

## Inheritance of fuzz and lint fiber initiation of cotton (*Gossypium hirsutum* L.)

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**Abstract:** Fibers of cultivated cotton are classified into two types, lint and fuzz. Fuzzless seeds are cotton seeds lacking fuzz on almost the whole surface of the seed except for small amounts of fuzz at the micropylar or chalazal regions. Fuzzless seeds provide a number of advantages such as avoiding delintation processes and increasing the quality of feed rations. Therefore, it is important to develop varieties having seeds without fuzz but with high fiber ratios. This study, in which three different  $F_2$  populations have been developed by using three distinct genotypes as parents, was conducted to investigate the quantitative inheritance of fuzz and fiber formation and to generate a genetic mapping population.  $F_2$  populations showed 3:1 segregation for fuzz initiation and 15:1 for fiber initiation, meaning that fuzz initiation was controlled by one dominant gene while fiber initiation was controlled by two dominant genes. The ranges were between 2% and 40% for gin turnout, between 0 and 0.04 g for lint index, and between 5.5 and 15.9 g for seed index in the Stoneville 453 × PI 528429 population, while the same characters ranged from 2% to 36%, from 0 to 0.046 g, and from 9.45 to 15.42 g, respectively, for the PI 528429 × Stoneville 453 population. The last  $F_2$  population (Fiberless × Stoneville 453) showed segregation values that varied between 0% and 42% for gin turnout, between 0 and 0.045 g for lint index, and between 5.56 and 12.98 g for seed index. Additionally, there was a significant ( $P < 0.01$ ) and positive correlation between gin turn out and lint index, between seed index and lint index, and between fuzz and gin turn out and lint index. These populations will provide a valuable genetic resource for fiber and fuzz initiation as well as quantitative trait locus mapping experiments.

**Key words:** *Gossypium hirsutum*, fuzzless, fuzzy, naked seed, initiation, gin turnout

### 1. Introduction

Cotton, as an annual crop, is mainly grown for its fiber and oil in the seed. Fibers of cultivated cotton are classified into two types: lint fibers, which are ginned off, and fuzz fibers that remain on the seed after ginning. The lint fibers initiate elongation on the day of anthesis or shortly thereafter, but the fuzz fibers initiate at 4–10 days postanthesis. After ginning the cotton seed, the leftover lint and fuzz fibers on the seed are called linters. Fibers are the most important raw material of the textile industry to be easily distinguished from seed; however, separation of linters from seeds is time-consuming and costly. In addition, the short fibers in the seed cake remaining after oil extraction have harmful effects in animal feed. Therefore, developing commercially valuable fuzzless cotton varieties with high fiber quality and understanding the inheritance of fuzz and lint fibers is important. Mutants were obtained and made available by several studies (Griffie and Ligon, 1929; Ware, 1940; Ware et al., 1947; Kohel, 1973; Turley and Kloth, 2002, 2008; Turley et al., 2007). Preferred features of these mutants may be used as a source of genes in developing new varieties and for understanding the molecular basis of fiber-forming traits.

It has been known that there are certain mutant genotypes whose seeds produce fibers that have no short fibers (linters) remaining after ginning as well as some other types of mutants that do not form fuzz or fibers (naked seed), which show a dominant inheritance character of fuzzlessness (Musaev and Abzalov, 1972; Nadarajan and Rangasamy, 1988; Zang and Pan, 1991; Du et al., 2001). In cotton, a number of genes related to fiber formation on species-specific chromosomes have been determined (Endrizzi et al., 1985; Percy and Kohel 1999; Karaca et al., 2002; Kohel et al., 2002). Of these genes,  $Li_1$  (Karaca et al., 2002) and  $Li_2$  have been reported to be monogenic and dominant, and the fact that they cause a reduction in fiber lengths (less than 10 mm) on immature seeds has been emphasized (Griffie and Ligon, 1929; Kohel et al., 1992). Thadani (1923, 1925) declared that a single gene,  $N-n$ , is effective on fuzzlessness. Some quantitative investigations were conducted on fiber and fuzz formation by hybridization of fuzzless/fiberless and fuzzy/fibery genotypes (Du et al., 2001; Turley et al., 2007; Turley and Kloth, 2002, 2008) and it was determined that the quality of having naked (fuzzless) seeds is controlled

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by dominant and recessive genes. A few genes are known for the existence and the quantity of fuzz (Endrizzi et al., 1984; Kohel, 1973). Among these genes, the naked seed locus,  $N_1N_1$  and  $n_1n_1$ , is characterized the best. Fuzzlessness of the seed is regulated by the dominant  $N_1$  locus (Turley and Kloth, 2002). In the case of having the  $N_1$  dominant allele, completely naked seeds, which are sometimes called fuzzless seeds, are formed. The recessive gene of  $n_2n_2$  is present in most commercial cotton varieties. Generally, there is more than 30% real fiber in these plants. Seeds are not completely naked, but only a small amount of fuzz is formed on the seed. Turley and Kloth (2002) determined a third fuzzless seed locus ( $n_3$ ) and found that  $N_1n_1$ ,  $N_2n_2$ , and  $N_3n_3$  genes affect the fiber percentage on cotton and that the fiber formed in genotypes with  $n_1n_1N_2N_3N_3$  genes is approximately 40.5%. These mutant cotton genotypes with the naked seed locus might have a key role in determining the quantitative trait locus (QTL) related to fuzz and fiber formation.

In this study, we aimed to investigate the quantitative inheritance of some commercially valuable traits, lint and fuzz fibers, gin turnout, lint index, and seed index, in three  $F_2$  cotton populations and to select genotypes having more fibers but no or less fuzz to develop new varieties.

## 2. Materials and methods

### 2.1. Plant material

Plant materials used in this study include Stoneville 453, PI 528429, and Fiberless that belong to *G. hirsutum* L. (Figure 1). These genotypes are used to develop hybrid  $F_2$  populations. Stoneville 453, having lint and fuzz fibers on the seed, is a high-yielding variety and has quality fibers. PI 528429 has few lint fibers and no fuzz, and the Fiberless genotype has no fibers and no fuzz on the seed (naked seed).

### 2.2. Construction of $F_2$ populations

Four different crossings were performed: Stoneville 453 × PI 528429, PI 528429 × Stoneville 453, Stoneville 453 ×

Fiberless, and Fiberless × Stoneville 453. The Fiberless × Stoneville 453 hybrid was excluded from the study due to the fact that an efficient number of  $F_2$  plants could not be obtained.

### 2.3. Phenotyping of fuzz and lint fiber initiation

Fuzz and lint fiber formations in the populations were classified as fuzzy/fuzzless and fibery/fiberless. The genotypes that did not form any fibers were defined as fiberless (no fuzz and lint fiber, naked) (Figure 2A), while those with no short fiber leftover after ginning and those with a very small amount of fuzz in the micropyle or chalazal region of the seed were defined as fuzzless (Figures 2A and B). The genotypes with intensive fuzz and lint fibers on the seed surface after ginning are called fuzzy (Figure 2C) (Du et al., 2001).

### 2.4. Phenotyping of fiber and seed properties

Fiber ratio (gin turnout), lint index, and seed index of populations were determined separately according to the formulas below.

$$\text{Gin Turnout (\%)} = \frac{\text{Fiber Wight (g)}}{\text{Fiber Wight (g)} + \text{Seed Wight (g)}} \times 100$$

$$\text{Lint Index (g)} = \frac{100 \text{ Seed Wight (g)} \times \text{Gin Turnout (\%)}}{100 - \text{Gin Turnout (\%)}} \times 100$$

**Seed index (g)** = Seeds of genotypes were delinted and weighed in groups of 100.

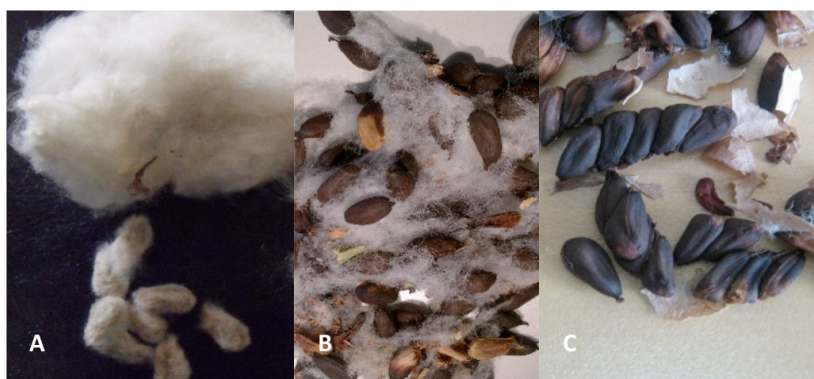
### 2.5. Statistical analyses

The frequencies in phenotypic data were analyzed using Microsoft Excel software while the correlations between the investigated properties were determined by JMP statistical software.

## 3. Results and discussion

### 3.1. Inheritance of fuzz and lint fiber initiation

Gin turnout values and estimated genotypes for fuzz and



**Figure 1.** The parents used in the study (A: Stoneville 453, B: PI 528429, C: Fiberless).

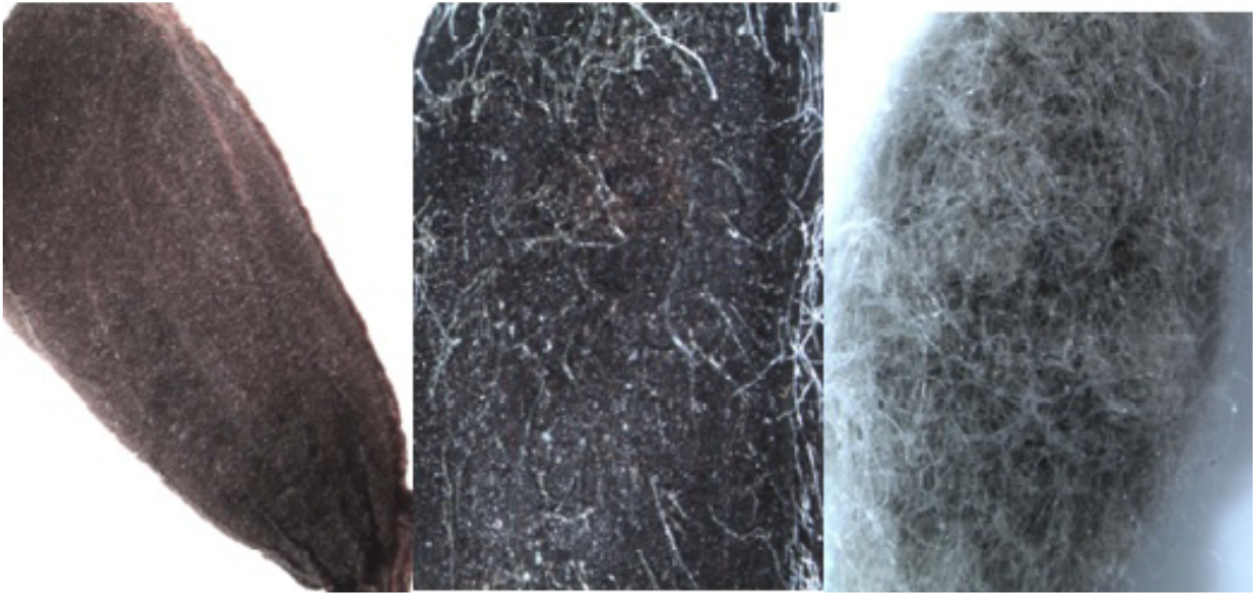


Figure 2. Fuzz in F<sub>2</sub> populations (A: no fuzz, B: little fuzz, C: fuzziness).

lint fibers of the parents are summarized in Table 1. It was observed that the lint fiber formation was dense and the seeds were fuzzless after ginning in all plants of the F<sub>1</sub> generation. The observation of intense lint fiber formation in the F<sub>1</sub> generation indicates that lint fiber formation is a dominant character. On the other hand, the fact that the seeds were fuzzless in the first generation points out the domination of fuzzlessness over fuzziness. F<sub>2</sub> segregation of mutant and wild-type genotypes yielded a 1 fuzzy : 3 fuzzless ratio (Figure 3), indicating that the fuzzless trait in the mutant is controlled by a dominant locus. Thus, fuzz formation seems to be controlled by the locus *n<sub>1</sub>n<sub>1</sub>* (Stoneville 453), and the fuzzlessness is controlled by the locus *N<sub>1</sub>N<sub>1</sub>* (PI 528429 and Fiberless) (Table 1). Thus, fuzz formation was mostly contributed by Stoneville 453, while fuzzlessness was contributed by the PI 528429 and Fiberless genotypes. The genotypic segregation of three populations was 1:3, a compatible ratio ( $P < 0.05$ ) determined by chi-square analysis. According to the results, segregation for fuzzlessness is the result of a single gene (*N<sub>1</sub>*), as described by Kearney and Harrison (1927), Thadani (1923), and Ware (1940). On the other hand, Turley and Kloth (2002)

reported 3 loci (*N<sub>1</sub>N<sub>1</sub>n<sub>2</sub>n<sub>2</sub>n<sub>3</sub>n<sub>3</sub>*) and Bechere et al. (2012) included one more locus (*n<sub>4</sub>n<sub>4</sub>*) controlling fuzzlessness. These differences in the loci may be result of the changes in genotypic backgrounds. Molecular mechanisms for fuzzless seed cannot be described at this time but it is documented that *N<sub>1</sub>* eliminates all fuzz fiber and has a greatly reduced percentage of lint (Kearney and Harrison, 1927; Ware, 1940).

F<sub>2</sub> segregation of mutant and wild-type genotypes yielded a 15 fibery: 1 fiberless ratio (Table 2), indicating that the fiberless trait in the mutant is controlled by two recessive loci and fiber formation is controlled by two dominant genes (*Li<sub>3</sub>-Li<sub>4</sub>*-), as also reported by Du et al. (2002). The fact that it is compatible with the expansion ( $P = 0.05$ ) was revealed as a result of chi-square analysis. Moreover, lint fiber formation seems to be controlled by the locus *Li<sub>3</sub>Li<sub>3</sub>Li<sub>4</sub>Li<sub>4</sub>* (Stoneville 453), *li<sub>3</sub>li<sub>3</sub>Li<sub>4</sub>Li<sub>4</sub>* or *Li<sub>3</sub>Li<sub>3</sub>li<sub>4</sub>li<sub>4</sub>* (PI 528429), and *li<sub>3</sub>li<sub>3</sub>li<sub>4</sub>li<sub>4</sub>* (Fiberless), as described by Du et al. (2001) (Table 1).

### 3.2. Segregation of fiber and seed properties

Means for gin turnout (GT), lint index (LI), and seed index (SI) results for each population are given in Table 3.

Table 1. Gin turnout values and estimated genotypes for fuzz and lint fibers of the parents.

Variety	Estimated genotypes		Gin turnout (%)
	Fuzz fiber	Lint fiber	
Stoneville 453	<i>n<sub>1</sub>n<sub>1</sub></i>	<i>Li<sub>3</sub>Li<sub>3</sub>Li<sub>4</sub>Li<sub>4</sub></i>	35.0
PI 528429	<i>N<sub>1</sub>N<sub>1</sub></i>	<i>li<sub>3</sub>li<sub>3</sub>Li<sub>4</sub>Li<sub>4</sub></i> or <i>Li<sub>3</sub>Li<sub>3</sub>li<sub>4</sub>li<sub>4</sub></i>	1.8
Fiberless	<i>N<sub>1</sub>N<sub>1</sub></i>	<i>li<sub>3</sub>li<sub>3</sub>li<sub>4</sub>li<sub>4</sub></i>	0

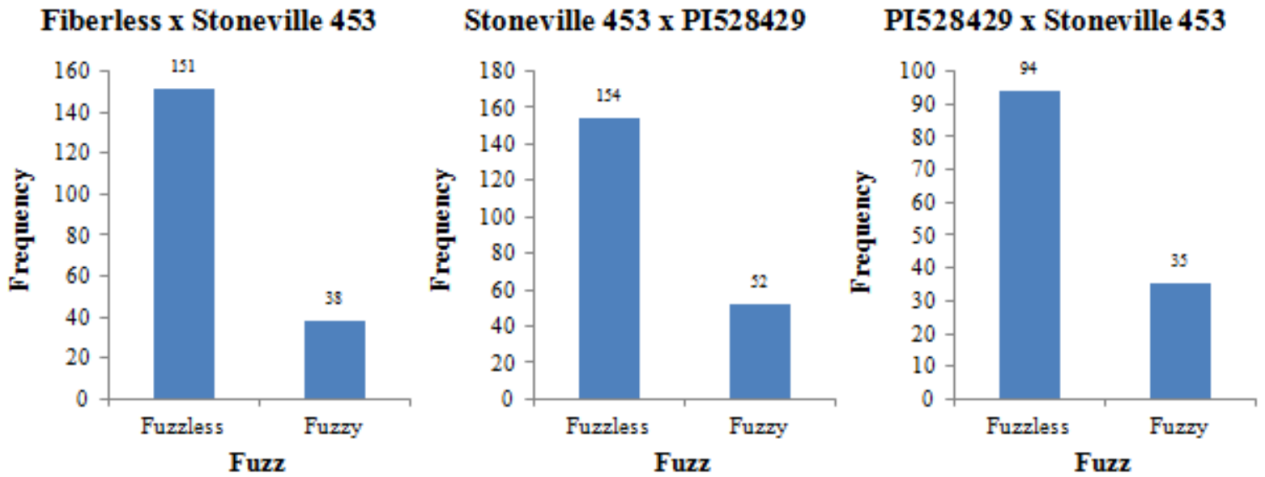


Figure 3. Frequency distribution of populations for fuzz (%).

Table 2. Inheritance (segregation) ratios of fuzz and lint fiber formation in F<sub>2</sub> populations.

	Generation	Plant number		ER	χ <sup>2</sup>	P = 0.05
		Fuzzy	Fuzzless			
PI × Stn 453	F <sub>2</sub>	35	94	1:3	1.01	3.84
Stn 453 × PI	F <sub>2</sub>	52	154	1:3	0.19	3.84
Fiberless × Stn 453	F <sub>2</sub>	38	151	1:3	2.89	3.84
		Fibery	Fiberless			
Fiberless × Stn 453	F <sub>2</sub>	171	11	15:1	3,04	3.84

PI: PI 528429, Stn 453: Stoneville 453, ER: expected ratio.

Table 3. Descriptive statistics for traits and populations.

	PI × Stn 453			Stn 453 × PI			Fiberless × Stn 453		
	GT (%)	LI (g)	SI (g)	GT (%)	LI (g)	SI (g)	GT (%)	LI (g)	SI (g)
NP	136	136	136	208	208	208	189	189	189
Mean	22	0.026	11.71	26	0.03	11.9	33	0.031	9.59
SD	8.5	0.01	1.11	10	0.01	1.68	9.6	0.0095	1.003
Min.	2	0	9.45	1	0	5.5	0	0	5.56
Max.	36	0.046	15.42	40	0.047	15.9	42	0.045	12.98

GT: Gin turnout, LI: lint index, SI: seed index, NP: number of plants, SD: standard deviation, PI: PI 528429, Stn 453: Stoneville 453.

The average GT was calculated as 22% in the PI 528429 × Stoneville 453 population, as 26% in Stoneville 453 × PI 528429, and as 33% in Fiberless × Stoneville 453. The maximum and minimum GT values observed in populations were 2%–36%, 2%–40%, and 0%–42%, respectively. The cross of Fiberless × Stoneville 453 shows

two-gene segregation but there are 3 groups observed in the frequency distribution graphs, meaning that higher gin turnout was controlled by *Li<sub>3</sub>Li<sub>3</sub>Li<sub>4</sub>Li<sub>4</sub>* while lower gin turnout was controlled by *li<sub>3</sub>li<sub>3</sub>Li<sub>4</sub>Li<sub>4</sub>* or *Li<sub>3</sub>Li<sub>3</sub>li<sub>4</sub>li<sub>4</sub>* and fiberlessness was controlled by the locus *li<sub>3</sub>li<sub>3</sub>li<sub>4</sub>li<sub>4</sub>* (Figure 4). The same trends in segregation were also seen in other



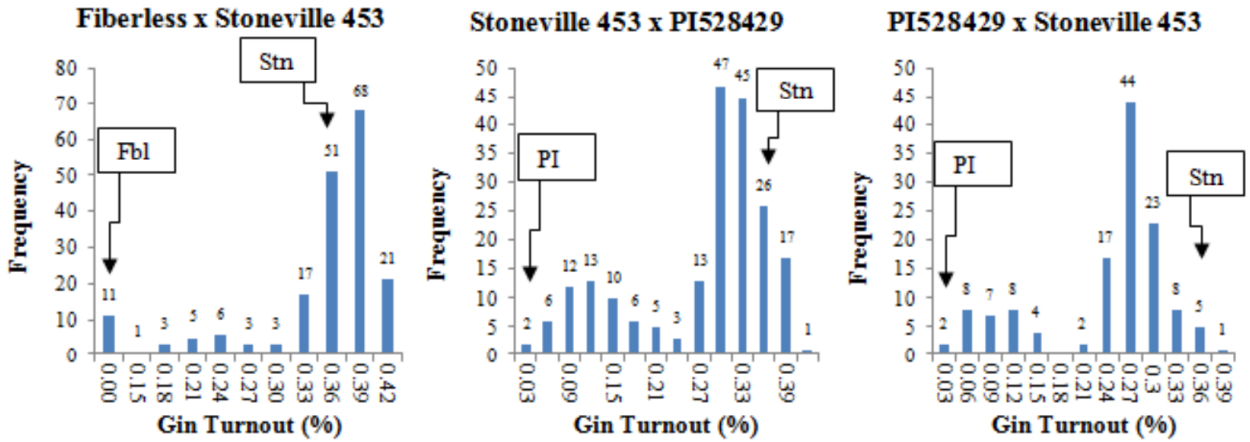


Figure 4. Frequency distribution of populations for gin turnout (%) (Stn: Stoneville 453, PI: PI 528429, Fbl: Fiberless).

populations but the homozygote recessive genotype was not observed in these populations. In other words, one of the genes controlling gin turnout is most probably homozygote recessive while the other one is either homozygote or heterozygote dominant ( $Li_3-li_4li_4$  or  $li_3li_3Li_4-$ ) when the gin turnout value is lower, being less than 20% in our study. It was reported that at least 1 dominant allele ( $Li_3Li_3$  or  $Li_4Li_4$ ) was needed for fiber development and one of these allele was required for fiber initiation, but no fiber development was seen when recessive homozygote alleles ( $li_3li_3li_4li_4$ ) were found together (Du et al., 2001). In a study conducted by An et al. (2010), in a hybrid F<sub>2</sub> population of MD17 × FM966, the average GT was calculated as 24.01% and the minimum and maximum values were found to be 0% and 40.76%, respectively. By considering the values presented in this study, we can declare that our populations show a similarly large segregation as in the previous research.

Lint index is described as the amount of fiber formed by a seed regardless of the seed size (Rong et al., 2005) In our study, the average lint indexes were determined as 0.026 g, 0.03 g, and 0.031 g for PI 528429 × Stoneville 453, Stoneville 453 × PI 528429, and Fiberless × Stoneville 453 populations, respectively. The minimum and maximum levels were detected as 0.00 and 0.046 g for PI 528429 × Stoneville 453, as 0.00 and 0.047 g for Stoneville 453 × PI 528429, and as 0.00 and 0.045 g for Fiberless × Stoneville 453 (Figure 5). It can be mentioned that each population has a large variation within itself in terms of lint index. Similar to our results, An et al. (2010) reported that the lint index of the hybrid MD17 × 181 ranged from 0.00 to 0.45 g.

Seed index is determined as the weight of 100 delinted seeds (He et al., 2005). We observed that the average seed index was similar in the PI 528429 × Stoneville 453 (11.71 g) and Stoneville 453 × PI 528429 (11.9 g) populations, while

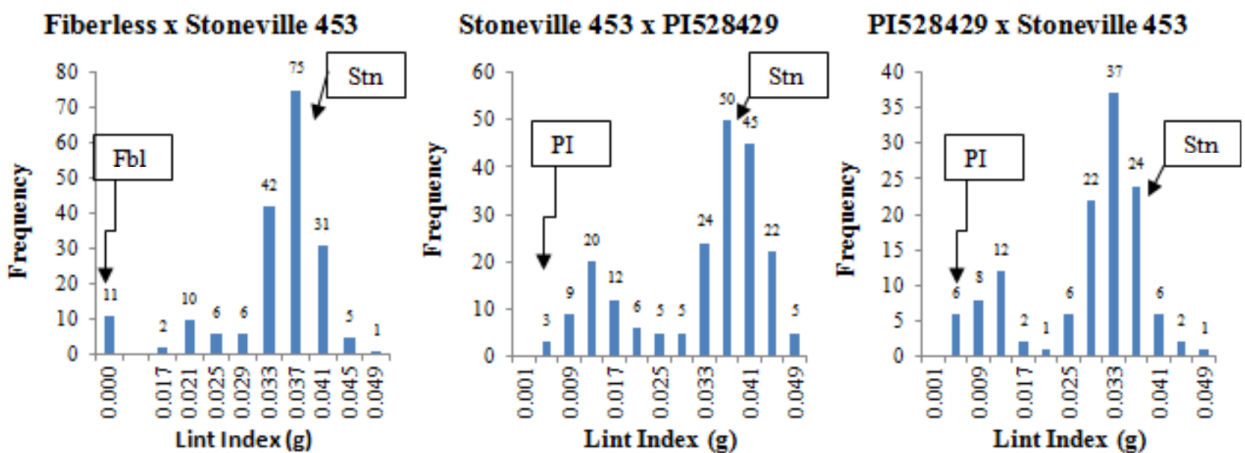


Figure 5. Frequency distribution of populations for lint index (g) (Stn: Stoneville 453, PI: PI 528429, Fbl: Fiberless).

it was lower in Fiberless × Stoneville 453 (9.59 g) compared to the others. In the PI 528429 × Stoneville 453 population, the minimum weight was 9.45 g while the maximum was 15.42 g. In the Stoneville 453 × PI 528429 population, these values were determined as 5.5 g and 15.9 g, respectively. As for the Fiberless × Stoneville 453 population, the values were found to be varied between 5.56 g and 12.98 g (Figure 6). When these values were compared to the ones reported by An et al. (2010), it was seen that the average values for the F<sub>2</sub> populations of MD17 × FM966 and MD17 × 181 were 10.29 g and 9.55 g, respectively, and they were relatively lower than the ones observed for our populations.

**3.3. Trait correlation**

In the PI 528429 × Stoneville 453 population, positive and significant correlations between GT and LI ( $r = 0.83^{**}$ ) and between GT and FZ ( $r = 0.74^{**}$ ) were detected. Similarly, positive and important correlations were also found not only between LI and FZ ( $r = 0.69^{**}$ ) but also between LI and SI ( $r = 0.46^{**}$ ). For the Stoneville 453 × PI 528429 F<sub>2</sub> population, positive and important correlations between GT and LI ( $r = 0.76^{**}$ ) and between GT and FZ ( $r = 0.82^{**}$ ) and a negative and important correlation between GT and SI ( $r = -0.40^{**}$ ) were detected. Once more, a positive and important correlation between LI and FZ ( $r = 0.67^{**}$ ) and a negative and important correlation between SI and FZ ( $r = -0.28^{**}$ ) were calculated. Lastly, in the Fiberless × Stoneville 453 F<sub>2</sub> population, the correlations between GT and LI ( $r = 0.67^{**}$ ), between GT and FZ ( $r = 0.58^{**}$ ), between LI and SI ( $r = 0.46^{**}$ ), and between LI and FZ ( $r = 0.48^{**}$ ) were all found to be positive and significant (Table 4).

According to the results presented above, it can be assumed that when GT increased, the LI and FZ ratio also increased while SI decreased. It was also observed that FZ decreased when SI increased. The relation between FZ and GT is especially important in breeding of fuzzless varieties.

With the results presented here, it can be understood that the genes related to fuzz ratio and GT were inherited in the next generation in conjunction; in other words, they are linked. Analogous relations have also been reported in previous studies (Turley et al., 2007). On the other hand, while a positive and important correlation between GT and LI was previously shown by another group (An et al., 2010), no previous report that shows a correlation between LI and SI and between LI and FZ has been found. Regarding these correlations, our study provides the literature with novel information.

**3.4. Conclusion**

It is quite important to breed new genotypes that have no fuzz on the seed and higher gin turnout. Fuzzless but fibery genotypes might be used to reach this goal. As a result of our study, it was found that there was single-gene inheritance in terms of fuzz formation in all populations while two genes are effective for fiber formation in one population. The populations were found to have a large variation for gin turnout, lint index, and seed index and so they can be efficiently used in QTL mapping experiments to find genes related to the traits mentioned above. In addition, the existence of significant correlations between these traits was determined and it was concluded that knowing the genetic structure that fundamentally affects these traits is essential in order to develop new varieties with desired quality since the determination of a DNA marker related to these traits will increase the success of the selection and bring us closer to the ideal of developing a genotype with high gin turnout and no fuzz formation. Because the populations that we developed showed extensive variations, these populations can be used in genetic mapping and marker development. Moreover, forming recombinant inbred lines from these populations can help more detailed genetic studies to be obtained.

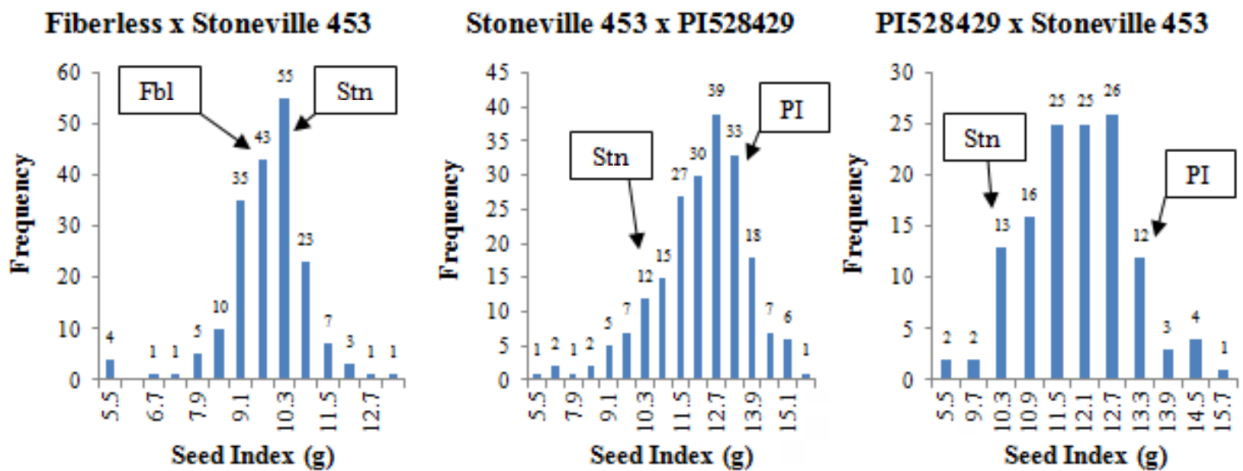


Figure 6. Frequency distribution of populations for seed index (g) (Stn: Stoneville 453, PI: PI 528429, Fbl: Fiberless).

**Table 4.** Pearson correlation coefficients among investigated traits in F<sub>2</sub> populations.

	PI 528429 × Stoneville 453			Stoneville 453 × PI 528429			Fiberless × Stoneville 453		
	GT	LI	SI	GT	LI	SI	GT	LI	SI
LI	0.83**			0.76**			0.67**		
SI	0.02	0.46**		-0.40**	0.17		-0.22	0.46**	
FZ	0.74**	0.69**	0.13	0.82**	0.67**	-0.28**	0.58**	0.48**	-0.10

GT: Gin turnout, LI: lint index, SI: seed index, FZ: fuzz, \*\*significant at 0.01 level.

## References

- An C, Jenkins JN, Wu J, Guo Y, McCarty JC (2010). Use of fiber and fuzz mutants to detect QTL for yield components, seed, and fiber traits of upland cotton. *Euphytica* 172: 21-34.
- Bechere E, Turley RB, Auld DL, Zeng L (2012). A new fuzzless seed locus in an upland cotton (*Gossypium hirsutum* L.) mutant. *American Journal of Plant Sciences* 3: 799-804.
- Du XM, Pan JJ, Wang RH, Zhang TZ, Shi Y (2001). Genetic analysis of presence and absence of lint and fuzz in cotton. *Plant Breeding* 120: 519-522.
- Endrizzzi JE, Turcotte EC, Kohel RJ (1984). Qualitative genetics, cytology and cytogenetics In: Kohel RJ, Lewis DF, editors. *Agronomy: Cotton*. Madison, WI, USA: American Society of Agronomy, pp. 59-80.
- Endrizzzi JE, Turcotte EL, Kohel RJ (1985). Genetics, cytogenetics and evolution of *Gossypium*. *Adv Genet* 23: 271-375.
- Griffee F, Ligon LL (1929). Occurrence of lintless cotton plants and the inheritance of the character 'Lintless'. *J Am Soc Agron* 21: 711-717.
- He DH, Lin ZX, Zhang XL, Nie YC, Guo XP, Feng CD, Stewart JM (2005). Mapping QTLs of traits contributing to yield and analysis of genetic effects in tetraploid cotton. *Euphytica* 144: 141-149.
- Karaca M, Saha S, Jenkins JN, Zipf A, Kohel R, Stelly DM (2002). Simple sequence repeat (SSR) markers linked to the LigonLintless (Li<sub>1</sub>) mutant in cotton. *J Hered* 93: 221-224.
- Kearney TH, Harrison RJ (1927). Inheritance of smooth seed in cotton. *J Agric Res* 35: 193-217.
- Kohel RJ (1973). Genetic nomenclature in cotton. *J Hered* 64: 291-295.
- Kohel RJ, Narbuth EV, Benedict C R (1992). Fiber development of Ligon Lintless-2 mutant of cotton. *Crop Sci* 32: 733-735.
- Kohel RJ, Stelly DM, Yu J (2002). Tests of six cotton (*Gossypium hirsutum* L.) mutants for association with aneuploids. *J Hered* 93: 130-132.
- Musaev JA, Abzalov MF (1972). Some questions concerning the inheritance of fuzzy in cotton seeds (*G. hirsutum* L.). *Genetika* 8: 7-16.
- Nadarajan N, Rangasamy SR (1988). Inheritance of the fuzzless-lintless character in cotton (*Gossypium hirsutum*). *Theor Appl Genet* 75: 728-730.
- Percy RG, Kohel RJ (1999). Qualitative genetics. In: Smith CW, Cothren JT, editors. (*Cotton: Origin, History, Technology, and Production*. New York, NY, USA: John Wiley & Sons.
- Rong J, Pierce GJ, Waghmare VN, Rogers CJ, Desai A, Chee PW, May OL, Gannaway JR, Wendel JF, Wilkins TA et al. (2005). Genetic mapping and comparative analysis of seven mutants related to seed fiber in cotton. *Theor Appl Genet* 111: 1137-1146.
- Thadani KI (1923). Linkage relations in the cotton plant. *Agric J India* 18: 572-579.
- Thadani KI (1925). Inheritance of certain characters in *Gossypium*. *Agric J India* 20: 37-42.
- Turley RB, Kloth RH (2002). Identification of a Third fuzzless seed locus in upland cotton (*Gossypium hirsutum* L.). *J Hered* 93: 359-364.
- Turley RB, Kloth RH (2008). The inheritance model for the fiberless trait in upland cotton (*Gossypium hirsutum* L.) line SL1-7-1: variation on a theme. *Euphytica* 164: 123-132.
- Turley RB, Vaughn KC, Scheffler JA (2007). Lint development and properties of fifteen fuzzless seed lines upland cotton (*Gossypium hirsutum* L.). *Euphytica* 156: 57-65.
- Ware JO (1940). Relation of fuzz pattern to lint in an upland cotton cross. *J Hered* 31: 489-498.
- Ware JO, Benedict LI, Rolfe WH (1947). A recessive naked-seed character in upland cotton. *J Hered* 38: 313-320.
- Zhang TZ, Pan JJ (1991). Genetic analysis of a fuzzless-lintless mutant in *Gossypium hirsutum* L. *Jiangsu Journal of Agricultural Science* 7: 13-16.