

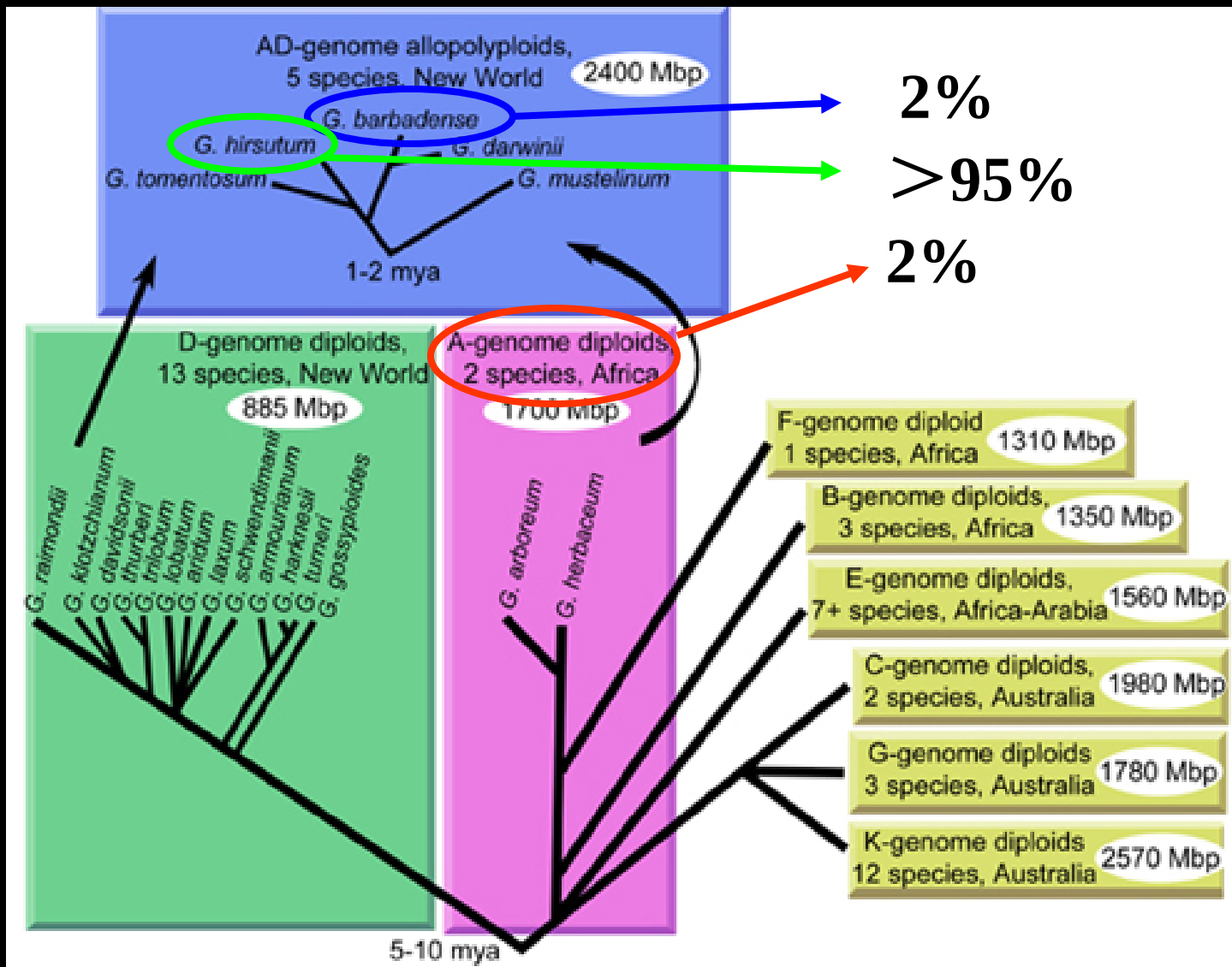
Genetic Map and QTL Mapping in Upland Cotton

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The interspecific maps of (*G. hirsutum* × *G. barbadense*) populations almost saturated.

Rong et al. (2004), 2584 loci, 4447.9 cM.

Guo et al. (2008), 2247 loci, 3425.8 cM.

Yu et al. (2011), 2316 loci, 4428.9 cM.

Our objectives are to construct high-density genetic map and to map QTL for agronomy traits.

Marker development

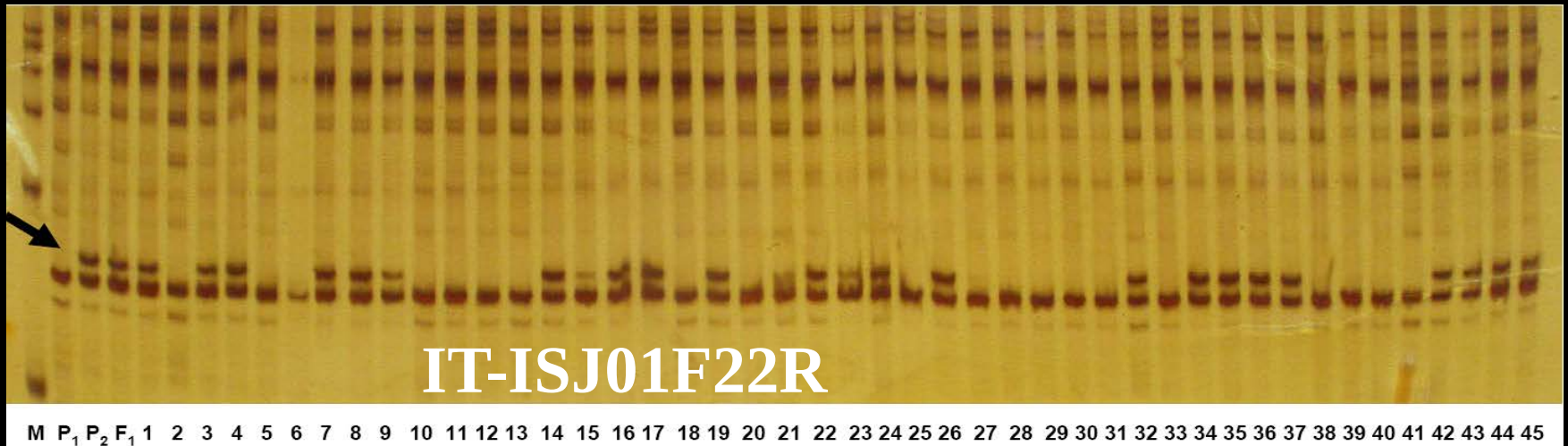
ISJ (intron-exon splice junction) marker

ET-ISJ (exon-targeted intron-exon splice junction)

4096 primer combinations

IT-ISJ (intron-targeted intron-exon splice junction)

4096 primer combinations



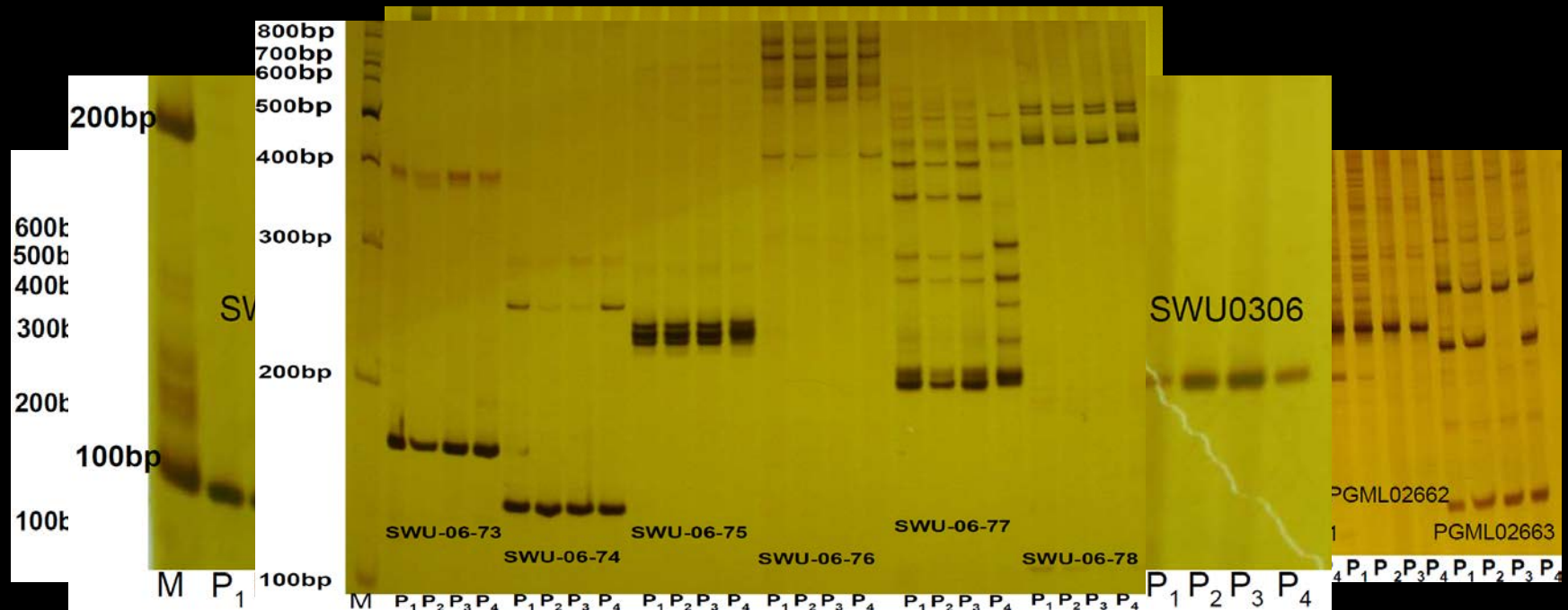
SSR marker

G. ramondii BAC-ends' SSR 5000 pairs

G. ramondii gnome SSR 953 pairs

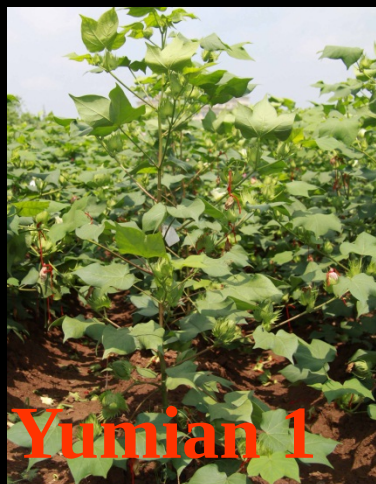
Transcription factor SSR 1592 pairs

RFLP probe 363 pairs SSR



Genetic map

Population parents



Fiber trait	Yumian 1	T586	CCRI35	7235
Length (mm)	29.2	20.5	29.2	33.2
Uniformity (%)	85.8	79.4	79.7	83.9
Micronaire	4.5	2.5	4.2	4.0
Elongation (%)	6.4	7.4	6.6	6.2
Strength (cN/tex)	36.7	19.5	30.7	35.8

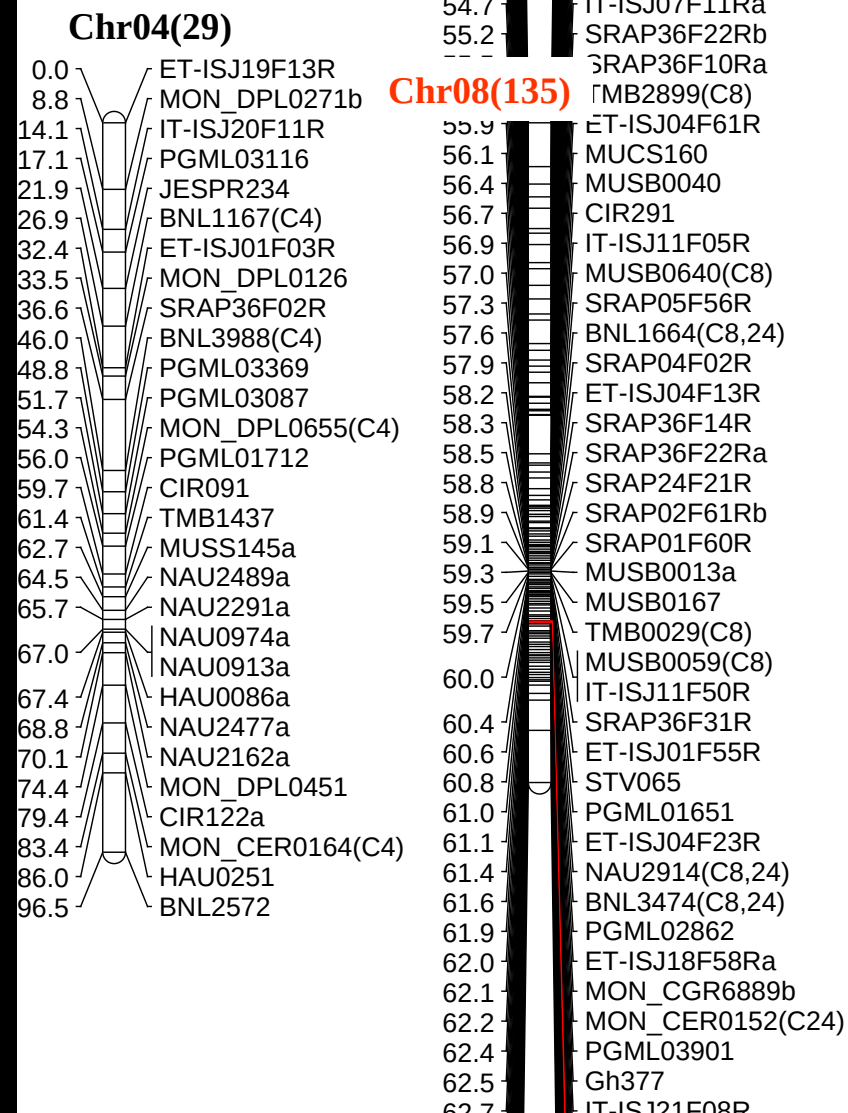
Population 1: (Yumian 1 × T586) RIL

270 lines

1775 loci

74 linkages

4250.6 cM



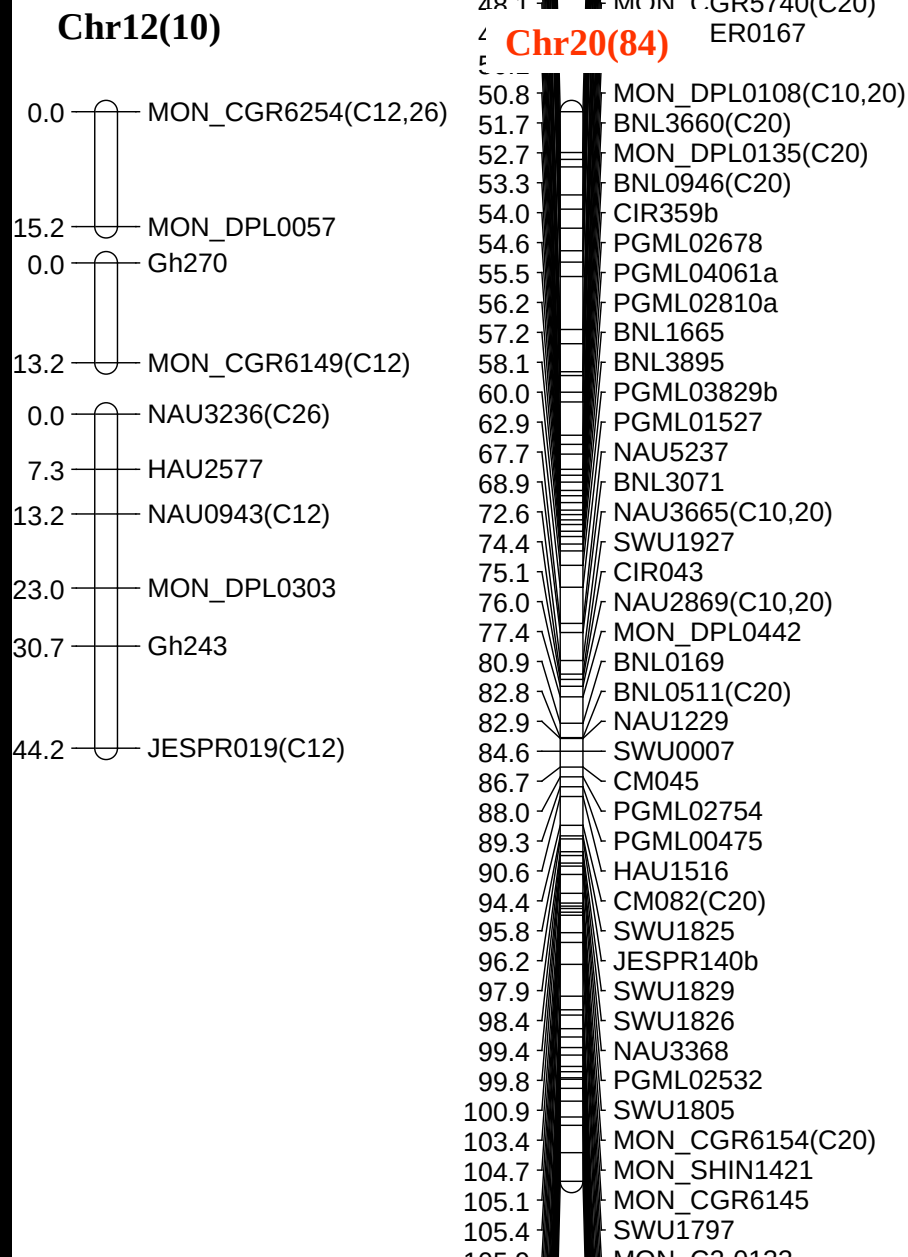
Population 2: (Yumian 1 × CCRI 35) RIL

180 lines

1132 loci

83 linkages

3729.7cM



Population 3

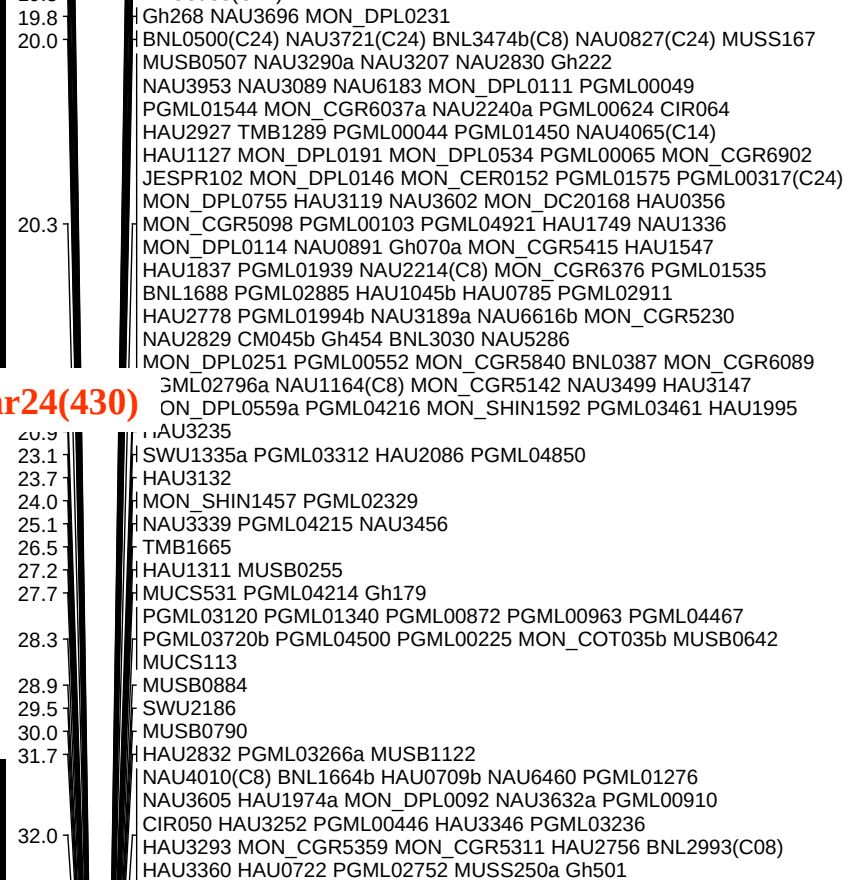
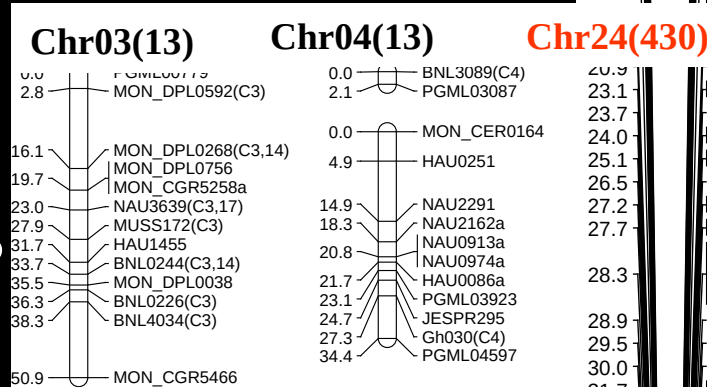
(Yumian 1 × 7235) RIL

180 lines

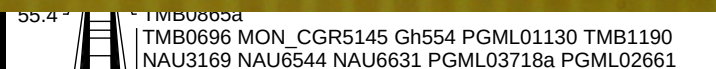
1444 loci

74 linkages

2887.7 cM



Gh455 (46-90)



Population 4

Composite cross population (CP)

(Yumian 1 × CCRI 35) × (Yumian 1 × ZB3)

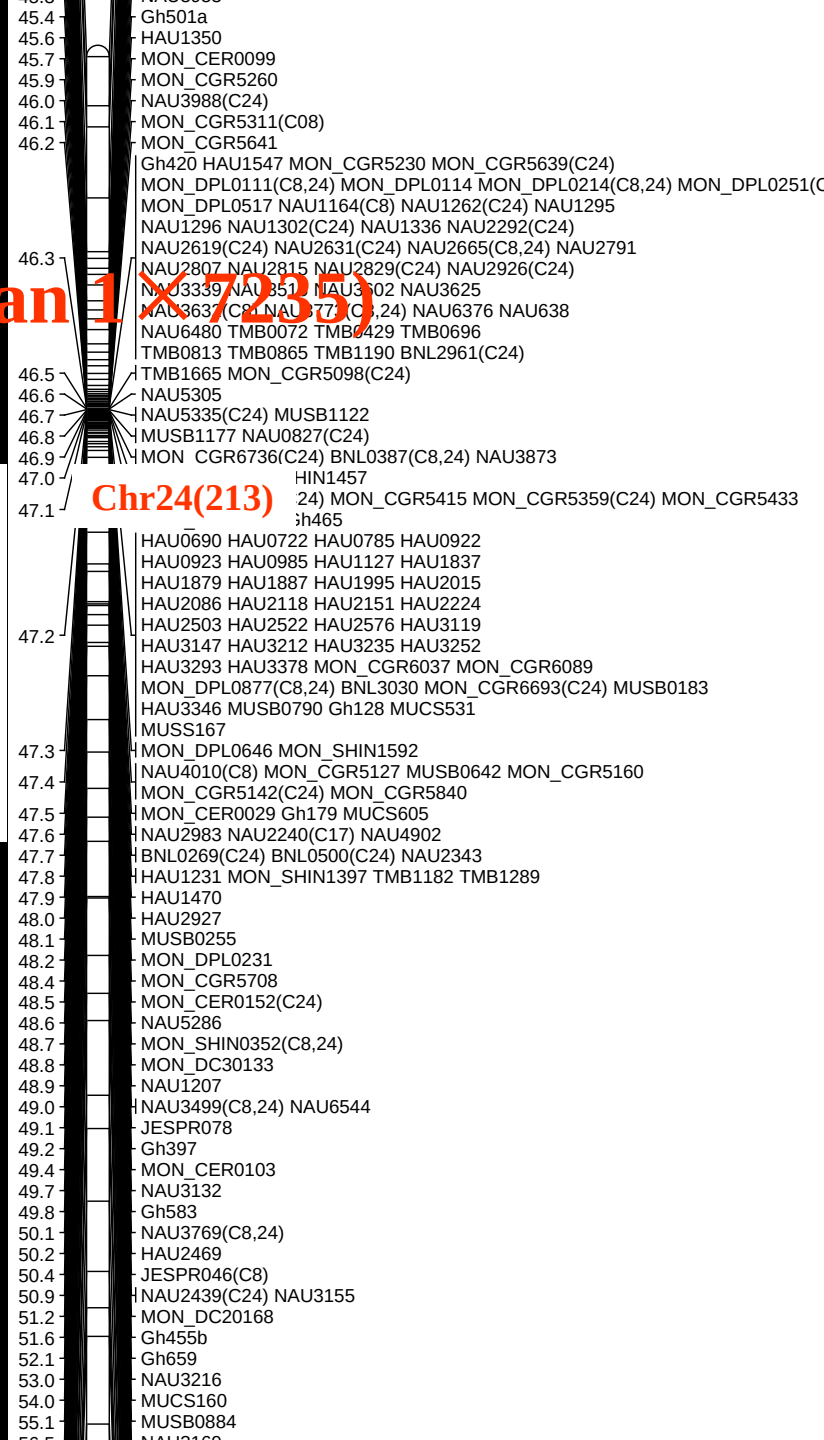
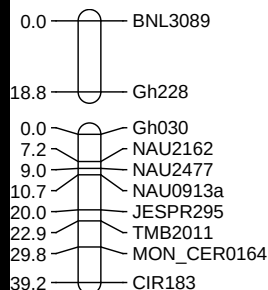
172 individuals

978 loci

69 linkages

4184.4 cM

Chr04(10)



QTL mapping for agronomy traits

Population 1: (Yumian 1 × T586) RIL

15 QTL for lint percent

55 QTL for 5 fiber quality traits

88 QTL for 6 seed-physical traits

57 QTL for 6 seed-nutritional traits

39 QTL for 5 photosynthetic traits

Population 2: (Yumian 1 × CCRI35) RIL

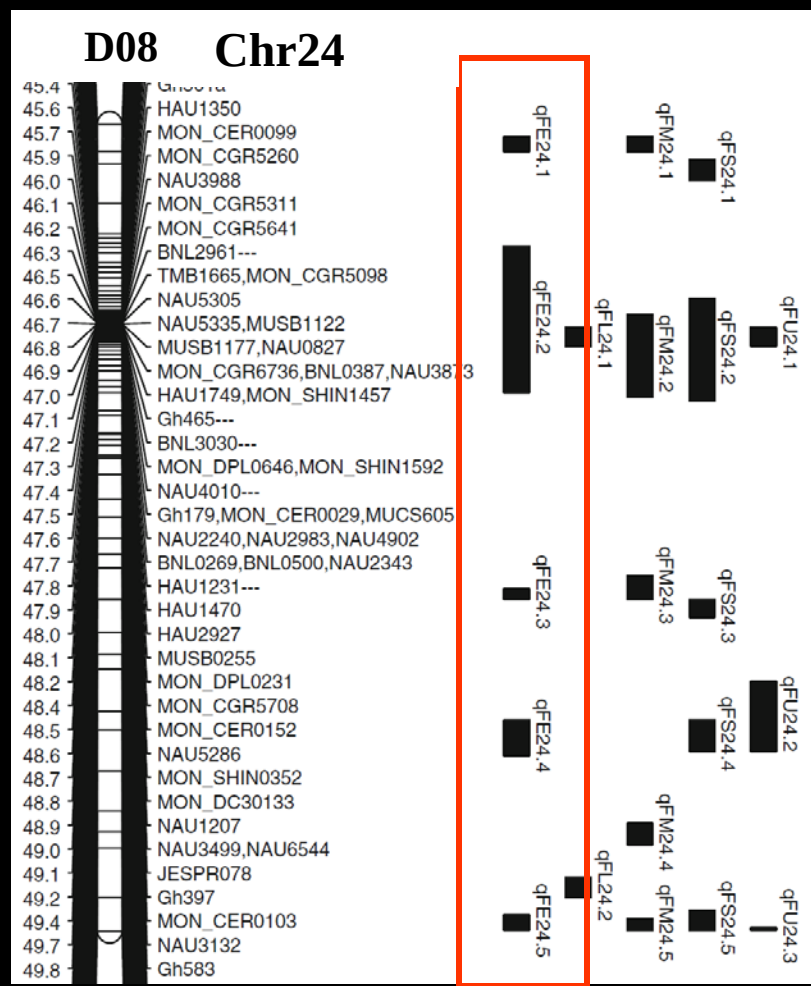
75 QTL for 5 fiber quality traits

35 QTL for 5 yield traits

Population 3: (Yumian 1 × 7235) RIL

54 QTL for 5 fiber quality traits

11 QTL for lint percent



Composite cross population

(Yumian 1 × CCRI 35) × (Yumian 1 × 7235)

63 QTL for 5 fiber quality traits

QTL	Chr	Near marker	a1	a2	% Expl.
qFL01.1	01	HAU1044	0.35	-0.58	48.5
qFL15.1	15	NAU0902	-0.27	0.88	50.8
qFL23.1	23	NAU1035	0.65	-0.57	42.0
qFS24.1	24	CGR5145	0.19	-0.54	16.2

Summary

(1) Tetraploid cotton genetic map

1) Markers unevenly distributed on genetic map

Chrom	POP1	POP2	POP3	Chrom	POP1	POP2	POP3
A01	54	46	21	D01	72	73	79
A02	33	45	35	D02	77	43	40
A03	37	24	13	D03	39	57	42
A04	29	21	13	D04	35	31	27
A05	70	57	53	D05	82	66	62
A06	140	34	35	D06	73	18	52
A07	57	36	21	D07	78	92	33
A08	153	29	74	D08	53	39	430
A09	37	31	45	D09	78	62	33
A10	40	23	30	D10	119	91	63
A11	72	28	41	D11	115	43	39
A12	50	10	38	D12	59	66	52
A13	78	19	33	D13	43	48	40
At	850	403	452	Dt	923	729	992

2) Although upland cotton has low genetic diversity, but **some chromosomes have much more diversity**. These chromosomes may be produced by interspecific introgression.

Chromosome	T586	CCRI35	7235	Chrom	T586	CCRI35	7235
A06	122	37	35	D06	73	18	52
A07	56	40	21	D07	61	85	33
A08	135	29	74	D08	49	38	430
A10	40	32	25	D10	98	84	63
A11	69	28	41	D11	110	43	18

3) Tetraploid D genome has higher genetic diversity than tetraploid A genome. This result suggest that A gnome evolved rapidly before the tetraploid formed, but D gnome evolved rapidly after the tetraploid formed.

The loci of At & Dt genome

Chromosome	T586	CCRI35	7235
At	850	403	452
Dt	923	729	992

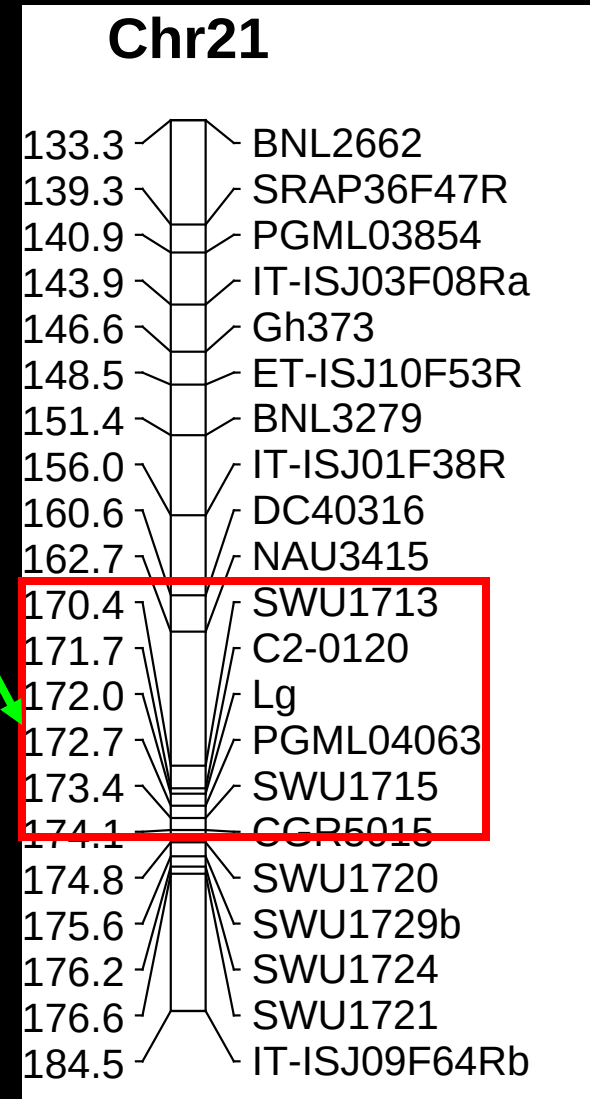
4) Some chromosomes have low genetic diversity among upland cultivars, even between *G. hirsutum* and *G. babadense*. These chromosomes may have important genes for cotton.

The loci of chromosome A04 & D04

Chromosome	T586	CCRI35	7235
A04	29	21	13
D04	35	31	27

5) Green fiber (Lg) was mapped at the end of chromosome Chr21 (D11)

Lg located on chromosome chr15 in the classical genetic map.



(2) QTL for agronomy traits

- 1) Many minor QTL controlled agronomy traits**
- 2) Different cotton cultivars have different alleles at some QTL loci**
- 3) Some QTL for yield, fiber quality and seed traits co-locate on the same chromosome region in cotton**
- 4) Some chromosome region clusters QTL for the same trait**

Acknowledgments

Prof. Yan pei

Prof. Andrew Paterson

Dr. Jian Zhang

Dr. Dajun Liu

Dr. Zhonghua Teng

Dr. Shiyi Tang

Dr. Dexin Liu

Dr. Ke Zhang

Mr. Zhaoyun Tan

Mr. Shunfeng Wang

Ms. Liu Fang



Mr. Gang Lin

Mr. Ling Li

Ms. Li Li

Ms. Huijuan Ni

Ms. Fengmin Zheng

Ms. Jing Zheng

Ms. Meichun Hu

Ms. Qun Wan