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Detection and verification of SNP related to cotton fiber quality in cotton cellulose synthase gene family

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Cellulose synthases (CesAs) are multi-subunit enzymes associated with the plasma membrane in plants, playing a pivotal role in cellulose production. In this study, the CesA gene coding sequences of four cotton species with sequenced genomes were aligned. The phylogenetic analysis indicated that the CesA gene family in *G. arboreum*, *G. raimondii*, *G. hirsutum* (“TM-1”) and *G. barbadense* (“Xinhai 21”) or *G. barbadense* (“3-79”) could be divided into 6 groups and 15 sub-groups, each group containing 2-5 homologous genes. A total of 544 SNPs were identified in the CesA gene family among the five cotton genomes, including 155 with including amino acid changes. An expression analysis of CesA genes through RNA-seq showed that one to four GhCesA genes were Differentially Expressed (DE) in 0 and 3 DPA ovules between the two BILs (NMGA-062 and NMGA-105) with different fiber lengths, but no DE gene was identified in 10 DPA fibers. Some SSR markers related to fiber quality were found around CesA Genes. Part of SNPs in the differentially expressed GhCesA genes was checked for fiber quality (in progress).

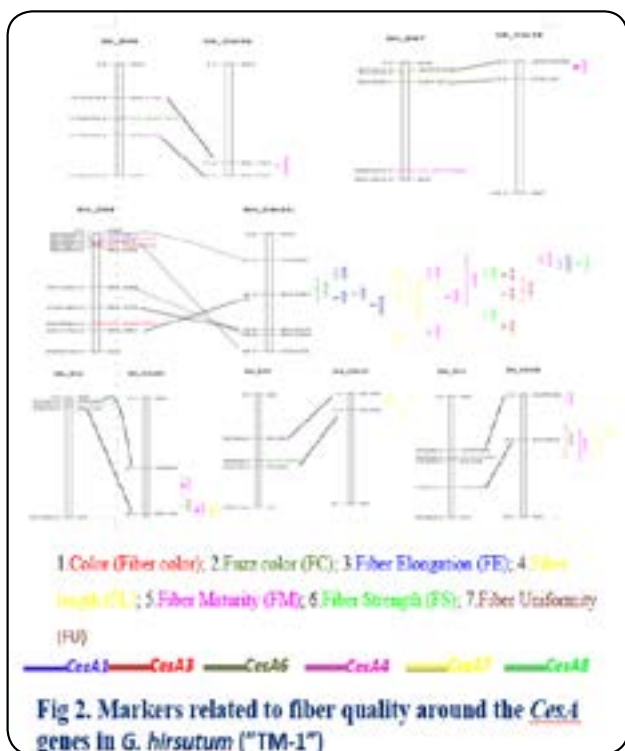


Table 2 Differential expression of *GhCesA* genes in ovules or fibers between NMGA-062 and NMGA-105 differing in fiber length.

CesA gene	Chr	Length (kb)	Divergence variation		Mutations	Group	Up or down regulated		
			Gh vs. Gh	Gh vs. Gb			0DPA	3DPA	10DPA
GH_A010400	A6	1303	3	3	0	CesA3	Down	Down	Down
GH_A010220	A11	1305	1	1	0	CesA5	Down	Down	Down
GH_D010220	D11	1304	1	0	0	CesA5	Down	Down	Down
GH_D010202	D05	1302	0	1	0	CesA5	Down	Down	Down
GH_D000120	D06	1300	11	1	0	CesA5	Down	Down	Down

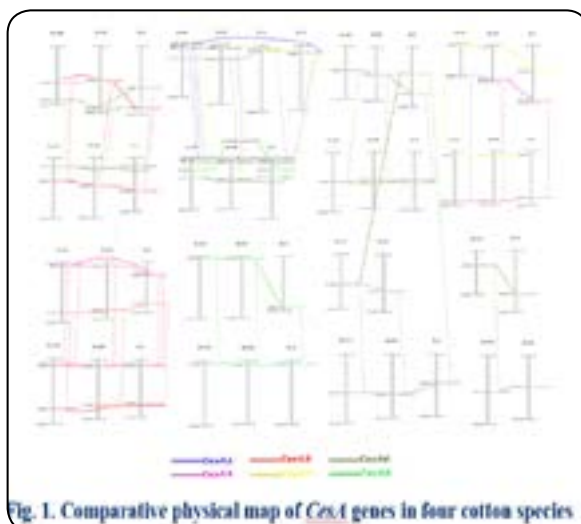
Table 3 Verification of SNPs in the exon region of the above *GhCesA* genes among different cotton materials (partial)

Gene	SNP	Cotton Materials					
		Material 1	Material 2	Material 3	Material 4	Material 5	Material 6
CesA3	SNP1	T	C	T	T	T	T
	SNP2	T	C	T	T	T	T
	SNP3	T	C	T	T	T	T
	SNP4	T	C	T	T	T	T
	SNP5	T	C	T	T	T	T
	SNP6	T	C	T	T	T	T
	SNP7	T	C	T	T	T	T
CesA5	SNP8	T	T	T	T	T	T
	SNP9	T	T	T	T	T	T

✓ Part of SNPs in the *GhCesA* genes were checked for fiber quality-In progress

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Recent Publications

1. Li F, Fan G, Wang K, Sun F, Yuan Y, Song G, Li Q, Ma Z, Lu C, Zou C, et al. (2014) Genome sequence of the cultivated cotton *Gossypium arboreum*. *Nature genetics* 46(6):567-573.
2. Wang K, Wang Z, Li F, Ye W, Wang J, Song G, Yue Z, Cong L, Shang H, Zhu S, et al. (2012) The draft genome of a diploid cotton *Gossypium raimondii*. *Nature Genetics* 44(10):1098-1103.
3. Li F, Fan G, Lu C, Xiao G, Zou C, Kohel R J, Ma Z, Shang H, Ma X, Wu J, et al., (2015) Genome sequence of cultivated upland cotton (*Gossypium hirsutum* TM-1) provides insights into genome evolution. *Nature biotechnology* 33(5):524-530.
4. Liu X, Zhao B, Zheng H, Hu Y, Lu G, Yang C, Chen J, Chen J, Chen D, Zhang L, et al., (2015) *Gossypium barbadense* genome sequence provides insight into the evolution of extra-long staple fiber and specialized metabolites. *Scientific reports* 5:14139.
5. Li A, Xia T and Xu W (2013) An integrative analysis of four CESA isoforms specific for fiber cellulose production between *Gossypium hirsutum* and *Gossypium barbadense*. *Planta* 237(6):1585–1597.

Biography

Xiangyun Zhang, professor, female, born in Hebei province, China. She is engaged in cotton breeding for over 30 years. She has won the National Scientific and Technological Progress Second Prize and China Agricultural Science and Technology Award, and now she obtains State Council special allowance. She and her team has successively presided and finished national or provincial cotton research projects more than 60 items, and nearly 20 high-yielding, disease-resistant and high-quality cotton varieties were bred, such as Ji228, Jiza 1, Jimian 958, Jiyouza69, Ji2000, etc. In addition, she presided over 18 invention patents and achievements. The team led by comrade Xiangyun Zhang laid the foundation of cotton breeding in Hebei province.

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