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Fibre quality evaluation of BG II converted 152 *G. hirsutum* cotton lines in F₆ generation with presence of Cry1Ac and Cry2Ab insect resistant transgene

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Abstract

The present study comprised of "Selection of *G. hirsutum* genotypes for superior fibre properties along with Bollgard II transgenes from segregating population" with the aim to develop *G. hirsutum* straight varieties with the Bollgard II version. The work was initiated at Cotton Research Station, Nanded (under jurisdiction of Vasantao Naik Marathwada Krishi Vidyapeeth, Parbhani, Maharashtra State). The experiment was laid in Randomized Block Design with three replications. The experiment comprises 152 qualitative promising genotypes with positive Cry1Ac and Cry2Ab transgene, sown and evaluated for quality fibre parameters. Fibre quality from pooled samples across three replications on upper half mean length (mm), fibre strength (g/tex), micronaire value ($\mu\text{g}/\text{inch}$), uniformity index (%) and fibre elongation (%) was recorded. The significant differences were observed for all the fibre parameters among the 152 genotypes. Out of 152 genotypes tested, for fibre length UHML (mm) the 45 genotypes observed long staple length (between 27.5 mm to 32.0 mm), 102 genotypes observed medium long staple length (between 25.0 mm to 27.5 mm) and five genotypes observed medium staple length (between 20.5 mm to 24.9). The range of micronaire ($\mu\text{g}/\text{inch}$) was observed from 2.9 ($\mu\text{g}/\text{inch}$) (S 6) to 4.9 ($\mu\text{g}/\text{inch}$) (S 24). Very fine micronaire value (below 3.0 $\mu\text{g}/\text{inch}$) was observed by S 6 (2.9 $\mu\text{g}/\text{inch}$), 85 genotypes observed fine micronaire (between 3.0 to 3.9 $\mu\text{g}/\text{inch}$) and 66 genotypes observed average micronaire value (between 4.0 to 4.9 $\mu\text{g}/\text{inch}$). Significant mean differences were observed for bundle strength (g/tex) in the testing genotypes. The range of bundle strength (g/tex) was observed from 23.1 (g/tex) to 32.5 (g/tex). One genotype showed good bundle strength S 87 (29.2 g/tex) (between 29.1 g/tex to 32.5 g/tex) among all the test genotypes. The 120 genotypes observed average bundle strength (g/tex) (between 25.1 to 29.0 g/tex) and 31 genotypes observed weak bundle strength (g/tex) (between 20.1 to 25.0 g/tex). The range of uniformity index (%) was observed from 79 (%) (S 143) to 86 (%) (S 36 and S 80). Two genotype S 36 and S 80 both showed excellent above 85% uniformity index among all the test genotypes. 117 genotypes observed average uniformity index (between 79% to 83%) and 33 genotypes observed good uniformity index (%) (between 83.1 to 85%). Fibre elongation (%) was observed from 4.3 (%) (S 129) to 6.3 (%) (S 14). Eight genotypes viz., S 14 (6.3%), S 27 (6.2%), S 30 (6.1%), S 57 (6.1%), S 58 (6.0%), S 108 (6.0%), S 110 (6.0%) and S 111 (6.0%) showed excellent fibre elongation (range 6.0% and above) and 98 genotypes observed good elongation (between 5.0% to 5.9%) of fibre among all the test genotypes. In this experiment long staple length genotypes S 87 (30 mm), S 80 (29.6 mm), S 138 (29.2 mm), S 152 (29.2 mm) and S127 (29.1 mm) having micronaire value S6 (2.9 $\mu\text{g}/\text{inch}$), S43 (3.0 $\mu\text{g}/\text{inch}$), S 8 and S49 (both 3.1 $\mu\text{g}/\text{inch}$) and bundle strength of S 87 (29.2 g/tex) and S80 (28.8 g/tex) observed promising for utilizing as parental source of BG II converted straight lines of *G. hirsutum* in further BG II hybrid development programme.

Keywords: Fibre quality, *G. hirsutum*, BG II straight variety, Cry1Ac and Cry2Ab, fibre improvement

Introduction

Research on cotton yield improvement worldwide receives immense importance on planting density, plant population and geometry including spatial arrangement. Nevertheless the fibre quality parameters have also immense importance for judging the cotton lint value to get the higher prices in market. Developing short to medium duration hybrids and varieties with erect, compact plant architecture, having necessary biotic and abiotic stress tolerant traits offers viable opportunities to increase yields and land use efficiencies. It is important to find the genotypes for their high seed cotton yield, which being a complex trait is highly influenced by the environmental conditions. Performance of any genotypes for a complex trait like seed cotton yield, it is very crucial to find the overall mean over diverse environments.

Along with this a high quality fibre which consists of good fibre strength, fibre length and fibre fineness is a pre-requisite for a textile industry. The demand for a high quality cotton is immensely increasing, thus there is a need to enhance the quality parameters by proper selections during breeding programmes. It is also very important to have prior knowledge about the environment and the genotype interactions as they have major role in assessment of elite cultivars.

In India, Bollgard I was introduced in 2002 consisting of *Cry IAc* protein and Bollgard II was introduced in 2008 consisting of *Cry IAc* and *Cry 2Ab* proteins. The Genetically Modified crops are regulated by Genetic Engineering Approval committee. Different Bt hybrids have different physiological and demographical difference. The *Cry IAc* I expression levels from one Bt cotton to another genotype is varying. The concentration of *cry IAc* in different genotypes are not identified (Nagappa *et al.*, 2018) [18].

Hence, the present research experiment was undertaken first time in public sector for development of the straight varieties of *G. hirsutum* into Bollgard II version (*Cry IAc* & *Cry 2Ab*) with an objective with improving the fibre quality.

Materials and Methods

The present study comprised of "Selection of *G.hirsutum* genotypes for superior fibre properties along with Bollgard II transgenes from segregating population" with the aim to develop *G hirsutum* straight varieties with the Bollgard II version. The work was initiated at Cotton Research Station, Nanded (under jurisdiction of Vasantrao Naik Marathwada Krishi Vidyapeeth, Parbhani, Maharashtra State). The experiment was laid in Randomized Block Design with three replications. The experiment comprises 152 qualitative promising genotypes with positive *Cry1Ac* and *Cry2Ab* transgene were sown and evaluated for quality fibre parameters with eight checks *viz.*, two BG II *intra hirsutum* hybrids *viz.*, Jadoo BG II and NHH BG II; two non bt hybrids *viz.*, NHH 44 and NHH 250; two bt straight varieties *viz.*, Suraj bt and PKV 081 bt; two straight varieties NH 615 and NH 545. Fibre quality from pooled samples across three replications on upper half mean length (mm), fibre strength (g/tex), micronaire value ($\mu\text{g}/\text{inch}$), uniformity index (%) and fibre elongation (%) was recorded. Two lint samples from each replication of each treatment were used to perform fibre quality analysis. Testing of the fibre parameters was done at the Ginning and Training Centre, Regional Centre, Central Institute for Research Cotton Technology, Nagpur.

Results and Discussion

Fibre parameters tested in the 152 genotypes showed varied results which are useful for the improvement of the genotype fibre quality.

Upper half mean length (UHML) (mm)

Significant mean differences were observed for upper half mean length (UHML) in the testing genotypes. The range of staple length was observed from 24.1 mm (S 144) to 30.0 mm (S 87). Out of 152 genotypes tested, 45 genotypes observed long staple length (between 27.5 mm to 32.0 mm) *viz.*, S 4 (28.1 mm), S 17 (28.1 mm), S 19 (28.5 mm), S 34 (27.5 mm), S 36 (29.0 mm), S 37 (28.0 mm), S 39 (28.2 mm), S 40 (27.7 mm), S 41 (27.7 mm), S 43 (29.0 mm), S 55 (28.1 mm), S 56 (27.9 mm), S 75 (28.0 mm), S 78 (27.6 mm), S 80 (29.6 mm),

S 81 (28.5 mm), S 82 (27.8 mm), S 84 (28.7 mm), S 85 (28.6 mm), S 86 (28.0 mm), S 87 (30.0 mm), S 88 (28.2 mm), S 89 (28.0 mm), S 117 (28.3 mm), S 118 (28.5 mm), S 124 (28.2 mm), S 125 (28.6 mm), S 126 (28.0 mm), S 127 (29.1 mm), S 128 (28.4 mm), S 129 (27.6 mm), S 130 (28.9 mm), S 131 (28.9 mm), S 132 (28.3 mm), S 134 (27.8 mm), S 135 (28.7 mm), S 136 (29.0 mm), S 137 (28.7 mm), S 138 (29.2 mm), S 139 (27.7 mm), S 140 (28.4 mm), S 142 (27.9 mm), S 147 (27.7 mm), S 148 (27.9 mm) and S 152 (29.2 mm). Total 102 genotypes observed medium long staple length (between 25.0 mm to 27.5 mm) *viz.*, S 2 (26.7 mm), S 3 (27.2 mm), S 5 (26.7 mm), S 6 (27.2 mm), S 7 (26.0 mm), S 8 (27.4 mm), S 9 (26.5 mm), S 10 (27.2 mm), S 11 (27.3 mm), S 12 (25.4 mm), S 13 (27.1 mm), S 14 (25.4 mm), S 15 (25.4 mm), S 16 (26.5 mm), S 18 (25.3 mm), S 20 (26.8 mm), S 21 (26.5 mm), S 22 (26.4 mm), S 23 (26.4 mm), S 24 (25.1 mm), S 25 (27.1 mm), S 26 (25.3 mm), S 27 (26.9 mm), S 28 (27.4 mm), S 29 (26.6 mm), S 30 (26.1 mm), S 31 (25.8 mm), S 32 (27.4 mm), S 33 (25.8 mm), S 35 (26.1 mm), S 38 (27.1 mm), S 42 (26.4 mm), S 44 (27.0 mm), S 45 (26.3 mm), S 46 (25.1 mm), S 47 (26.1 mm), S 48 (26.1 mm), S 49 (25.7 mm), S 50 (26.6 mm), S 51 (25.5 mm), S 53 (26.3 mm), S 54 (25.3 mm), S 57 (26.4 mm), S 58 (27.3 mm), S 59 (26.1 mm), S 60 (27.1 mm), S 61 (25.6 mm), S 63 (26.5 mm), S 64 (26.6 mm), S 65 (26.4 mm), S 66 (26.1 mm), S 67 (25.8 mm), S 68 (26.6 mm), S 69 (26.7 mm), S 70 (26.7 mm), S 71 (27.1 mm), S 72 (27.4 mm), S 73 (26.9 mm), S 74 (25.8 mm), S 76 (27.0 mm), S 77 (27.4 mm), S 79 (27.4 mm), S 83 (27.3 mm), S 90 (26.1 mm), S 91 (25.7 mm), S 92 (25.5 mm), S 93 (27.2 mm), S 94 (27.4 mm), S 95 (26.9 mm), S 96 (26.2 mm), S 97 (27.1 mm), S 98 (27.2 mm), S 99 (26.1 mm), S 100 (25.3 mm), S 102 (25.6 mm), S 103 (26.4 mm), S 104 (25.0 mm), S 105 (25.9 mm), S 106 (26.6 mm), S 107 (25.8 mm), S 108 (27.2 mm), S 109 (26.4 mm), S 110 (26.6 mm), S 111 (26.4 mm), S 112 (27.1 mm), S 113 (26.4 mm), S 114 (26.3 mm), S 115 (26.3 mm), S 116 (26.4 mm), S 119 (27.4 mm), S 120 (26.3 mm), S 121 (25.7 mm), S 122 (26.0 mm), S 123 (26.1 mm), S 133 (26.7 mm), S 141 (26.3 mm), S 143 (25.6 mm), S 145 (27.1 mm), S 146 (25.4 mm), S 149 (26.7 mm), S 150 (26.8 mm) and S 151 (27.3 mm). Five genotypes observed medium staple length (between 20.5 mm to 24.9 mm) *viz.*, S 1 (24.8 mm), S 52 (24.2 mm), S 62 (24.8 mm), S 101 (24.5 mm) and S 144 (24.1 mm) (Table 1). Similar results for significant differences for the fibre length was observed by Patil *et al.*, (2009) [21], Zeng and Meredith (2009) [25], Ashokkumar and Ravi (2010) [2], Karademir *et al.*, (2010) [10], Imran *et al.*, (2011) [9], Magadum *et al.*, (2012) [12], Erande *et al.*, (2014) [5], Farooq *et al.*, (2014) [7], Khan *et al.*, (2014) [11], Malagouda *et al.*, (2014) [14], Santoshkumar Pujer *et al.*, (2014) [24], Bajwa *et al.*, (2015) [3], Bayyapu Reddy *et al.*, (2015) [4], Arshad *et al.*, (2016) [1], Eswari *et al.*, (2017) [6], Methre *et al.*, (2017) [16], Mohan Kumar *et al.*, (2018) [17], Nawaz *et al.*, (2019) [19], Gnanasekaran *et al.*, (2020) [8], Mahesh *et al.*, (2020) [13], Rehman *et al.*, (2020) [22], Sahar *et al.*, (2021) [23], Meena *et al.*, (2022) [15], Nisar *et al.*, (2022) [20].

Fibre micronaire ($\mu\text{g}/\text{inch}$)

Significant mean differences were observed for micronaire ($\mu\text{g}/\text{inch}$) in the testing genotypes. The range of micronaire ($\mu\text{g}/\text{inch}$) was observed from 2.9 ($\mu\text{g}/\text{inch}$) (S 6) to 4.9 ($\mu\text{g}/\text{inch}$) (S 24). Out of 152 genotypes tested, 85 genotypes observed fine micronaire (between 3.0 to 3.9 $\mu\text{g}/\text{inch}$) *viz.*, S 5 (3.7 $\mu\text{g}/\text{inch}$), S 7 (3.8 $\mu\text{g}/\text{inch}$), S 8 (3.1 $\mu\text{g}/\text{inch}$), S 9 (3.3

$\mu\text{g}/\text{inch}$), S 10 (3.7 $\mu\text{g}/\text{inch}$), S 14 (3.6 $\mu\text{g}/\text{inch}$), S 17 (3.2 $\mu\text{g}/\text{inch}$), S 20 (3.6 $\mu\text{g}/\text{inch}$), S 21 (3.8 $\mu\text{g}/\text{inch}$), S 29 (3.8 $\mu\text{g}/\text{inch}$), S 30 (3.7 $\mu\text{g}/\text{inch}$), S 31 (3.7 $\mu\text{g}/\text{inch}$), S 32 (3.6 $\mu\text{g}/\text{inch}$), S 33 (3.7 $\mu\text{g}/\text{inch}$), S 34 (3.8 $\mu\text{g}/\text{inch}$), S 35 (3.5 $\mu\text{g}/\text{inch}$), S 36 (3.4 $\mu\text{g}/\text{inch}$), S 38 (3.5 $\mu\text{g}/\text{inch}$), S 39 (3.4 $\mu\text{g}/\text{inch}$), S 40 (3.8 $\mu\text{g}/\text{inch}$), S 42 (3.7 $\mu\text{g}/\text{inch}$), S 43 (3.0 $\mu\text{g}/\text{inch}$), S 45 (3.3 $\mu\text{g}/\text{inch}$), S 48 (3.3 $\mu\text{g}/\text{inch}$), S 49 (3.1 $\mu\text{g}/\text{inch}$), S 50 (3.0 $\mu\text{g}/\text{inch}$), S 51 (3.3 $\mu\text{g}/\text{inch}$), S 53 (3.5 $\mu\text{g}/\text{inch}$), S 54 (3.5 $\mu\text{g}/\text{inch}$), S 55 (3.5 $\mu\text{g}/\text{inch}$), S 56 (3.4 $\mu\text{g}/\text{inch}$), S 58 (3.5 $\mu\text{g}/\text{inch}$), S 64 (3.9 $\mu\text{g}/\text{inch}$), S 77 (3.7 $\mu\text{g}/\text{inch}$), S 80 (3.8 $\mu\text{g}/\text{inch}$), S 83 (3.6 $\mu\text{g}/\text{inch}$), S 84 (3.7 $\mu\text{g}/\text{inch}$), S 86 (3.8 $\mu\text{g}/\text{inch}$), S 87 (3.5 $\mu\text{g}/\text{inch}$), S 88 (3.9 $\mu\text{g}/\text{inch}$), S 89 (3.7 $\mu\text{g}/\text{inch}$), S 92 (3.9 $\mu\text{g}/\text{inch}$), S 94 (3.8 $\mu\text{g}/\text{inch}$), S 95 (3.8 $\mu\text{g}/\text{inch}$), S 96 (3.8 $\mu\text{g}/\text{inch}$), S 97 (3.7 $\mu\text{g}/\text{inch}$), S 98 (3.8 $\mu\text{g}/\text{inch}$), S 102 (3.8 $\mu\text{g}/\text{inch}$), S 104 (3.2 $\mu\text{g}/\text{inch}$), S 105 (3.6 $\mu\text{g}/\text{inch}$), S 106 (3.8 $\mu\text{g}/\text{inch}$), S 107 (3.8 $\mu\text{g}/\text{inch}$), S 108 (3.5 $\mu\text{g}/\text{inch}$), S 109 (3.3 $\mu\text{g}/\text{inch}$), S 110 (3.8 $\mu\text{g}/\text{inch}$), S 112 (3.7 $\mu\text{g}/\text{inch}$), S 113 (3.7 $\mu\text{g}/\text{inch}$), S 114 (3.8 $\mu\text{g}/\text{inch}$), S 115 (3.7 $\mu\text{g}/\text{inch}$), S 117 (3.4 $\mu\text{g}/\text{inch}$), S 118 (3.7 $\mu\text{g}/\text{inch}$), S 119 (3.4 $\mu\text{g}/\text{inch}$), S 120 (3.7 $\mu\text{g}/\text{inch}$), S 121 (3.4 $\mu\text{g}/\text{inch}$), S 122 (3.4 $\mu\text{g}/\text{inch}$), S 123 (3.6 $\mu\text{g}/\text{inch}$), S 125 (3.7 $\mu\text{g}/\text{inch}$), S 127 (3.8 $\mu\text{g}/\text{inch}$), S 130 (3.8 $\mu\text{g}/\text{inch}$), S 131 (3.7 $\mu\text{g}/\text{inch}$), S 133 (3.8 $\mu\text{g}/\text{inch}$), S 135 (3.3 $\mu\text{g}/\text{inch}$), S 136 (3.7 $\mu\text{g}/\text{inch}$), S 137 (3.7 $\mu\text{g}/\text{inch}$), S 138 (3.6 $\mu\text{g}/\text{inch}$), S 139 (3.6 $\mu\text{g}/\text{inch}$), S 140 (3.6 $\mu\text{g}/\text{inch}$), S 143 (3.2 $\mu\text{g}/\text{inch}$), S 144 (3.2 $\mu\text{g}/\text{inch}$), S 145 (3.5 $\mu\text{g}/\text{inch}$), S 146 (3.5 $\mu\text{g}/\text{inch}$), S 147 (3.3 $\mu\text{g}/\text{inch}$), S 148 (3.7 $\mu\text{g}/\text{inch}$), S 149 (3.2) and S 150 (3.7 $\mu\text{g}/\text{inch}$). Total 66 genotypes observed average micronaire (between 4.0 to 4.9 $\mu\text{g}/\text{inch}$) viz., S 1 (4.3 $\mu\text{g}/\text{inch}$), S 2 (4.1 $\mu\text{g}/\text{inch}$), S 3 (4.5 $\mu\text{g}/\text{inch}$), S 4 (4.0 $\mu\text{g}/\text{inch}$), S 11 (4.1 $\mu\text{g}/\text{inch}$), S 12 (4.7 $\mu\text{g}/\text{inch}$), S 13 (4.1 $\mu\text{g}/\text{inch}$), S 15 (4.2 $\mu\text{g}/\text{inch}$), S 16 (4.0 $\mu\text{g}/\text{inch}$), S 18 (4.0 $\mu\text{g}/\text{inch}$), S 19 (4.2 $\mu\text{g}/\text{inch}$), S 22 (4.7 $\mu\text{g}/\text{inch}$), S 23 (4.1 $\mu\text{g}/\text{inch}$), S 24 (4.9 $\mu\text{g}/\text{inch}$), S 25 (4.6 $\mu\text{g}/\text{inch}$), S 26 (4.8 $\mu\text{g}/\text{inch}$), S 27 (4.6 $\mu\text{g}/\text{inch}$), S 28 (4.6 $\mu\text{g}/\text{inch}$), S 37 (4.1 $\mu\text{g}/\text{inch}$), S 41 (4.4 $\mu\text{g}/\text{inch}$), S 44 (4.1 $\mu\text{g}/\text{inch}$), S 46 (4.2 $\mu\text{g}/\text{inch}$), S 47 (4.1 $\mu\text{g}/\text{inch}$), S 52 (4.1 $\mu\text{g}/\text{inch}$), S 57 (4.1 $\mu\text{g}/\text{inch}$), S 59 (4.3 $\mu\text{g}/\text{inch}$), S 60 (4.4 $\mu\text{g}/\text{inch}$), S 61 (4.2 $\mu\text{g}/\text{inch}$), S 62 (4.2 $\mu\text{g}/\text{inch}$), S 63 (4.1 $\mu\text{g}/\text{inch}$), S 65 (4.0 $\mu\text{g}/\text{inch}$), S 66 (4.4 $\mu\text{g}/\text{inch}$), S 67 (4.4 $\mu\text{g}/\text{inch}$), S 68 (4.4 $\mu\text{g}/\text{inch}$), S 69 (4.0 $\mu\text{g}/\text{inch}$), S 70 (4.7 $\mu\text{g}/\text{inch}$), S 71 (4.1 $\mu\text{g}/\text{inch}$), S 72 (4.0 $\mu\text{g}/\text{inch}$), S 73 (4.4 $\mu\text{g}/\text{inch}$), S 74 (4.2 $\mu\text{g}/\text{inch}$), S 75 (4.0 $\mu\text{g}/\text{inch}$), S 76 (4.1 $\mu\text{g}/\text{inch}$), S 78 (4.2 $\mu\text{g}/\text{inch}$), S 79 (4.1 $\mu\text{g}/\text{inch}$), S 81 (4.0 $\mu\text{g}/\text{inch}$), S 82 (4.0 $\mu\text{g}/\text{inch}$), S 85 (4.1 $\mu\text{g}/\text{inch}$), S 90 (4.3 $\mu\text{g}/\text{inch}$), S 91 (4.6 $\mu\text{g}/\text{inch}$), S 93 (4.1 $\mu\text{g}/\text{inch}$), S 99 (4.7 $\mu\text{g}/\text{inch}$), S 100 (4.7 $\mu\text{g}/\text{inch}$), S 101 (4.1 $\mu\text{g}/\text{inch}$), S 103 (4.0 $\mu\text{g}/\text{inch}$), S 111 (4.1 $\mu\text{g}/\text{inch}$), S 116 (4.1 $\mu\text{g}/\text{inch}$), S 124 (4.1 $\mu\text{g}/\text{inch}$), S 126 (4.2 $\mu\text{g}/\text{inch}$), S 128 (4.1 $\mu\text{g}/\text{inch}$), S 129 (4.1 $\mu\text{g}/\text{inch}$), S 132 (4.0 $\mu\text{g}/\text{inch}$), S 134 (4.2 $\mu\text{g}/\text{inch}$), S 141 (4.1 $\mu\text{g}/\text{inch}$), S 142 (4.0 $\mu\text{g}/\text{inch}$), S 151 (4.1 $\mu\text{g}/\text{inch}$) and S 152 (4.0 $\mu\text{g}/\text{inch}$). Very fine micronaire value (below 3.0 $\mu\text{g}/\text{inch}$) was observed by o S 6 (2.9 $\mu\text{g}/\text{inch}$) (Table 1). Similar micronaire results were recorded by Patil *et al.*, (2009) [21], Zeng and Meredith (2009) [25], Ashokkumar and Ravi (2010) [2], Karademir *et al.*, (2010) [10], Imran *et al.*, (2011) [9], Magadum *et al.*, (2012) [12], Erande *et al.*, (2014) [5], Farooq *et al.*, (2014) [7], Khan *et al.*, (2014) [11], Malagouda *et al.*, (2014) [14], Santoshkumar Pujer *et al.*, (2014) [24], Bajwa *et al.*, (2015) [3], Bayyapu Reddy *et al.*, (2015) [4], Arshad *et al.*, (2016) [1], Eswari *et al.*, (2017) [6], Methre *et al.*, (2017) [16], Mohan Kumar *et al.*, (2018) [17], Nawaz *et al.*, (2019) [19], Gnanasekaran *et al.*, (2020) [8], Mahesh *et al.*, (2020) [13], Rehman *et al.*, (2020) [22], Sahar *et al.*, (2021) [23], Meena *et*

al., (2022) [15], Nisar *et al.*, (2022) [20].

Bundle strength (g/tex)

Significant mean differences were observed for bundle strength (g/tex) in the testing genotypes. The range of bundle strength (g/tex) was observed from 23.1 (g/tex) to 32.5 (g/tex).

One genotype S 87 (29.2 g/tex) showed good bundle strength (between 29.1 g/tex to 32.5 g/tex) among all the test genotypes. Out of 152 genotypes tested, 120 genotypes observed average bundle strength (g/tex) (between 25.1 to 29.0 g/tex) viz., S 2 (25.7 g/tex), S 3 (26.3 g/tex), S 4 (27.3 g/tex), S 5 (25.8 g/tex), S 6 (26.9 g/tex), S 7 (25.2 g/tex), S 8 (26.4 g/tex), S 9 (25.6 g/tex), S 10 (26.7 g/tex), S 11 (26.2 g/tex), S 13 (26.8 g/tex), S 14 (25.5 g/tex), S 16 (25.9 g/tex), S 17 (27.4 g/tex), S 19 (27.8 g/tex), S 20 (26.2 g/tex), S 21 (25.8 g/tex), S 22 (26.0 g/tex), S 23 (25.6 g/tex), S 25 (26.8 g/tex), S 27 (26.2 g/tex), S 28 (26.8 g/tex), S 29 (26.0 g/tex), S 30 (25.9 g/tex), S 31 (25.2 g/tex), S 32 (26.8 g/tex), S 34 (26.9 g/tex), S 35 (25.7 g/tex), S 36 (28.7 g/tex), S 37 (27.6 g/tex), S 38 (26.8 g/tex), S 39 (27.8 g/tex), S 40 (27.1 g/tex), S 41 (27.3 g/tex), S 42 (25.8 g/tex), S 43 (28.7 g/tex), S 44 (26.5 g/tex), S 45 (25.6 g/tex), S 47 (25.8 g/tex), S 48 (25.5 g/tex), S 50 (26.0 g/tex), S 53 (25.8 g/tex), S 55 (27.7 g/tex), S 56 (27.2 g/tex), S 57 (26.8 g/tex), S 58 (26.8 g/tex), S 59 (25.7 g/tex), S 60 (26.9 g/tex), S 63 (25.8 g/tex), S 64 (26.1 g/tex), S 65 (25.9 g/tex), S 66 (25.8 g/tex), S 67 (25.1 g/tex), S 68 (26.1 g/tex), S 69 (26.0 g/tex), S 70 (25.9 g/tex), S 71 (26.4 g/tex), S 72 (26.8 g/tex), S 73 (26.1 g/tex), S 75 (27.4 g/tex), S 76 (26.7 g/tex), S 77 (26.8 g/tex), S 78 (26.9 g/tex), S 79 (26.5 g/tex), S 80 (28.8 g/tex), S 81 (27.1 g/tex), S 82 (26.7 g/tex), S 83 (26.5 g/tex), S 84 (27.2 g/tex), S 85 (27.6 g/tex), S 86 (27.5 g/tex), S 88 (27.3 g/tex), S 89 (27.4 g/tex), S 90 (25.8 g/tex), S 93 (26.4 g/tex), S 94 (26.7 g/tex), S 95 (26.1 g/tex), S 96 (25.8 g/tex), S 97 (26.7 g/tex), S 98 (26.3 g/tex), S 99 (25.8 g/tex), S 103 (25.4 g/tex), S 107 (25.1 g/tex), S 108 (26.7 g/tex), S 109 (25.5 g/tex), S 110 (25.3 g/tex), S 112 (26.4 g/tex), S 113 (25.1 g/tex), S 114 (25.2 g/tex), S 115 (25.1 g/tex), S 116 (25.3 g/tex), S 117 (27.3 g/tex), S 118 (27.5 g/tex), S 119 (26.3 g/tex), S 120 (25.4 g/tex), S 124 (27.1 g/tex), S 125 (27.2 g/tex), S 126 (26.9 g/tex), S 127 (28.1 g/tex), S 128 (27.0 g/tex), S 129 (26.7 g/tex), S 130 (28.1 g/tex), S 131 (27.8 g/tex), S 132 (27.1 g/tex), S 133 (25.3 g/tex), S 134 (26.1 g/tex), S 135 (27.8 g/tex), S 136 (28.4 g/tex), S 137 (27.1 g/tex), S 138 (27.9 g/tex), S 139 (25.8 g/tex), S 140 (27.1 g/tex), S 141 (25.3 g/tex), S 142 (26.5 g/tex), S 145 (25.8 g/tex), S 147 (26.3 g/tex), S 148 (26.4 g/tex), S 150 (25.7 g/tex), S 151 (26.9 g/tex) and S 152 (28.1 g/tex). Total 31 genotypes observed weak bundle strength (g/tex) (between 20.1 to 25.0 g/tex) viz., S 1 (24.1 g/tex), S 12 (24.6 g/tex), S 15 (24.8 g/tex), S 18 (24.7 g/tex), S 24 (24.8 g/tex), S 26 (24.7 g/tex), S 33 (24.7 g/tex), S 46 (24.9 g/tex), S 49 (24.9 g/tex), S 51 (24.5 g/tex), S 52 (23.7 g/tex), S 54 (24.9 g/tex), S 61 (24.6 g/tex), S 62 (24.4 g/tex), S 74 (24.9 g/tex), S 91 (24.9 g/tex), S 92 (25.0 g/tex), S 100 (24.7 g/tex), S 101 (23.8 g/tex), S 102 (24.8 g/tex), S 104 (24.6 g/tex), S 105 (24.9 g/tex), S 106 (24.6 g/tex), S 111 (24.9 g/tex), S 121 (24.3 g/tex), S 122 (24.8 g/tex), S 123 (24.9 g/tex), S 143 (24.2 g/tex), S 144 (23.1 g/tex), S 146 (23.8 g/tex), and S 149 (25.0 g/tex) (Table 4.5). Significant differences for the bundle strength was also reported by Patil *et al.*, (2009) [21], Zeng and Meredith (2009) [25], Ashokkumar and Ravi (2010) [2], Imran *et al.*, (2011) [9],

Karademir *et al.*, (2010) ^[10], Magadam *et al.*, (2012) ^[12], Erande *et al.*, (2014) ^[5], Farooq *et al.*, (2014) ^[7], Khan *et al.*, (2014) ^[11], Malagouda *et al.*, (2014) ^[14], Santoshkumar Pujer *et al.*, (2014) ^[24], Bayyapu Reddy *et al.*, (2015) ^[4], Eswari *et al.*, (2017) ^[6], Methre *et al.*, (2017) ^[16], Mohan Kumar *et al.*, (2018) ^[17], Nawaz *et al.*, (2019) ^[19], Gnanasekaran *et al.*, (2020) ^[8], Mahesh *et al.*, (2020) ^[13], Rehman *et al.*, (2020) ^[22], Sahar *et al.*, (2021) ^[23], Meena *et al.*, (2022) ^[15], Nisar *et al.*, (2022) ^[20] in the cotton genotypes.

Uniformity index (%)

Significant mean differences were observed for uniformity index (%) in the testing genotypes. The range of uniformity index (%) was observed from 79 (%) (S 143) to 86 (%) (S 36 and S 80). Two genotype S 36 and S 80 both showed excellent above 85% uniformity index among all the test genotypes. Out of 152 genotypes tested, 117 genotypes observed average uniformity index (between 79% to 83%) viz., S 1 (82%), S 2 (83%), S 3 (82%), S 4 (83%), S 5 (82%), S 6 (83%), S 7 (83%), S 8 (83%), S 9 (83%), S 10 (83%), S 11 (83%), S 12 (82%), S 14 (83%), S 15 (82%), S 16 (83%), S 17 (82%), S 18 (83%), S 19 (83%), S 41 (82%), S 42 (83%), S 45 (83%), S 46 (81%), S 43 (83%), S 48 (83%), S 49 (83%), S 50 (82%), S 51 (80%), S 52 (81%), S 53 (81%), S 54 (82%), S 55 (82%), S 56 (83%), S 57 (82%), S 58 (82%), S 59 (83%), S 60 (81%), S 61 (82%), S 62 (81%), S 63 (83%), S 64 (83%), S 65 (83%), S 66 (83%), S 67 (81%), S 68 (82%), S 69 (83%), S 70 (83%), S 71 (83%), S 72 (83%), S 73 (83%), S 77 (83%), S 78 (83%), S 79 (83%), S 84 (83%), S 86 (81%), S 90 (82%), S 91 (82%), S 92 (81%), S 93 (82%), S 94 (82%), S 95 (82%), S 96 (82%), S 97 (82%), S 98 (82%), S 99 (82%), S 100 (82%), S 101 (81%), S 102 (81%), S 103 (81%), S 104 (81%), S 105 (81%), S 106 (81%), S 107 (81%), S 108 (81%), S 109 (82%), S 110 (81%), S 111 (81%), S 112 (81%), S 113 (82%), S 114 (81%), S 115 (80%), S 116 (82%), S 117 (80%), S 118 (81%), S 119 (80%), S 120 (81%), S 121 (80%), S 122 (81%), S 123 (81%), S 124 (80%), S 125 (80%), S 126 (80%), S 127 (81%), S 128 (82%), S 129 (82%), S 130 (82%), S 131 (81%), S 132 (81%), S 133 (81%), S 134 (80%), S 135 (81%), S 136 (82%), S 137 (80%), S 138 (80%), S 139 (81%), S 140 (82%), S 141 (82%), S 142 (80%), S 143 (79%), S 144 (80%), S 145 (80%), S 146 (81%), S 147 (80%), S 148 (81%), S 149 (80%), S 150 (80%), S 151 (80%), and S 152 (80%). Total 33 genotypes observed good uniformity index (%) (between 83.1 to 85%) viz., S 13 (84%), S 20 (84%), S 21 (84%), S 22 (84%), S 23 (85%), S 24 (85%), S 25 (84%), S 26 (84%), S 27 (85%), S 28 (25%), S 29 (84%), S 30 (84%), S 31 (84%), S 32 (84%), S 33 (85%), S 34 (85%), S 35 (85%), S 37 (84%), S 38 (84%), S 39 (84%), S 40 (84%), S 43 (84%), S 44 (84%), S 74 (84%), S 75 (84%), S 76 (84%), S 81 (84%), S 82 (84%), S 83 (84%), S 85 (84%), S 87 (85%), S 88 (84%) and S 89 (85%) (Table 1). Uniformity index quality parameter in cotton genotypes was also done by Patil *et al.*, (2009) ^[21], Zeng and Meredith (2009) ^[25], Karademir *et al.*, (2010) ^[10], Imran *et al.*, (2011) ^[9], Erande *et al.*, (2014) ^[5], Khan *et al.*, (2014) ^[11], Malagouda *et al.*, (2014) ^[14], Santoshkumar Pujer *et al.*, (2014) ^[24], Bayyapu Reddy *et al.*, (2015) ^[4], Eswari *et al.*, (2017) ^[6], Methre *et al.*, (2017) ^[16], Nawaz *et al.*, (2019) ^[19], Gnanasekaran *et al.*, (2020) ^[8], Mahesh *et al.*, (2020) ^[13], Sahar *et al.*, (2021) ^[23].

Fibre elongation (%)

Significant mean differences were observed for fibre elongation (%) in the testing genotypes. The range of fibre elongation (%) was observed from 4.3 (%) (S 129) to 6.3 (%) (S 14). Eight genotypes viz., S 14 (6.3%), S 27 (6.2%), S 30 (6.1%), S 57 (6.1%), S 58 (6.0%), S 108 (6.0%), S 110 (6.0%) and S 111 (6.0%) showed excellent fibre elongation (range 6.0% and above) among all the test genotypes. Out of 152 genotypes tested, 98 genotypes observed good elongation (between 5.0% to 5.9%) of fibre viz., S 2 (5.0%), S 4 (5.5%), S 5 (5.5%), S 6 (5.7%), S 7 (5.2%), S 8 (5.2%), S 9 (5.5%), S 10 (5.3%), S 11 (5.8%), S 13 (5.7%), S 15 (5.2%), S 16 (5.1%), S 17 (5.2%), S 20 (5.4%), S 21 (5.9%), S 22 (2.1%), S 25 (5.5%), S 26 (5.1%), S 28 (5.8%), S 29 (5.3%), S 31 (5.7%), S 32 (5.8%), S 33 (5.9%), S 34 (5.0%), S 35 (5.4%), S 36 (5.3%), S 37 (5.1%), S 38 (5.1%), S 39 (5.3%), S 40 (5.3%), S 43 (5.6%), S 45 (5.1%), S 46 (5.7%), S 47 (5.7%), S 48 (5.6%), S 49 (5.9%), S 50 (5.5%), S 51 (5.4%), S 52 (5.2%), S 53 (5.5%), S 54 (5.5%), S 55 (5.5%), S 56 (5.9%), S 59 (5.0%), S 60 (5.8%), S 61 (5.3%), S 68 (5.0%), S 70 (5.4%), S 71 (5.2%), S 72 (5.1%), S 73 (5.4%), S 74 (5.6%), S 75 (5.4%), S 76 (5.2%), S 77 (5.4%), S 78 (5.2%), S 79 (5.3%), S 80 (5.4%), S 82 (5.4%), S 83 (5.2%), S 84 (5.3%), S 85 (5.3%), S 86 (5.0%), S 88 (5.3%), S 89 (5.2%), S 90 (5.5%), S 92 (5.3%), S 93 (5.1%), S 94 (5.2%), S 95 (5.7%), S 99 (5.5%), S 100 (5.4%), S 101 (5.4%), S 102 (5.5%), S 103 (5.2%), S 104 (5.3%), S 105 (5.6%), S 106 (5.4%), S 107 (5.7%), S 109 (5.9%), S 115 (5.3%), S 122 (5.3%), S 126 (5.3%), S 130 (5.8%), S 131 (5.0%), S 133 (5.0%), S 134 (5.2%), S 135 (5.4%), S 137 (5.0%), S 140 (5.3%), S 141 (5.5%), S 142 (5.0%), S 143 (5.4%), S 148 (5.1%), S 149 (5.2%), S 150 (5.5%), S 151 (5.5%) and S 152 (5.1%). Total 46 genotypes observed average fibre elongation (%) (between 4.5 to 4.9%) viz., S 1 (4.9%), S 3 (4.8%), S 12 (4.7%), S 18 (4.9%), S 19 (4.9%), S 23 (4.9%), S 24 (4.8%), S 41 (4.5%), S 42 (4.9%), S 44 (4.9%), S 62 (4.4%), S 63 (4.6%), S 64 (4.6%), S 65 (4.4%), S 66 (4.5%), S 67 (4.5%), S 69 (4.4%), S 81 (4.9%), S 87 (4.9%), S 91 (4.6%), S 96 (4.7%), S 97 (4.8%), S 98 (4.9%), S 112 (4.9%), S 113 (4.6%), S 114 (4.6%), S 116 (4.8%), S 117 (4.7%), S 118 (4.9%), S 119 (4.7%), S 120 (4.9%), S 121 (4.9%), S 123 (4.8%), S 124 (4.9%), S 125 (4.7%), S 127 (4.5%), S 128 (4.4%), S 129 (4.3%), S 132 (4.9%), S 136 (4.8%), S 138 (4.7%), S 139 (4.8%), S 144 (4.5%), S 145 (4.6%), S 146 (4.7%) and S 147 (4.7%) (Table 1). The important fibre elongation studies were also done previously by Patil *et al.*, (2009) ^[21], Zeng and Meredith (2009), Karademir *et al.*, (2010) ^[10], Imran *et al.*, (2011) ^[9], Erande *et al.*, (2014) ^[5], Khan *et al.*, (2014) ^[11], Malagouda *et al.*, (2014), Bayyapu Reddy *et al.*, (2015) ^[4], Methre *et al.*, (2017) ^[16], Nawaz *et al.*, (2019) ^[19], Mahesh *et al.*, (2020) ^[13].

The main fibre qualities for the textile industries are the staple length, bundle strength and micronaire. In this experiment regarding to the long staple length genotypes S 87 (30 mm), S 80 (29.6 mm), S 138 (29.2 mm), S 152 (29.2 mm) and S 127 (29.1 mm), for micronaire value S 6 (2.9 µg/inch), S 43 (3.0 µg/inch), S 8 and S 49 (both 3.1 µg/inch) and bundle strength of S 87 (29.2 g/tex) and S 80 (28.8 g/tex) observed promising for utilizing as parental source of BG II converted straight lines of *G. hirsutum* in further BG II hybrid development programme.

Table 1: Fibre parameter of putative cotton plants in F6 generation with presence of Cry1Ac and Cry2Ab insect resistant transgene gene in elite single plant selections during 2021-22

Sr. No	Genotype	UHML (mm)	MIC ($\mu\text{g}/\text{inch}$)	BS (g/tex)	UI (%)	Elongation (%)
1	S-1	24.8	4.3	24.1	82	4.9
2	S-2	26.7	4.1	25.7	83	5.0
3	S-3	27.2	4.5	26.3	82	4.8
4	S-4	28.1	4.0	27.3	83	5.5
5	S-5	26.7	3.7	25.8	82	5.5
6	S-6	27.2	2.9	26.9	83	5.7
7	S-7	26.0	3.8	25.2	83	5.2
8	S-8	27.4	3.1	26.4	83	5.2
9	S-9	26.5	3.3	25.6	83	5.5
10	S-10	27.2	3.7	26.7	83	5.3
11	S-11	27.3	4.1	26.2	83	5.8
12	S-12	25.4	4.7	24.6	82	4.7
13	S-13	27.1	4.1	26.8	84	5.7
14	S-14	25.4	3.6	25.5	83	6.3
15	S-15	25.4	4.2	24.8	82	5.2
16	S-16	26.5	4.0	25.9	83	5.1
17	S-17	28.1	3.2	27.4	82	5.2
18	S-18	25.3	4.0	24.7	83	4.9
19	S-19	28.5	4.2	27.8	83	4.9
20	S-20	26.8	3.6	26.2	84	5.4
21	S-21	26.5	3.8	25.8	84	5.9
22	S-22	26.4	4.7	26.0	84	5.1
23	S-23	26.4	4.1	25.6	85	4.9
24	S-24	25.1	4.9	24.8	85	4.8
25	S-25	27.1	4.6	26.8	84	5.5
26	S-26	25.3	4.8	24.7	85	5.1
27	S-27	26.9	4.6	26.2	85	6.2
28	S-28	27.4	4.6	26.8	84	5.8
29	S-29	26.6	3.8	26.0	84	5.3
30	S-30	26.1	3.7	25.9	84	6.1
31	S-31	25.8	3.7	25.2	84	5.7
32	S-32	27.4	3.6	26.8	84	5.8
33	S-33	25.8	3.7	24.7	85	5.9
34	S-34	27.5	3.8	26.9	85	5.0
35	S-35	26.1	3.5	25.7	85	5.4
36	S-36	29.0	3.4	28.7	86	5.3
37	S-37	28.0	4.1	27.6	84	5.1
38	S-38	27.1	3.5	26.8	84	5.1
39	S-39	28.2	3.4	27.8	84	5.3
40	S-40	27.7	3.8	27.1	84	5.3
Sr. No	Genotype	UHML (mm)	MIC ($\mu\text{g}/\text{inch}$)	Bundle strength (g/tex)	UI (%)	Elongation (%)
41	S-41	27.7	4.4	27.3	82	4.5
42	S-42	26.4	3.7	25.8	83	4.9
43	S-43	29.0	3.0	28.7	84	5.6
44	S-44	27.0	4.1	26.5	84	4.9
45	S-45	26.3	3.3	25.6	83	5.1
46	S-46	25.1	4.2	24.9	81	5.7
47	S-47	26.1	4.1	25.8	83	5.7
48	S-48	26.1	3.3	25.5	83	5.6
49	S-49	25.7	3.1	24.9	83	5.9
50	S-50	26.6	3.0	26.0	82	5.5
51	S-51	25.5	3.3	24.5	80	5.4
52	S-52	24.2	4.1	23.7	81	5.6
53	S-53	26.3	3.5	25.8	81	5.5
54	S-54	25.3	3.5	24.9	82	5.5
55	S-55	28.1	3.5	27.7	82	5.5
56	S-56	27.9	3.4	27.2	83	5.9
57	S-57	26.4	4.1	26.8	82	6.1
58	S-58	27.3	3.5	26.8	82	6.0
59	S-59	26.1	4.3	25.7	83	5.0
60	S-60	27.1	4.4	26.9	81	5.8
61	S-61	25.6	4.2	24.6	82	5.3
62	S-62	24.8	4.2	24.4	81	4.4
63	S-63	26.5	4.1	25.8	83	4.6

64	S-64	26.6	3.9	26.1	83	4.6
65	S-65	26.4	4.0	25.9	83	4.4
66	S-66	26.1	4.4	25.8	83	4.5
67	S-67	25.8	4.4	25.1	81	4.5
68	S-68	26.6	4.4	26.1	82	5.0
69	S-69	26.7	4.0	26.0	83	4.4
70	S-70	26.7	4.7	25.9	83	5.4
71	S-71	27.1	4.1	26.4	83	5.2
72	S-72	27.4	4.0	26.8	83	5.1
73	S-73	26.9	4.4	26.1	83	5.4
74	S-74	25.8	4.2	24.9	84	5.6
75	S-75	28.0	4.0	27.4	84	5.4
76	S-76	27.0	4.1	26.7	84	5.2
77	S-77	27.4	3.7	26.8	83	5.4
78	S-78	27.6	4.2	26.9	83	5.2
79	S-79	27.4	4.1	26.5	83	5.3
80	S-80	29.6	3.8	28.8	86	5.4
Sr. No	Genotype	UHML (mm)	MIC (μg/inch)	Bundle strength (g/tex)	UI (%)	Elongation (%)
81	S-81	28.5	4.0	27.1	84	4.9
82	S-82	27.8	4.0	26.7	84	5.4
83	S-83	27.3	3.6	26.5	84	5.2
84	S-84	28.7	3.7	27.2	83	5.3
85	S-85	28.6	4.1	27.6	84	5.3
86	S-86	28.0	3.8	27.5	81	5.0
87	S-87	30.0	3.5	29.2	85	4.9
88	S-88	28.2	3.9	27.3	84	5.3
89	S-89	28.0	3.7	27.4	85	5.2
90	S-90	26.1	4.3	25.8	82	5.5
91	S-91	25.7	4.6	24.9	82	4.6
92	S-92	25.5	3.9	25.0	81	5.3
93	S-93	27.2	4.1	26.4	82	5.1
94	S-94	27.4	3.8	26.7	82	5.2
95	S-95	26.9	3.8	26.1	82	5.7
96	S-96	26.2	3.8	25.8	82	4.7
97	S-97	27.1	3.7	26.7	82	4.8
98	S-98	27.2	3.8	26.3	82	4.9
99	S-99	26.1	4.7	25.8	82	5.5
100	S-100	25.3	4.7	24.7	82	5.4
101	S-101	24.5	4.1	23.8	81	5.4
102	S-102	25.6	3.8	24.8	81	5.5
103	S-103	26.4	4.0	25.4	81	5.2
104	S-104	25.0	3.2	24.6	81	5.3
105	S-105	25.9	3.6	24.9	81	5.6
106	S-106	25.6	3.8	24.6	81	5.4
107	S-107	25.8	3.8	25.1	81	5.7
108	S-108	27.2	3.5	26.7	81	6.0
109	S-109	26.4	3.3	26.5	82	5.9
110	S-110	26.6	3.8	25.3	81	6.0
111	S-111	26.4	4.1	24.9	81	6.0
112	S-112	27.1	3.7	26.4	81	4.9
113	S-113	26.4	3.7	25.1	82	4.6
114	S-114	26.3	3.8	25.2	81	4.6
115	S-115	26.3	3.7	25.1	80	5.3
116	S-116	26.4	4.1	25.3	82	4.8
117	S-117	28.3	3.4	27.3	80	4.7
118	S-118	28.5	3.7	27.5	81	4.9
119	S-119	27.4	3.4	26.3	80	4.7
120	S-120	26.3	3.7	25.4	81	4.9
Sr. No	Genotype	UHML (mm)	MIC (μg/inch)	Bundle strength (g/tex)	UI (%)	Elongation (%)
121	S-121	25.7	3.4	24.3	80	4.9
122	S-122	26.0	3.4	24.8	81	5.3
123	S-123	26.1	3.6	25.9	81	4.8
124	S-124	28.2	4.1	27.1	80	4.9
125	S-125	28.3	3.7	27.2	80	4.7
126	S-126	28.0	4.2	26.9	80	5.3
127	S-127	29.1	3.8	28.1	81	4.5
128	S-128	28.4	4.1	27.0	82	4.4

129	S-129	27.6	4.1	26.7	82	4.3
130	S-130	28.9	3.8	28.1	82	5.8
131	S-131	28.9	3.7	27.8	81	5.0
132	S-132	28.3	4.0	27.1	81	4.9
133	S-133	26.7	3.8	25.3	81	5.0
134	S-134	27.8	4.2	26.1	80	5.2
135	S-135	28.7	3.3	27.8	81	5.4
136	S-136	29.0	3.7	28.4	82	4.8
137	S-137	28.7	3.7	27.1	80	5.0
138	S-138	29.2	3.6	27.9	80	4.7
139	S-139	27.7	3.6	25.8	81	4.8
140	S-140	28.4	3.6	27.1	82	5.3
141	S-141	26.3	4.1	25.3	82	5.5
142	S-142	27.9	4.0	26.5	80	5.0
143	S-143	25.6	3.2	24.2	79	5.4
144	S-144	24.1	3.2	23.1	80	4.5
145	S-145	27.1	3.5	25.8	80	4.6
146	S-146	25.4	3.5	23.8	81	4.7
147	S-147	27.7	3.3	26.3	80	4.7
148	S-148	27.9	3.7	26.4	81	5.1
149	S-149	26.7	3.2	25.0	80	5.2
150	S-150	26.8	3.7	25.7	80	5.5
151	S-151	27.3	4.1	26.9	80	5.5
152	S-152	29.2	4.0	28.1	80	5.1
Checks						
153	NH-615	28.0	4.2	27.2	81	5.2
154	NH-545	24.4	4.5	22.3	81	5.7
155	Suraj	26.3	3.7	25.4	81	5.4
156	PKV081	27.0	3.5	26.3	81	5.5
157	NHH250	26.1	4.5	25.7	82	5.1
158	NHH44	25.0	4.0	24.1	81	5.0
159	NHH44 BG II	26.2	4.4	25.2	81	5.2
160	Jadoo BG II	28.2	4.1	27.8	82	4.7

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