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BOOK OF ABSTRACTS

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typically last at least 60 days, directly determine cotton fibre quality characteristics. The goal of this work was to identify differentially expressed genes at two different stages during cotton fibre development i.e. 0 dpa and 10 dpa. The techniques, suppression substractive hybridization (SSH) and qRT-PCR were followed using the isogenics representing FL (Fuzzy linted) and Fl (Fuzzy-lintless) linesof G.arboreum. The scanning electron microscopy (SEM) revealed no difference in the fibre initials except for the fuzz development in Fl (Fuzzy-lintless) line which is due to the down-regulation of the some genes necessary for the fibre development. In SSH, based on the putative functions of genes preferentially or specifically expressed in fibre elongation stage in cotton fibre development BLAST results showed that many novel genes were contained in forward library and a few had been previously reported. On the basis of previous reports and the putative functions of the genes which are involved in fibre development and how those genes regulate fibre growth were reported in the database. This include actin depolymerizing factor 2 (ACT2), acyl- oxidase 1 (ACO1), beta-galactosidase (β-galactosidase) from Ricinus communis. There were contigs showing the homology to the beta-glucanase (β-glucanase), β-ketoacyl-Coa synthase family protein, beta-tubulin 19 (β-tubulin 19), elongation factor 1 (EF1), glucose-6-phosphate 1-epimerase, malate dehydrogenase, xyloglucan endotransglucosylase hydrolase protein 32 (XTH32/XET32). Genes like calcineurin b-like protein (CBL), calmodulin binding (CaM), mitogen-activated protein kinase 16 (MAPK/ MPK16), diacylglycerol acyltransferase (ACY) Phospholipase-C (PLC), phosphatidylcholine transferases (PCY), Phospholipase-C (PLC) were also found in the database and attempt was made for some of this genes to validate by the Quantitave real-time PCR which confirmed the chance of the undergrowth of the fibre in the Fl line. Comparative analysis fibre specific genes between tetraploid and diploid cotton is made to specify genomic location of these genes.

14. Tak Fa 86-5: GREEN-STAPLE COTTON CULTIVAR

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Cotton improvement for natural-color fiber is not only adding value to fiber product, but is also environmental friendly in reducing nature pollution from a dying process. Thus in 2000, the long stable (fiber or lint) Takfa 2 cotton was crossed a green-short staple cotton variety; thereafter (2001-2002), backcrossing to Takfa 2 and selection for good green-lint yielding cotton plants for four generations was made. In each backcrossing, seed (after ginning or separation from seed cotton) was collected in bulk from individual green- lint cotton plants exhibiting the plant type of Takfa 2. The seeds of BC_4F_1 were then sown in 2003, plants with green fiber or lint were selected and their seeds were used for planting as BC_4F_2 in 2004 for pedigree method of selection. From all planted BC_4F_2 plants, 574 plants were individually selected from this generation. Then 574 families of BC_4F_3 seeds or lines were used for further planting for selection (in the plant-to-row pattern) in 2005. Two

hundred and eight green-lint yielding rows with the plant type or canopy similar to Takfa 2 were selected, in which 675 plants were selected for fiber quality examination. Sixty-six plants (from 30 rows) had a standard fiber quality with the average of 24% ginning out turn fiber percentage), 1.24-inch fiber length, 18.3 g tex^{-1} fiber strength, 47 uniformity and 0.9 micronaire fiber fineness. In 2006, seeds of 66 selected plants were then planted as 66 rows (plant-to-row) and 96 rows (boll-to-row) of BC_4F_4 families or lines. Only 27 rows or lines with good plant type uniformity were selected. The bulk-collected seeds of 27 individual lines were planted as BC_4F_5 lines in 2007. Only 20 lines with good uniformity green-lint yield and plant type were selected their mean fiber qualities were 24% ginning out turn, 1.24 inch fiber length, 23 g tex^{-1} fiber strength, 49 uniformity and 2.0 micronaire fiber fineness. The lines with uniformity in good plant type and green fiber quality were evaluated for yield potential in 2008-2011. The promising, Tak Fa 86-5 was a selection as outstanding in green-stable quality, high yield and leaf roll disease resistance.

15. EXPLOITATION OF HETEROTIC GROUP THROUGH RECIPROCAL SELECTION FOR COMBINING ABILITY IN COTTON (Gossypium hirsutm L.)

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Exploitation of heterosis through hybrids has led to improvement in productivity of both selfand cross pollinated crops. In cross pollinated crops hybrid breeding program is supported by population improvement schemes aimed at improving combining ability. There are very few studies on grouping genotypes based on heterotic pattern and exploiting them in self pollinated crops. At Dharwad, efforts are made to constantly observe most potential crosses and understand the basis of complementationcausing high heterosis. These efforts have lead to formation of different heterotic groups like Stay green x Compact, Robust x Compact, Robust x Higher RGR and Stay green x high RGR which in general give potential hybrids.Further efforts are alsomade to identify elite combiners within each group and utilize this knowledge to exploit these groups by Patil (2013).

In an attempt to exploit these diverse heterotic groups, attempts are made to enhance genetic distance between opposite heteroticpopulations following modified reciprocal recurrent selection scheme between opposite populations. The main objectives of the present study were framed on creation of recombinational variability for combining ability and assess the nature and magnitudes of variability released for combining ability in F_4 generations and explore possibility of improving combining ability as a trait in developing better hybrids.

The experimental material was constituted by a HeteroticBox involving two diverse single cross F_1s viz DSC-7x DSC-68 from compact heterotic group and DSMR-10 x DSG3-5 from robust and stay green heterotic group which were identified as base populations through the principal of predicted double cross performance.. These crosses were advanced to F_4 generation and seventy four lines of DSC-7 x DSC-68 and thirty seven