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A dense reference map for *Lupinus angustifolius*: A foundation for building lupin genome research

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Summary



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- Background
- Approach
- The new reference map
- Syntenic relations
- Applications



RIL population development



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Domestic
(83A:476)

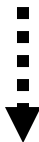
X



F₁



F₂



F₈

Wild
(P27255)



Population developed
at DAFWA

106 RILs

Two maps have been published



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CONSTRUCTION OF A GENETIC LINKAGE MAP USING MELP AND IDENTIFICATION OF MOLECULAR MARKERS LINKED TO DOMESTICATION GENES IN NARROW-LEAFED LUPIN (*Lupinus angustifolius* L.)

JEFFREY G. BOERSMA^{1,2*}, MARGARET PALLOTTA¹, CHENGDAO LI¹, BEVAN J. BUIRCHELL¹, KRISHNAPILLAI SIVASITHAMPARAM² and HUAAN YANG¹

- 7 traits mapped
- 521 anonymous MELP markers
- 21 linkage groups

The first gene-based map of *Lupinus angustifolius* L.-location of domestication genes and conserved synteny

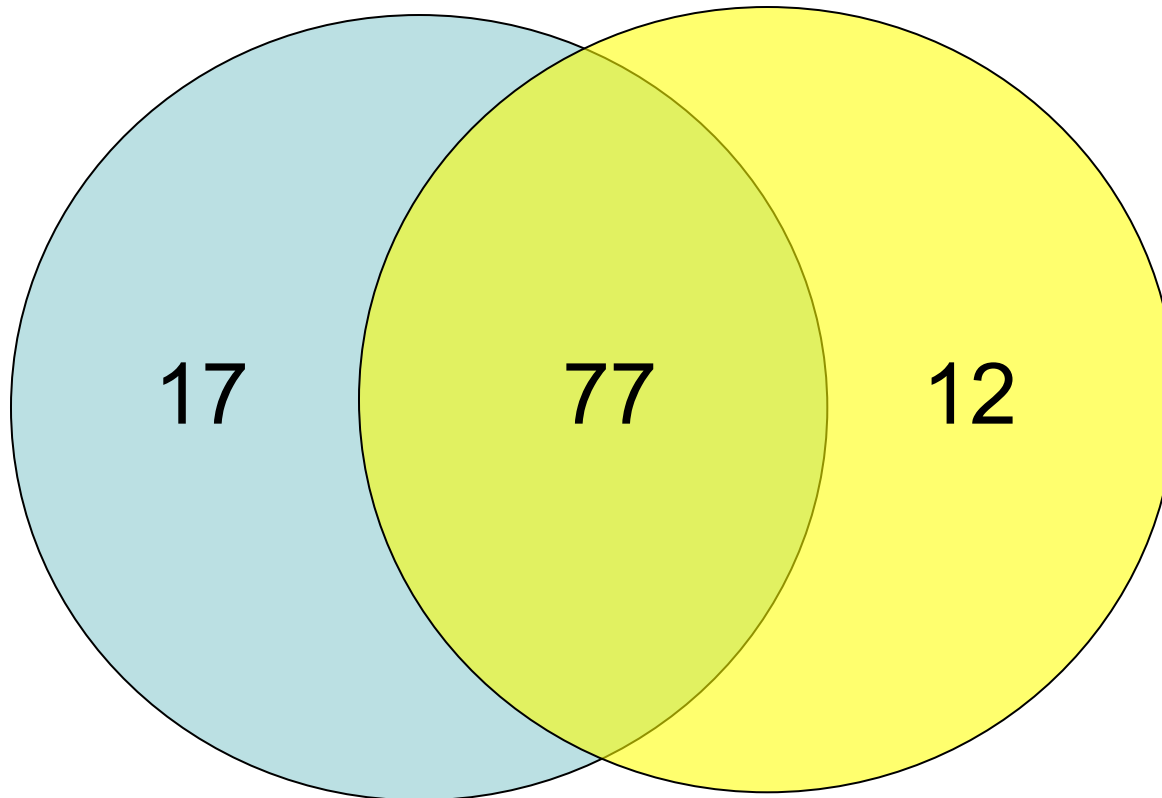
- 5 traits mapped with *Medicago truncatula*
- 300 locus-specific AFLP markers
- 75 anonymous AFLP markers
- 20 linkage groups

Maohua Chen · Xueping Chen · Phan · Simon R. Ellwood · Paula M. Moolhuijzen · James Hill · Angela McQuinn · Clare E. O'Lone · John Fosu-Nyarko · Marie Scobie · Mehmet Cakir · Michael G. K. Jones · Matthew Bellgard · Michał Książkiewicz · Bogdan Wolko · Susan J. Barker · Richard P. Oliver · Wallace A. Cowling

Different RIL subsets were used in previous studies



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Nelson et al. 2006

Boersma et al. 2005

Strategy for generating a combined map



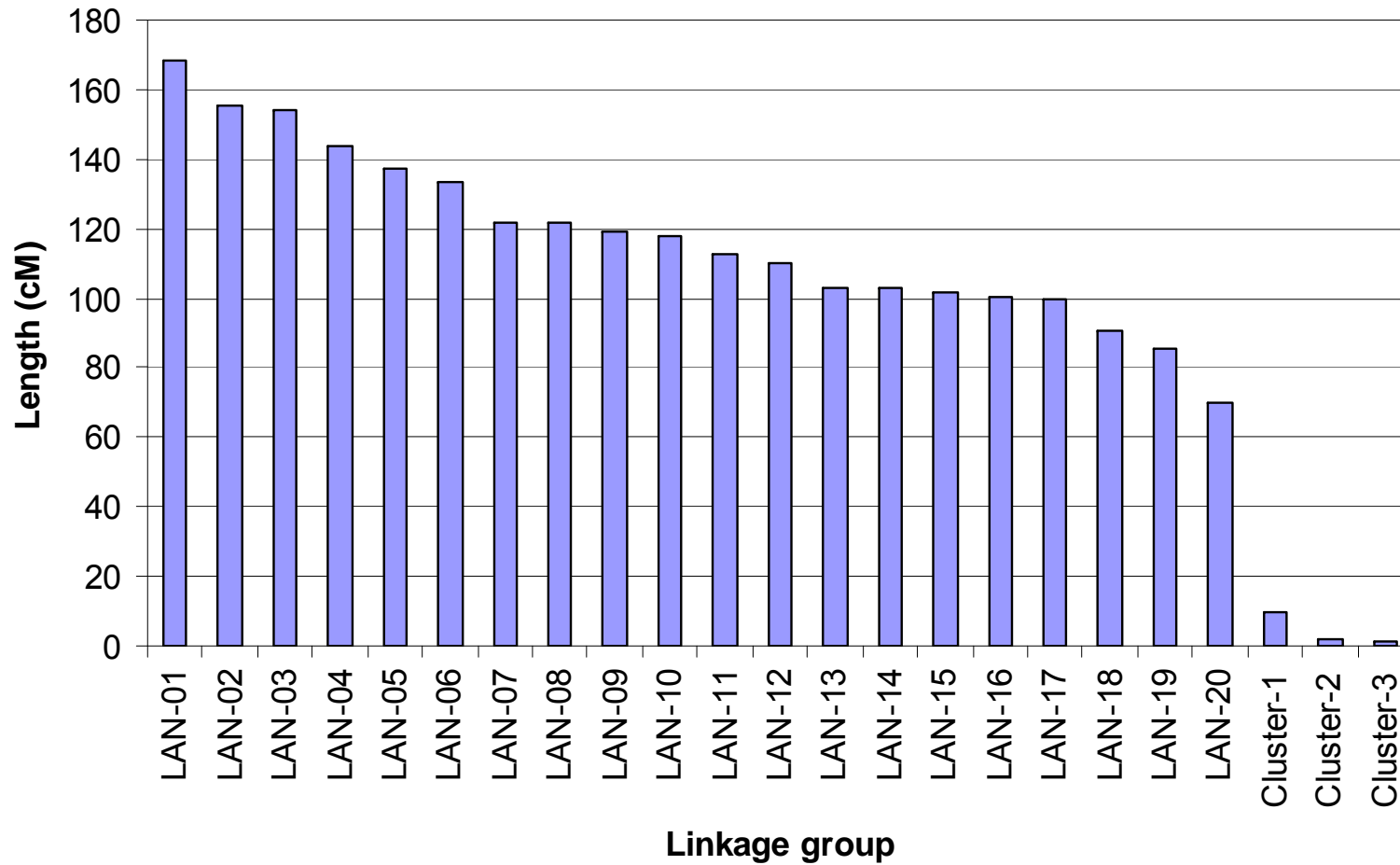
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- Pool together data from two mapping studies
- New loci:
 - *Tardus* and various trait-linked loci (Boersma et al)
 - 80 new gene based markers
- Create linkage map based on 106 RILs using MultiPoint software

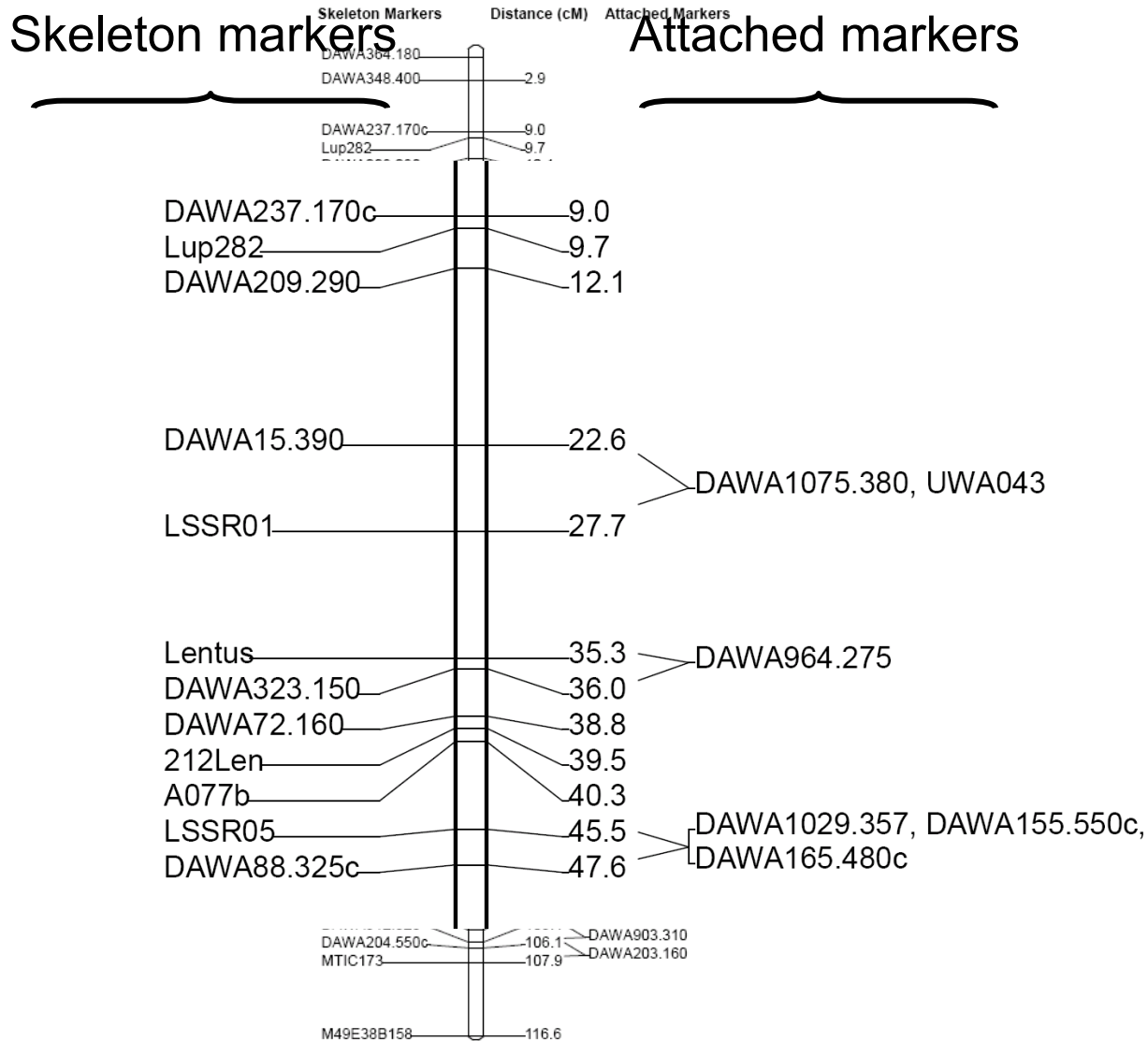


Features of the new reference map

1080 loci in 20 solid groups ($n = 20$)



641 skeleton + 449 attached markers



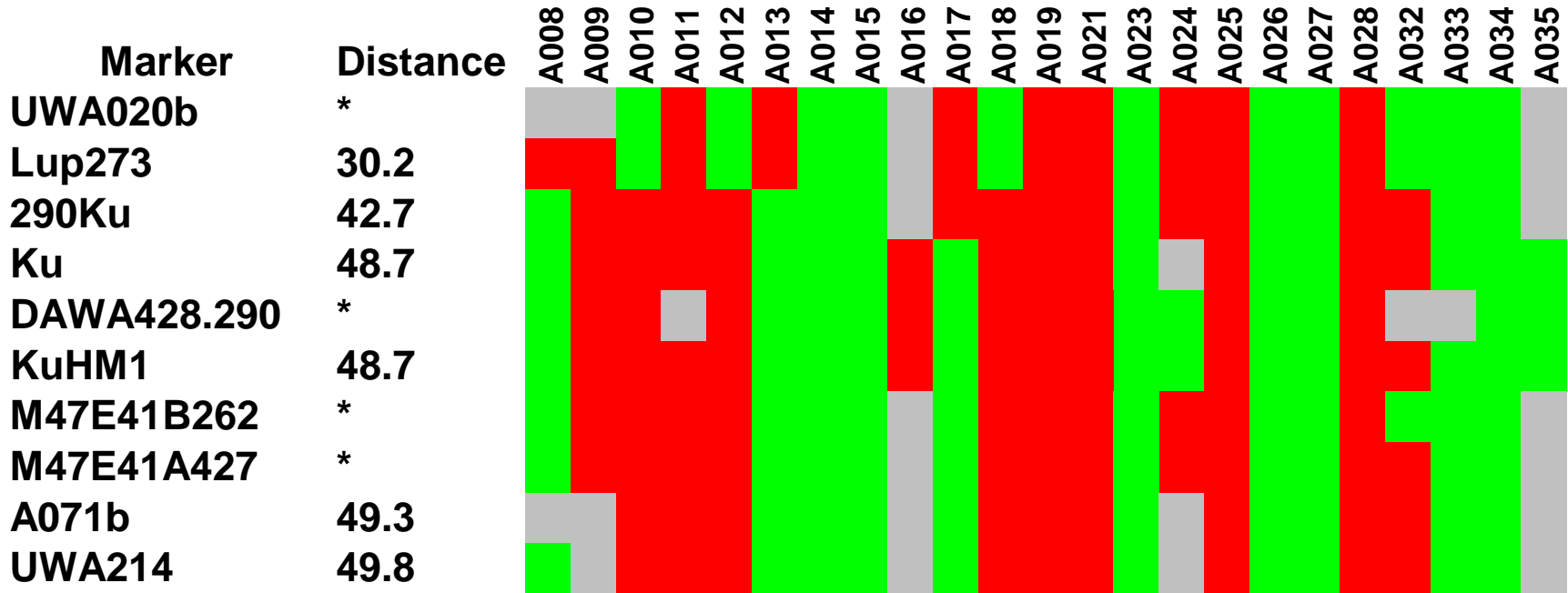
A reference map for genome research in *Lupinus angustifolius*



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- Publication of the new reference map in an international journal
- Standardised linkage group names will allow easier comparison between studies
- Provision of RILs and genotyping data will assist collaboration among group

Graphical genotype data will be released





Where next?

Linkage group = chromosome?



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- Lupin chromosomes are hard to distinguish cytologically
- Poznań group is attempting to allocate linkage groups to chromosomes
- Using molecular cytogenetic probes on chromosome spreads

Anchoring physical maps



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- Bacterial Artificial Chromosome (BAC) libraries are used for physical mapping
- Typically consist of 10,000's of clones with ~100kb genomic DNA
- BAC libraries for NLL have been developed by groups Poznań and Perth
- A genetic map is required to orientate BAC contigs (overlapping series of BACs)

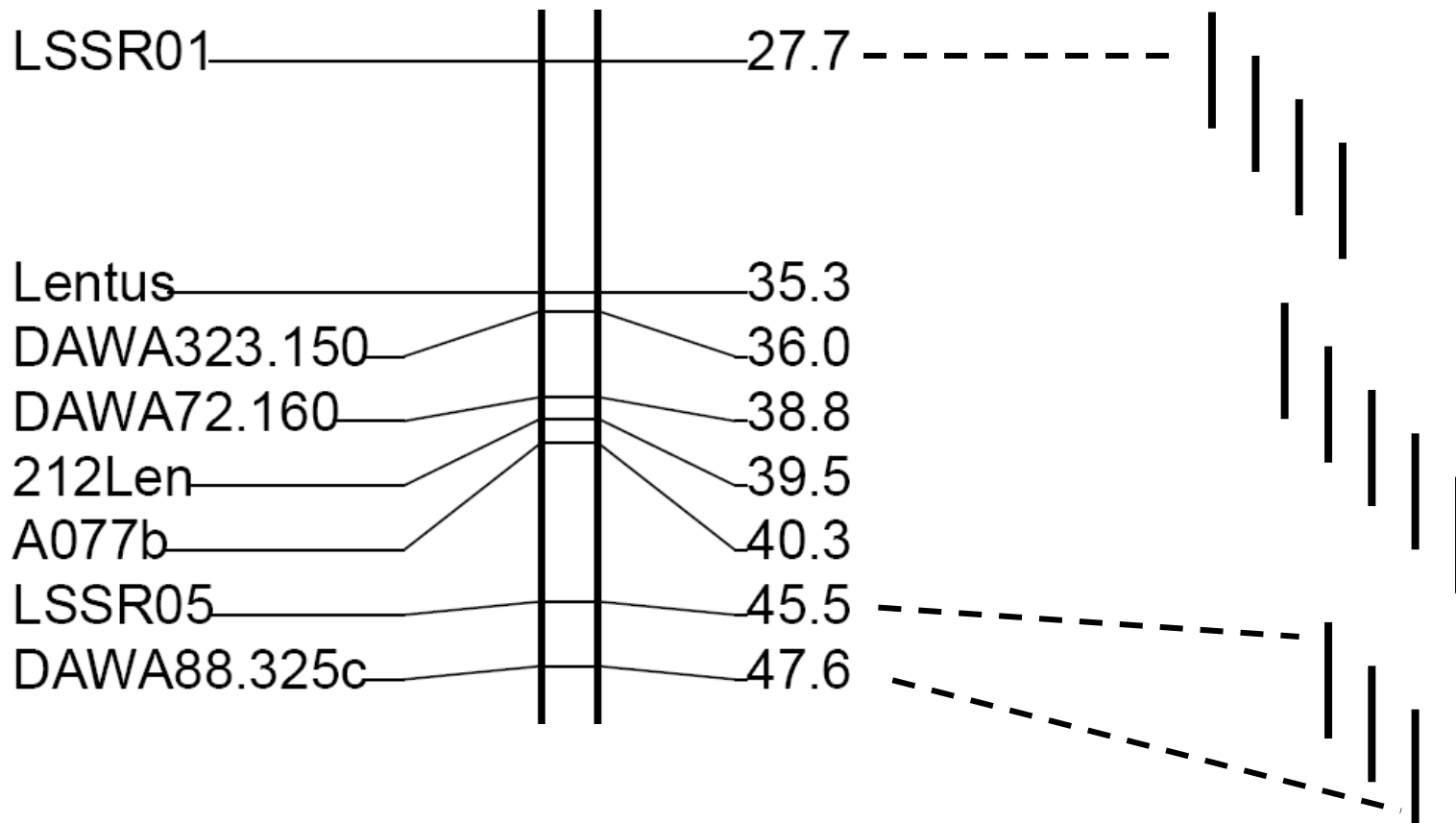
Anchoring physical maps



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Genetic map

BAC contigs



Genome sequencing



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- DNA sequencing technology is advancing at a breathtaking rate
- The first genome sequence of a species is still hard to obtain
- Sequencing further accessions is relatively cheap and straightforward
- Completing the first NLL genome will require an integrated approach including physical, genetic and cytogenetic tools

Association mapping



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- A powerful approach for gene discovery and validation of candidate genes
- Potentially much higher resolution than traditional linkage mapping
- Requires:
 - a diverse, preferably unstructured, population
 - high quality phenotyping
 - a suite of markers with known locations

Status and Prospects of Association Mapping in Plants

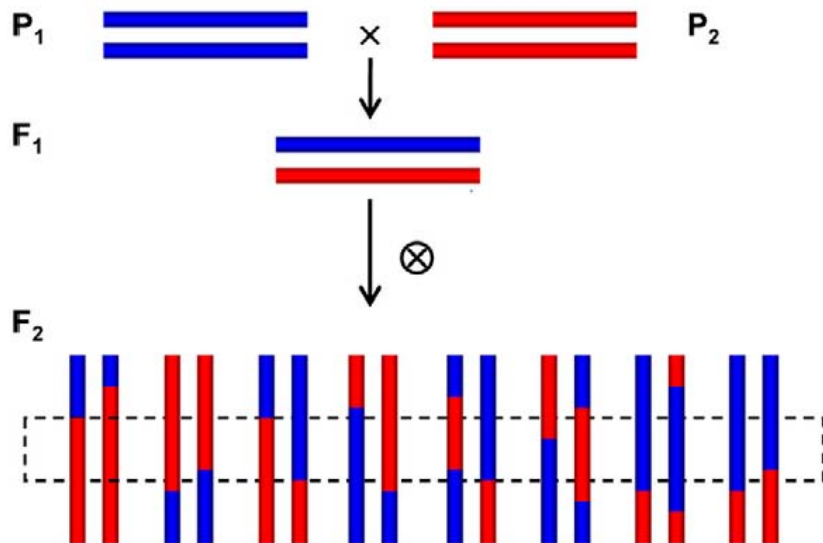


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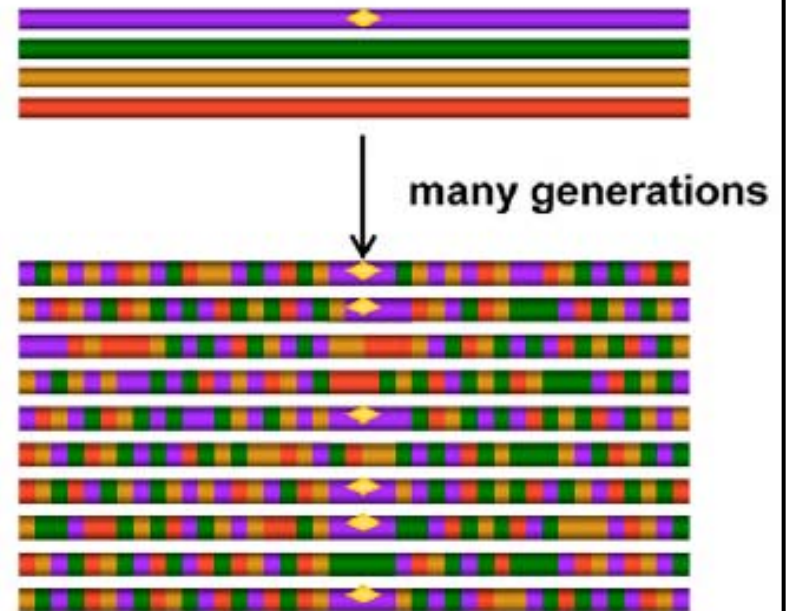
Chengsong Zhu, Michael Gore, Edward S. Buckler, and Jianming Yu*

THE PLANT GENOME ■ JULY 2008 ■ VOL. 1, NO. 1

Linkage mapping



Association mapping



NLL is ready for association mapping



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- Excellent phenotypic data is already available (and increasing) for NLL (DAFWA, CSIRO)
- DArT marker information for 1000+ accessions
- A core collection has been defined
- Initial low resolution association mapping can be conducted with 300 mapped DArT markers
- For higher resolution mapping, 1000s of SNP markers could be developed relatively cheaply



In summary

A new framework map for NLL



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- A dense standard map to aid communication and collaboration in the research community
- A foundation for physical mapping, cytogenetic analysis and genome sequencing
- A pre-requisite for association mapping
- A tool for accessing model genome resources *via* comparative mapping

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