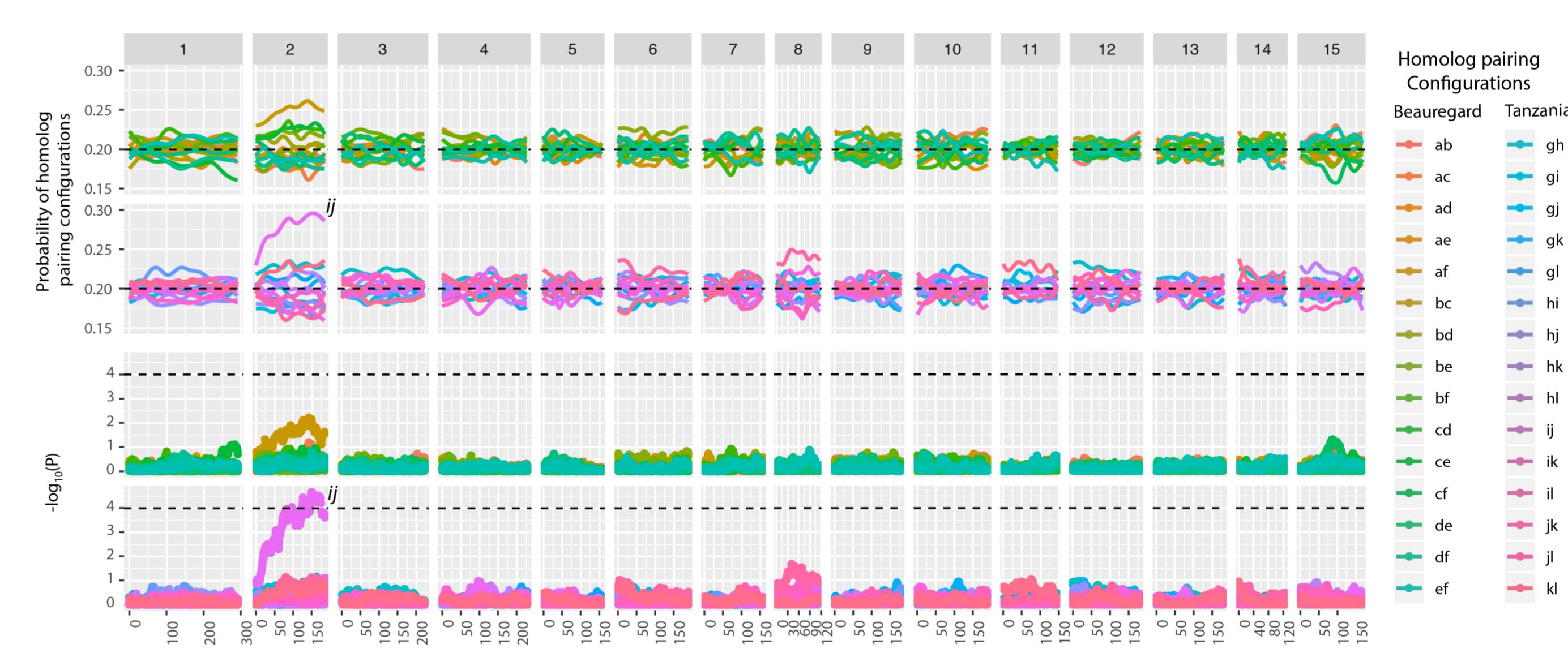


Figure 4: Probability profiles for 15 homolog pairs in parents 'Beauregard' and 'Tanzania' across 15 linkage groups. The dashed lines in the probability profiles indicate the pairing probability expected under random pairing ($\frac{3}{15} = 0.2$). The lower panels indicate $-\log_{10} P$ of a χ^2 independence test for all possible homolog pairs. Dashed lines indicate $P < 10^{-4}$. Homologs *i* and *j* presented a low, but significant preferential pairing in linkage group 2.

Conclusion

- Although compute-intensive, the construction of multipoint genetic maps in complex polyploids has several advantages, including error modeling, computation of preferential pairing profiles, and construction of haplotypes in the offspring.
- The resulting sweetpotato genetic map revealed 96.5% collinearity between the hexaploid *I. batatas* and its diploid relative *I. trifida*.
- We showed that sweetpotato inheritance is vastly autopolypliod-like and random chromosome pairing enables recombination between all homologous across generations.
- We speculate that the hexasomic-bivalent inheritance promotes stability to the allelic transmission in sweetpotato.

Related talk in this conference: Sweetpotato Genomics Workshop - Characterization of Sweetpotato Inheritance Using Ultradense Multilocus Genetic Map (Royal Palm Salon 5-6, Wednesday, Jan 15, 1:55 PM)

References

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