

IDENTIFICATION OF QTLs FOR FIBER QUALITY IN A M5 MUTANT SEGREGATING POPULATION



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Objectives

- Identify new molecular markers related to fiber quality characteristics in segregating M₅ mutant cotton (*Gossypium hirsutum* L.) population.
- Identify QTLs with practical applicability for Bulgarian cotton breeding programs.



Materials and methods

- Apply mutagenic treatment to standard Bulgarian variety (Chirpan 603)
- Develop segregating population
- Screen the segregating population for polymorphisms of known SSR markers related to fiber quality
- Use ISSR primers to discover new markers
- Associate marker segregation with trait variability

Materials and methods – cont' d

- Gamma ray treatment
- Selfing for 6 generations + phenotyping
- Application of core set of SSRs to the developed population
- Application of the only 3 described so far ISSRs
- Assessing the applicability of further (in house developed) ISSRs
- QTL mapping

Traits of interest

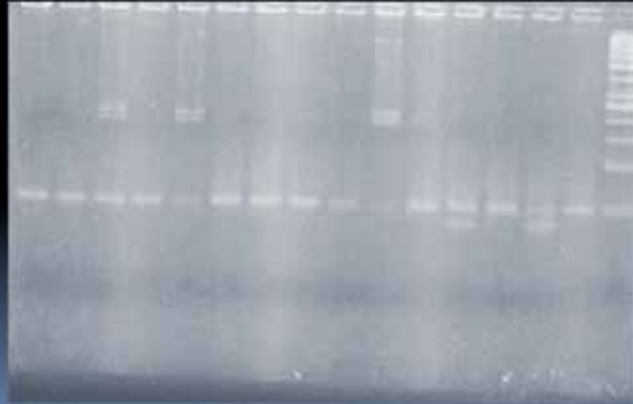
- Fiber length
- Fiber strength
- Uniformity
- Elongation
- Maturity
- Micronaire

Results and discussion

- 13 SSR primer pairs used
 - Common for different cotton maps (Lacape et al., 2003; Rong et al., 2004; Liu et al., 2006; Ma et al., 2008)
 - Useful polymorphisms identified in relation to fiber quality

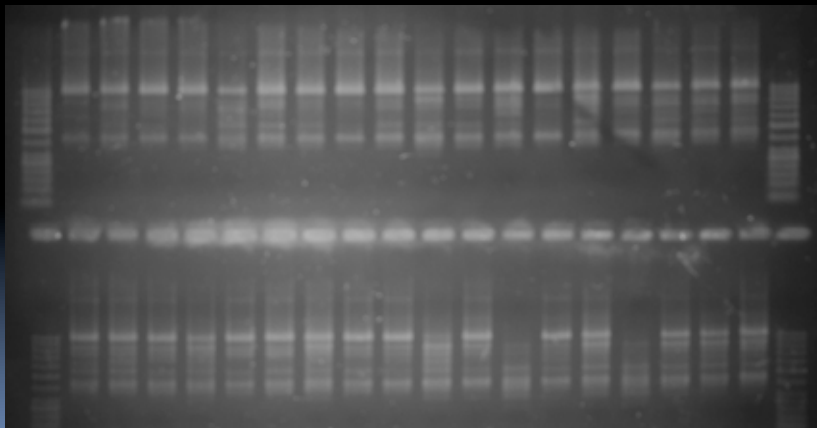
Results and discussion

- Low number of SSR marker polymorphisms identified => low number of useful markers



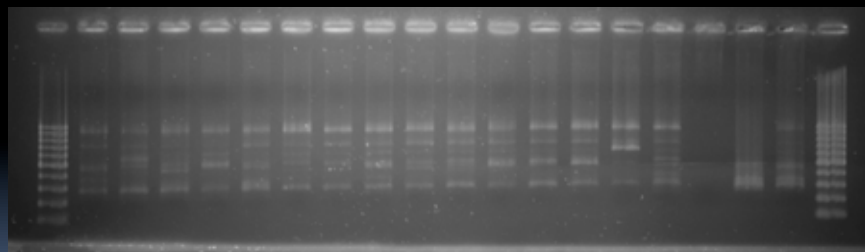
Results and discussion

- Number of ISSR marker polymorphisms => number of useful markers



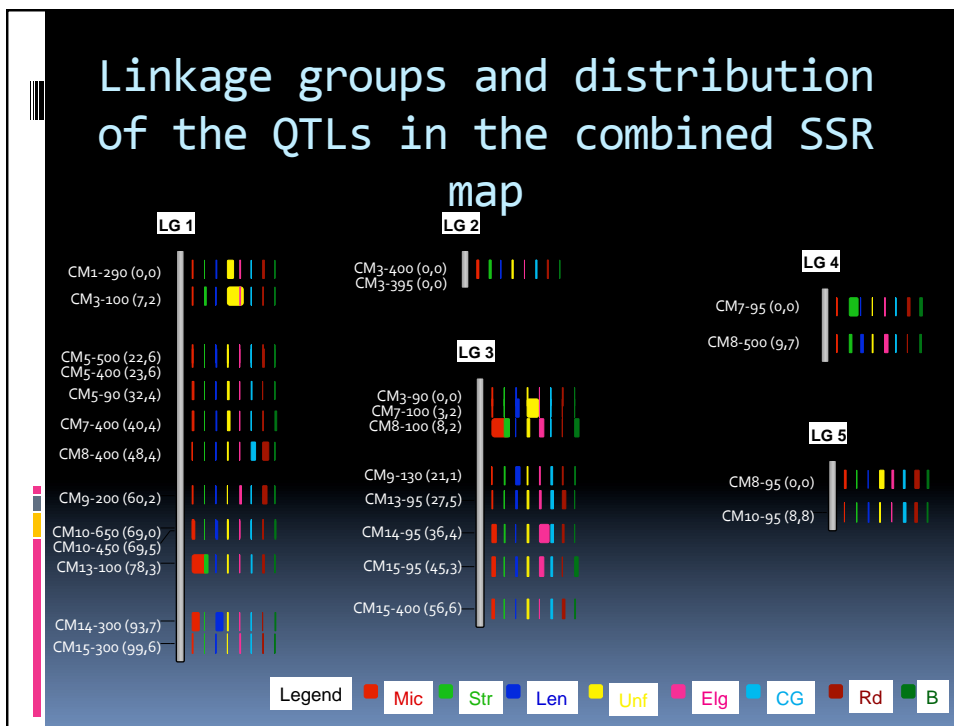
Results and discussion

- Higher number of ISSR marker polymorphisms identified per reaction as compared to SSR markers



Results and discussion

Genotype	Fiber characteristics							
	Mic	Strength	Length	Uniformity	Elongation	C-G	Rd	+b
M 20	3,9	26,8	30,1	83,3	10,2	53,2	63,0	9,6
M 8	4,5	31,4	29,3	83,7	9,1	53,4	60,5	10,5
M 72	3,8	30,4	29,0	79,3	9,2	52,2	63,6	9,3
M 19	4,0	28,1	29,0	84,6	9,8	62,1	62,0	8,5
M 4	3,6	29,5	28,9	84,4	9,8	53,4	61,1	10,6
M 65	3,6	25,9	28,9	80,7	7,2	52,2	62,3	9,2
M 6	4,9	30,4	28,6	83,8	9,6	52,1	65,0	9,0
M 18	4,2	31,4	28,2	82,0	9,6	62,1	60,6	9,1
M 61	3,7	31,6	28,1	84,3	6,9	53,2	63,6	9,6
M 23	4,3	28,5	28,0	82,6	15,2	53,1	65,4	10,2
...								
....								
M 56	4,7	29,2	24,5	83,2	7,8	53,2	60,9	9,5
M 14	6,2	27,8	23,8	83,0	7,5	43,1	67,5	10,6
M 74	4,0	26,1	23,7	82,8	7,6	53,3	61,9	10,9
M 38	5,4	27,2	23,3	80,5	10,7	52,2	62,2	8,9



Relative distance and significance of the effects of the QTLs in the ISSR map

ISSR marker N°	cM	len	Unf	Str	Elg	Mat
1	0,0	1,94	0,12	0,89	2,21	2,68
...
10	0,0	0,31	0,11	0,19	0,03	3,95 *
11	18,3	3,32	0,76	0,52	0,03	0,58
12	25,1	4,58 *	8,68 **	0,32	0,16	0,50
...
25	41,5	0,09	2,79	1,41	5,11 *	0,01
...
28	0,0	1,52	1,16	3,95 *	2,51	17,54 ****
29	6,1	0,63	0,06	0,00	7,94 **	0,00
30	0,0	6,14 *	3,87	3,77	3,58	0,05
...
35	0,0	0,02	0,26	0,80	0,12	0,04

Conclusions

- SSR markers developed in intraspecific crosses can be useful in mutation breeding
- Most of the loci affect single trait
- Regions were identified with possible clustering of genes / pleiotropic effects
- The information obtained in SSR mapping can be complemented through the use of ISSR markers

Thank you!



Faculty of Agronomy