Cluster and Principal Component Analysis for Seed Coat Resistibility and Its Related Traits of Cotton (*Gossypium spp.*) Genotypes

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Abstract— *During the ginning of seed cotton, the seeds can be broken and mixed into the fibers. The number of seed coat particles passing into the fibers and the amount of neps caused by the seed coat is an important factor that negatively affects the yarn quality and creates problems in dyeing. In this study, 200 different cotton genotypes were evaluated in terms of 100-seed weight, seed coat ratio, seed coat thickness and seed coat resistibility. As a result of the study, it was determined that 100-seed weights of genotypes varied between 7.23 - 15.43 g, seed coat ratios between 15.53 - 38.27%, seed coat thickness between 0.41 - 1.00 mm and seed coat resistibility between 41.07 - 107.21 newton. TxNo:142 genotype had the highest seed coat resistibility. In addition, it was determined that there was a positive and significant relationship between seed coat resistibility and 100-seed weight. In principal components analysis, two out of 4 principal components were selected with Eigen value >1. The two principal components contributed 59.3% towards variability. In cluster analysis, 200 genotypes were allocated in five clusters. Cluster II was the largest by having 90 genotypes while cluster V, cluster III, cluster I and cluster IV having 54, 28, 20 and 8 genotypes, respectively.*

Keywords— Cotton, seed traits, seed coat.

I. INTRODUCTION

Cotton, which constitutes the raw material of more than fifty industries, especially the textile and food industries, is one of the most important industrial plants. Cotton is the raw material of the textile and cellulose industry with its fiber, of the vegetable oil industry with the oil obtained from the kernel, and of the feed industry with its seed and meal. Approximately 90% of the fiber crops cultivation areas in the world are cotton. In our country, according to 2024 data, cotton was cultivated on approximately 467 000 hectares and 2.24 million tons of seed cotton was produced (Anonymous, 2024). According to Aydın Commodity Exchange data, in the 2023/2024 season, Turkey is the fourteenth country in terms of cultivation area, sixth in terms of fiber cotton yield obtained from unit area, seventh in terms of fiber cotton production amount, fifth in terms of fiber cotton consumption and fourth in terms of fiber cotton imports in the world cotton market (Anonymous, 2023).

Seed cotton harvested from the field contains fibers and kernels before processing. In order for the seed cotton to be sent to spinning mills, it must be cleaned from the kernels and other foreign materials (vegetable parts, dust, etc.). The process of separating cotton into kernel and fiber is called ginning (Kıllı, 2001). After the ginning process, fiber cotton is obtained as the main product and cotton seed is obtained as a by-product. On average, 35-40% of the seed cotton consists of fiber and 60-65% of seed.

The seed cotton obtained after harvesting is separated from the seeds by ginning. During ginning, the seeds may break and mix with the fiber cotton. After ginning, the number of seed coat particles and the amount of neps caused by seed coat is an important problem that negatively affects the yarn quality, creates problems in dyeing and reduces the quality and value of textiles (yarn and fabric). In our country, approximately 40% of baled cotton has seed coat problem (Özbek, 2017). The cotton seed coat has a 5-layered structure (Figure 1) (Yan et al., 2009).

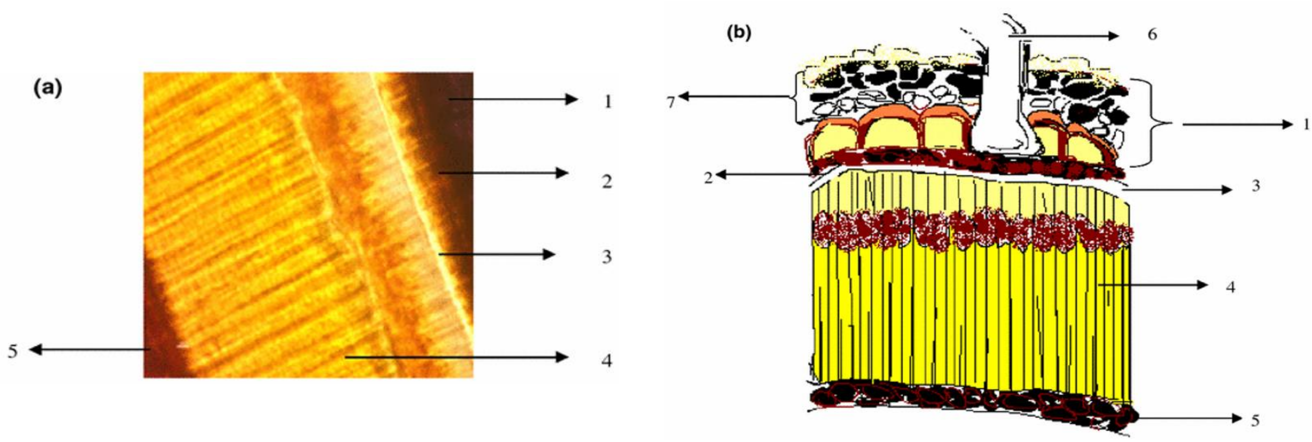

FIGURE 1: Cotton seed coat structure a) Light microscope image of seed coat section b) Schematic view of seed coat anatomical structure. 1) epidermis layer, 2) outer pigment layer, 3) colorless layer, 4) palisade layer, 5) inner pigment layer, 6) cotton fiber, 7) cutin (Yan et al., 2009).

Cellulose and pectin are the main components of the epidermal layer surrounded by cutin and wax; pectin, hemicellulose and lignin are the main components of the palisade layer; and lignin-like compounds are the main components of the inner and outer pigment layer (Yan et al., 2009). During the ginning of seed cotton after harvest, seed coats can be broken and mixed into the fibers. Approximately 30% of the negative effects in textile products are attributed to seed coat particles and it is emphasized that seed coat particles in ginned fiber cotton can vary by 50% depending on cotton varieties (Bel and Xu, 2011).

Principal component analyses (PCA) and biplot approaches are an approach that provides the opportunity to visually present and evaluate the relationships between the examined parameters and genotypes at the same time (Kahraman et al., 2021). There is a need to use principal component analysis to demonstrate the results of cotton breeding research. Therefore, many researchers (Abasianyanga et al., 2017; Nandhini et al., 2018; Shah et al., 2018; Vinodhana and Gunasekaran, 2019; Abdel-Monaem et al., 2020; and Yehia and El-Hashash, 2021) have used PCA to know the relationships among yield and yield components, as well as to evaluate the relationship and diversity among various cotton germplasms. This study aimed to evaluate the genotypes and the relationship between seed coat breaking resistance and seed weight, seed coat ratio and seed coat thickness traits in 200 different cotton genotypes.

II. MATERIALS AND METHODS

2.1 Experimental site:

The experiment was conducted in the research area of the Department of Field Crops, KSU Faculty of Agriculture, during the 2018 cotton growing season. The province of Kahramanmaras, where the experiment was conducted, is located between 37°11' and 38°36' north latitude and 36°15' and 37°42' east longitude. The average temperature and precipitation during the experimental years (2018) and the long-term averages over time are presented in Figure 2. The average temperature of May - November in the research year and long years were 18.54°C and 17.47°C, respectively. The total monthly precipitation in May - November was 240.4 mm and the average monthly relative humidity was 56.09%. There was no precipitation in July, August and September. The soils of the test area have a clay loam texture with a pH of 7.72, salinity of 0.15% and low organic matter content (1.55%).

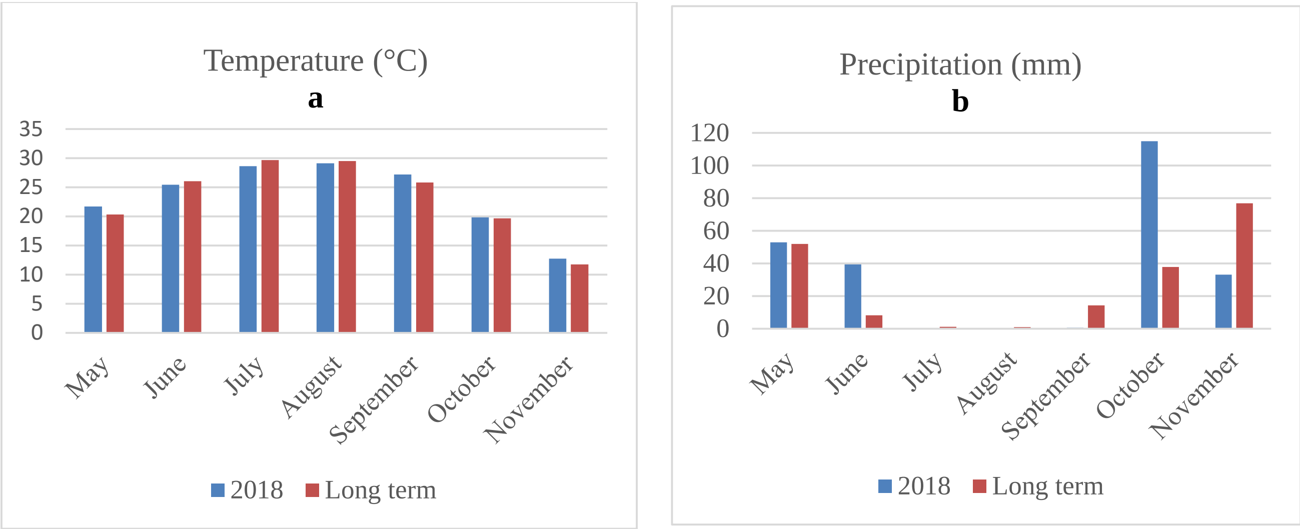

FIGURE 2: The average climate data for the experimental years; (a) Temperature; (b) Precipitation

2.2 Experimental materials:

In the study, 200 different cotton genotypes obtained from the genetic stocks of Nazilli Cotton Research Institute (CRI-Nazilli/Turkey) were used as material. The sequence numbers and names of the cotton genotypes used are given in Table 1.

2.3 Experimental design and field management:

The research was carried out according to the randomized block design with three replications. The experimental area was plowed deeply with a plow in the fall, and after spending the winter in this way, it was made ready for sowing by cultivating the soil with a cultivator and tapping it while the soil was at the right level before sowing according to the weed status of the field. The seeds of the varieties used in the experiment were sown by hand on May 11, 2018 in 5 m long plots with a row spacing of 70 cm in accordance with the experimental design. After emergence, cotton seedlings were thinned by hand in the 2- to 4-leafed period with a row spacing of 20 cm. Before sowing, 300 kg of 20-20-0 compound fertilizer containing 60 kg N and P_2O_5 per hectare was applied as sprinkling. As a top fertilizer, 200 kg ha^{-1} of urea fertilizer containing 46% nitrogen was applied by hand before the second irrigation. In order to protect the developing cotton seedlings from weeds, to prevent the loss of water in the soil by evaporation, to ensure the development and deepening of the roots of the seedlings, hand hoeing was done 2 times and tractor hoeing 3 times. Cotton plants were irrigated 7 times during the vegetation period by furrow irrigation method, taking into account their development status. During the growing season, cotton plants were sprayed four times against sucking insects (*Aphis gossypii* and *Empoasca spp*) and once against green bollworm (*Helicoverpa armigera*) pests. Harvesting was done twice by hand on October 8 and November 1, 2018.

TABLE 1
AVERAGE VALUES OF 200 COTTON GENOTYPES FOR INVESTIGATED CHARACTERS

Genotype No	Genotype name	100-SW (g)	SCR (%)	SCT (mm)	SCRe (Newton)
1	MNH-786	9,02	29,54	0,56	62,26
2	BH-118	9,99	33,72	0,67	47,30
3	Ziroatkar-68	11,59	31,85	0,63	66,90
4	Sindh-1	9,71	29,50	0,66	68,46
5	AGC 85	11,55	34,63	0,50	59,84
6	CIM 401	9,27	34,16	0,76	71,69
7	Frego Cluster	10,36	26,07	0,49	69,87
8	AzGR-11468	11,90	29,97	0,66	67,28
9	CIM-506	10,63	19,34	0,56	53,01
10	Sohni	8,60	29,54	0,58	66,82
11	CIM-70	10,21	19,68	0,55	54,91
12	994	9,87	25,42	1,00	45,53
13	VH 260	9,43	22,25	0,61	44,89
14	Stoneville 474	9,85	38,27	0,54	79,72
15	Malmal-MNH-786	9,34	20,33	0,60	55,05
16	AzGR-11836	11,01	32,15	0,62	82,08

17	Marvi	8,42	30,88	0,49	55,38
18	Ziroatkar-81	12,29	23,85	0,47	75,65
19	AzGR-11834	11,43	22,17	0,42	82,53
20	AzGR-11839	12,29	19,50	0,58	80,87
21	Stoneville 506	10,45	27,38	0,45	69,06
22	Nibge-2	11,02	20,55	0,69	67,56
23	MNH-990	8,97	33,06	0,52	66,50
24	Sadori	10,06	29,63	0,49	57,37
25	Penta	11,35	29,36	0,54	86,79
26	Abroginal 79	9,91	33,29	0,60	71,46
27	Nova	10,95	29,25	0,98	73,10
28	Shazbaz	7,72	27,64	0,48	45,72
29	Deltapine 5816	11,57	34,10	0,51	82,68
30	Deltapine 565	12,87	32,63	0,52	71,84
31	Stoneville 2B	10,39	30,48	0,43	70,43
32	Deltapine 50 –vert	9,06	31,54	0,56	58,32
33	MNH-493	7,37	33,44	0,57	47,15
34	Stoneville 508	10,83	29,84	0,55	86,37
35	AzGR-7711	12,53	33,56	0,70	71,68
36	Stoneville 256	10,75	21,69	0,67	74,65
37	Stoneville 5A	10,92	27,75	0,65	80,57
38	Tamcot Sphinx	10,05	25,55	0,57	72,16
39	Bulgar 73	10,90	29,70	0,59	79,11
40	Stoneville 618 BBR	9,02	29,31	0,41	99,38
41	Carolina Queen	9,79	27,19	0,60	80,13
42	AfricaES(20025)	10,33	36,25	0,56	81,22
43	Acala Tex	11,32	36,27	0,67	75,01
44	Tx No: 1412	11,11	17,31	0,55	107,21
45	Karnak 55	13,68	18,03	0,94	102,54
46	Mex 106	14,60	33,66	0,47	92,76
47	Dpl 5540-85-subokra	11,59	24,39	0,50	78,39
48	Deltapine 120	11,48	23,61	0,57	73,63
49	Acala 1517-70	11,43	28,30	0,57	79,93
50	TAM C155 - 22 ELS	11,66	27,48	0,48	88,31
51	Deltapine 45 – vert	13,61	21,46	0,66	71,82
52	Acala 44	13,94	27,50	0,61	91,41
53	Deltapine 15A	11,87	26,44	0,57	79,22
54	Brown Egyptian	9,96	21,84	0,55	72,35
55	Deltapine 12	12,20	24,11	0,61	78,00
56	Deltapine 25	9,96	29,13	0,69	92,55
57	Acala Nunn's	10,53	33,31	0,59	75,52
58	Acala 1517 D	7,23	31,03	0,51	101,63
59	Acala Morell	12,59	32,72	0,48	89,14
60	TAM B147 – 21	11,81	31,50	0,57	83,65
61	TAM 87 G3- 27	12,06	31,47	0,48	69,74
62	Acala Glandless	10,46	26,17	0,65	86,84
63	Acala 4-42	14,27	26,51	0,57	79,66
64	Acala 442	12,69	20,16	0,69	92,25
65	TAM C66 - 26	14,56	28,33	0,57	82,55
66	Deltapine Staple	11,88	30,29	0,47	79,52
67	Togo	11,66	25,41	0,58	71,97
68	NIAB-KIRN	12,33	39,58	0,52	76,97
69	Sivon	8,99	30,21	0,58	75,64
70	Alba Acala 70	11,25	20,47	0,65	74,19
71	NIA-UFAQ	12,22	29,09	0,45	59,24
72	Giza 7	9,05	26,17	0,54	77,99
73	Cris-134	11,21	23,35	0,49	58,21
74	Acala Naked	8,70	26,13	0,62	78,34

75	Samos	10,73	27,31	0,47	71,88
76	Agdas 6	10,62	34,87	0,49	73,74
77	Zeta 2	11,95	34,07	0,49	77,69
78	Agdas 7	11,78	32,92	0,44	75,71
79	AGC 375	9,82	27,21	0,45	73,58
80	Haridost	10,66	21,10	0,64	59,51
81	Viky (ES-20021)	9,64	29,57	0,57	65,09
82	Sorbon	9,68	31,70	0,44	80,09
83	Agdas 3	8,04	27,99	0,52	79,38
84	Sugdiyon-2	10,11	22,33	0,59	81,85
85	CIM-240	12,41	25,32	0,51	77,45
86	Sure Grow 125	10,26	30,49	0,63	69,41
87	AzGR-3775	9,72	25,50	0,55	83,62
88	Ujchi 2 Uzbek	11,36	26,42	0,62	87,51
89	Ziroatkar-64	10,71	29,73	0,58	79,77
90	AGC 208	9,97	22,28	0,55	71,31
91	B557	10,31	30,65	0,43	56,92
92	Cris-342	8,37	31,10	0,53	64,85
93	MNH-814	9,21	23,97	0,57	43,34
94	Korina	9,73	24,16	0,50	76,67
95	FH 142	10,61	28,96	0,83	41,07
96	TX No: 1416	8,16	15,53	0,58	84,18
97	Stoneville 213	14,38	30,19	0,50	73,03
98	Acala SJ 3	9,71	33,70	0,51	76,09
99	Mex 123	10,28	38,52	0,62	73,37
100	Fibermax 832	10,20	27,61	0,49	69,66
101	Giza 75	9,78	24,46	0,60	84,68
102	Tex 844	12,26	23,48	0,60	81,06
103	Tx No: 2383	11,93	25,79	0,54	83,16
104	Bulgar 6396	11,02	26,31	0,55	82,59
105	Deltapine 20	10,14	28,87	0,49	77,05
106	Agala Sindou	10,16	22,92	0,51	70,33
107	Tex 1152	10,03	25,92	0,48	70,18
108	NIAB 111	12,07	35,10	0,59	67,91
109	Mehrgon	9,80	29,36	0,45	82,44
110	Campu	10,66	26,71	0,59	74,64
111	Stoneville 3202	11,72	26,43	0,79	74,47
112	Stoneville 62	10,27	30,59	0,51	72,92
113	Giza 70	10,80	27,95	0,58	66,28
114	Deltapine 62	10,61	25,23	0,61	75,55
115	Acala Okra	11,49	31,19	0,49	78,08
116	Acala Young's	10,05	27,48	0,58	73,27
117	TAM B182	10,91	26,68	0,73	76,78
118	Deltapine SR-5	13,73	32,60	0,61	75,65
119	TAM C147 -42	10,14	27,93	0,51	70,69
120	Acala 8	11,93	27,44	0,45	79,25
121	Acala 1064	12,30	21,11	0,48	76,72
122	Acala Cluster	10,79	28,08	0,60	77,18
123	Auborn 56	9,96	23,15	0,48	70,85
124	TAM 94 L 25 P1	10,82	27,59	0,55	68,23
125	Aden	12,32	35,70	0,49	86,46
126	Acala Okra VA2-4	10,55	31,36	0,69	78,28
127	Deltapine 905	12,11	32,87	0,64	76,96
128	Acala 29	10,95	18,23	0,71	78,45
129	Giza 45	13,01	23,60	0,63	74,62
130	Earlipima	12,28	21,60	0,70	82,22
131	Acala 1517 SR2 – vert	15,43	25,88	0,82	73,94
132	Acala N 28-5	12,23	25,88	0,53	66,84

133	Deltapine 26	10,18	28,13	0,60	72,17
134	AzGR-11835	11,14	26,64	0,65	75,29
135	Rantos	11,51	20,99	0,61	70,40
136	Agdas 17	12,38	27,67	0,95	78,82
137	NIAB-111	11,56	29,07	0,61	50,70
138	Tex 1216	9,97	25,29	0,48	78,42
139	Mex 122	12,13	26,16	0,56	77,46
140	Tx No: 2700	11,60	24,39	0,57	80,23
141	Stoneville 014	12,27	26,57	0,56	70,47
142	Stonville 108 SR	11,02	22,51	0,61	67,56
143	TX No: 2382	11,99	22,97	0,51	74,69
144	Hopicala – vert	12,33	26,25	0,50	75,43
145	Eva	12,44	26,62	0,55	70,12
146	Mex 102	10,53	23,56	0,53	77,24
147	NIAB 78	11,32	28,12	0,72	63,94
148	Stoneville 731N	10,09	24,83	0,70	73,24
149	Taashkent	11,00	26,18	0,49	99,65
150	Stonville 504	10,86	27,20	0,55	64,36
151	Cascot L7	10,67	28,46	0,61	73,40
152	Avesto	11,02	18,27	0,48	61,61
153	Darmi	11,07	25,82	0,63	86,54
154	Giza 59	12,15	26,09	0,59	78,80
155	Tadla 25	11,87	23,70	0,71	72,76
156	New Mexican Acala	11,82	27,31	0,73	79,44
157	Giza 83	12,45	22,91	0,53	79,59
158	Stoneville 256-315	12,68	22,43	0,49	79,55
159	Arcota-129	12,19	24,85	0,53	65,40
160	NIAB 846	11,67	26,82	0,56	59,58
161	Mex 68	10,07	20,76	0,48	77,01
162	Europa	12,84	23,83	0,54	82,74
163	TX No: 1389	11,74	18,70	0,59	75,98
164	Ionia	12,28	28,00	0,54	75,88
165	Helius	11,31	23,97	0,53	75,96
166	NIAB 874	12,11	21,38	0,51	63,61
167	Ligur	11,22	25,75	0,58	74,79
168	NIAB 777	10,36	23,77	0,58	64,03
169	Tex 2167	10,51	27,90	0,48	69,54
170	Fibermax 819	11,13	31,72	0,58	67,76
171	Tex 843	10,51	27,54	0,50	76,07
172	Acala 32	11,12	31,50	0,52	78,92
173	Acala 1-13-3-1	10,47	28,04	0,60	60,63
174	Deltapine 61	12,83	35,17	0,64	71,45
175	Deltapine 15	10,85	27,41	0,65	69,47
176	Deltapine 14	10,58	35,77	0,58	72,52
177	Acala Shafter Station	9,40	28,35	0,48	72,86
178	Acala 1517-91	10,11	24,78	0,72	91,65
179	Acala Tex	12,18	25,01	0,80	77,24
180	Deltapine 714 GN	12,18	32,49	0,60	68,98
181	Acala 1517 C	10,87	27,45	0,63	69,90
182	Acala 44 WR	11,65	23,04	0,52	78,87
183	Deltapine 50	12,29	25,69	0,54	73,83
184	Acala SJ1	10,87	21,85	0,56	83,77
185	Crumpled	12,51	20,75	0,64	92,68
186	Deltapine 41	13,49	31,62	0,60	68,22
187	TAM C66 - 16	10,11	28,20	0,57	73,70
188	TAM 01 E - 22	14,35	31,31	0,54	70,46
189	Acala Harper	12,70	29,02	0,51	60,62
190	Acala-55-5	10,68	25,69	0,50	67,54

191	Deltapine 80	10,12	26,38	0,55	83,10
192	Tropical 225	10,63	23,62	0,51	77,88
193	TAM 04 WB - 33	13,28	25,97	0,58	74,83
194	Acala Mexican	12,07	27,67	0,54	89,12
195	Acala 3080	11,85	30,59	0,49	80,84
196	Acala 51	11,99	25,96	0,53	80,66
197	TAM A106- 16ELS	11,95	34,92	0,58	80,24
198	TAM B139 - 17 ELS	11,95	28,62	0,62	75,25
199	Deltapine SR4	12,66	29,59	0,60	83,28
200	Acala SS 2280	10,46	23,23	0,59	77,59
Average		11,09	27,35	0,57	74,20

2.4 Data collected:

100 seed weight (100-SW, g): Harvested seed cotton from each plot was ginned in micro ginning machine and seeds were obtained. From the seeds obtained by ginning, 100 cotton seeds were counted 4 times, weighed and averaged.

Seed coat ratio (SCR, %): One hundred seed samples from each plot were delinted with dilute sulphuric acid (50%) and weighed after drying for 48 hours under room conditions (Boykin, 2010). The seeds were then cut in half with a scalpel and the inner parts were removed. After weighing the shells obtained, the seed coat ratio was calculated as percentage according to the following formula.

SCR (%) = [100 seed coat weight (g) / 100-SW (g)]) x 100 (1)

Seed coat thickness (SCT, mm): The hulls of 100 cotton seeds were measured from 3 different places with a digital caliper and the seed coat thickness was determined by averaging (Boykin, 2010).

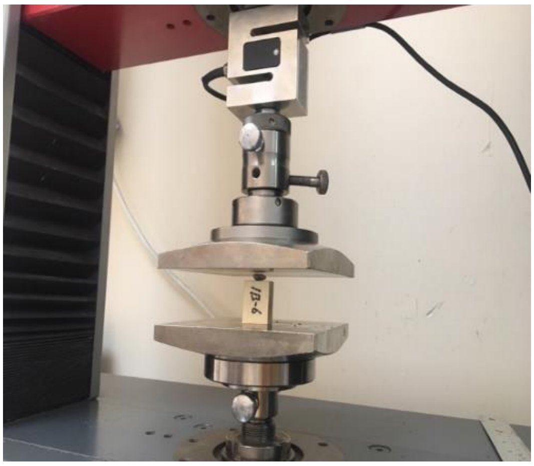

FIGURE 3. HIT5, 5P by ZwickTM instrument

Seed coat resistibility (SCRe, Newton): It was determined by working on 10 seed samples in 3 replicates (10x3= 30 seeds) randomly selected from the seeds obtained as a result of ginning the cotton harvested from each plot. Seed coat resistibility was determined by applying Zwick 10kN pressure at a speed of 2 mm min^{-1} on HIT5.5P by ZwickTM device (Figure 3) to seeds containing 8.0±0.5% moisture in KSU Faculty of Forestry test laboratory (Mengeloglu et al., 2015).

2.5 Data analyses:

The variance analyses of the data obtained for the traits examined in the study were carried out using SAS statistical package programme according to the random blocks experimental design. Duncan multiple comparison test was applied to compare the means of the significant sources of variation. Due to the high number of genotypes, averages for each trait were given and letter groupings were not shown. Pearson correlation analysis was utilized to examine the relationships between the traits (Sarwar et al., 2021). Principal component analyses were calculated on average data and evaluated with the biplot approach (JMP 15.1 SAS Institute Inc, 2020). Cluster analysis was based on SCRe and related seed traits. Cluster analysis was conducted following the agglomerative hierarchical clustering ward's method, in order to categorize genotypes into different homogeneous groups using XLSTAT (XLSTAT, 2014).

III. RESULTS AND DISCUSSION

Analysis of variance for investigated characteristics are presented in (Table 2). The result showed the existence of highly significant ($P \leq 0.01$) variation among genotypes for 100-SW, SCR, SCT and SCRe.

TABLE 2
MEAN SQUARES FROM ANALYSIS OF VARIANCE FOR 4 CHARACTERS OF 200 COTTON GENOTYPES

Source of variance	DF	100-SW	SCR	SCT	SCRe
Replication	2	0.56	27.78	0.0026	34.87
Genotype	199	5.48**	73.62**	0.0200**	329.35**
Eror	398	0.14	11.35	0.0051	51.31
CV %		3.43	12.24	12,31	9,66

, ** , ns, significant at P ≤ 0.05, P ≤ 0.01 and non-significant, respectively. 100-SW: Hundred seed weight, SCR: Seed coat ratio, SCT: Seed coat thickness, SCRe: Seed coat resistibility.

3.1 100-SW (g):

Cotton genotypes showed statistically significant difference in terms of 100-SW at p<0.01 level (Table 2). The average 100-SW value of the cotton genotypes used as material in the study was 11.04 g and they varied between 7.23 g and 15.43 g (Table 1). The highest 100-SW values were obtained from Acala 1517 SR2-vert (15.43 g), Mex 106 (14.60 g), TAM C66-26 (14.56 g) and Stoneville 213 (14.38 g) genotypes; the lowest 100-SW values were obtained from Acala 1517 D (7.23 g), MNH-493 (7.37 g) and Shazbaz (7.72 g) genotypes, respectively. Patel et al. (2003) reported that 100-SW values differed among cotton varieties; Efe et al. (2013) reported that 100-SW values of some mutant cotton varieties from Azerbaijan varied between 9.4 - 12.7 g in Southeastern Anatolia Region; Yuka (2014) reported that 100-SW values of 13 different cotton genotypes varied between 8.13-10.71 g; Tekeli (2016) reported that 100-SW values varied between 9.03-13.28 g; Kıllı and Beycioglu (2020a) reported that 100-SW values varied between 9.34-13.05 g in their study with 46 different cotton genotypes; Kıllı and Beycioglu (2020c) reported that 100-SW values varied between 9.11-12.65 g in different cotton genotypes. The fact that the 100-SW values obtained in the study showed a wide variation between approximately 7 g and 15 g and also differed from the findings of the researchers may be due to the presence of genotypes from different species and the high number of genotypes.

3.2 SCR (%):

Cotton genotypes showed statistically significant difference in terms of SCR at p<0.01 level (Table 2). The average SCR value of the cotton genotypes used as material in the study was 27.35 % and the SCR values varied between 15.53 % and 38.27 % (Table 1). The highest SCR values were obtained from Stoneville 474 (38.27 %), Acala Tex (36.25 %) and Africa ES (20025) (36.27 %) genotypes; the lowest SCR values were obtained from TxNo: 1416 (15.53 %) and TxNo: 1412 (17.31 %) genotypes, respectively. The wide variation between 15 % and 38 % of the SCR values obtained in the study was due to the presence of genotypes from different species, the large number of genotypes, and the different values of SCT and 100-SW.

3.3 SCT (mm):

Cotton genotypes showed statistically significant difference in terms of SCT at p<0.01 level (Table 2). The average SCT value of the cotton genotypes used as material in the study was 0.57 mm and SCT values varied between 0.41 mm and 1.00 mm (Table 1). The highest SCT values were obtained from Genotypes 994 (1.00 mm), FH 142 (0.83 mm) and Acala 1517 SR2-vert (0.82 mm); the lowest SCT values were obtained from Genotypes Stoneville 618 BBR (0.41 mm), Stoneville 2B (0.43 mm), B557 (0.43 mm), Agdaş 7 (0.44 mm) and Sorbon (0.43 mm), respectively. The wide variation between 0.41 mm and 1.00 mm in the SCT values we obtained in the study may be due to the presence of genotypes from different species, the number of genotypes being quite high, and the different SCR and 100-SW values.

3.4 SCRe (N):

The cotton genotypes used as material in the study showed statistically significant differences at p<0.01 level in terms of SCRe (Table 2). The average SCRe value over all genotypes was 74.20 N and SCRe values varied between 41.07 N and 107.21 N (Table 1). The highest SCRe values were obtained from TxNo:142 (107.21 N), Karnak 55 (102.54 N), Acala 1517D (101.63 N), Taashkent (99.65 N) and Stoneville 618 BBR (99. 38 N) genotypes; the lowest SCBR values were obtained from FH 142 (41.07 N), MNH-184 (43.34 N), VH 260 (44.89 N), Genotype 994 (45.53 N), Shazbaz (45.72 N), MNH 493 (47.15 N) and BH

118 (47.30 N) genotypes, respectively. Bolek et al. (2007) reported that the difference between varieties was significant in the study in which they investigated the SCR of 10 cotton varieties of *G. hirsutum* L. species; Down et al. (2019) reported that cotton seeds with different genetic structure showed differences in terms of break resistance. The results of SCRe obtained in this study are similar to the findings of the researchers. The difference between the lowest and highest SCRe values obtained from the genotypes was quite high as 66 Newton. The wide variation of the genotypes in terms of SCRe was due to the presence of genotypes from different species and the high number of genotypes. Armijo et al. (2006 a and b) reported that the amount of seed coat neps was 3 times higher in cotton varieties with easily breakable seed coat. The seed coat problems encountered in post ginning fibre cottons can be reduced by developing varieties with more robust, in other words, less brittle seed coat characteristics or by transferring seed coat robustness to existing varieties.

3.5 Pearson's Correlation:

Basic statistics for the traits analysed show that there is a sufficient amount of variability among the 200 cotton genotypes (Table 3). When the basic statistics are analysed, it is seen that among the 4 traits studied, except 100 seed weight, the other traits have relatively high coefficients of variation. This situation shows that there is a possibility to obtain new individuals from the existing genotypes and to create new combinations by crosses in the selections to be made in terms of the aforementioned traits.

TABLE 3
SOME DESCRIPTIVE STATISTICS FOR INVESTIGATED TRAITS

Traits	Minimum	Maximum	Mean	Variance	Standard deviation	Coefficient of variation (%)
100-SW (g)	7,23	15,43	11,09	1,89	1,37	3.43
SCR (%)	15,53	39,58	27,35	19,66	4,43	12.24
SCT (mm)	0,41	1,00	0,57	0,009	0,095	12.31
SCRe (N)	41,07	107,21	74,20	111,84	10,57	9.66

Pearson's correlation coefficients showing the relationships between the 4 traits investigated in 200 cotton genotypes are given in Table 4. When the relationships between the traits were analyzed, it was determined that 100-SW showed positive but insignificant relationship with SCT (r=0.124) and positive and significant relationship with SCRe (r=0.249**). The relationships between other traits were not statistically significant.

TABLE 4
PEARSON'S CORRELATION COEFFICIENT BETWEEN TRAITS OF 200 COTTON GENOTYPES

	SCR	SCT	SCRe
100-SW	-0.033	0.124	0.249**
SCR		-0.108	-0.063
SCT			-0.044

3.6 Principal component analysis:

Variance is decomposed into its components for the conservation and utilization of genetic diversity. Principal component analysis (PCA) simplifies complex data by transforming the number of correlated variables into a smaller number of principal components ((Said and Hefny, 2021), it is also a useful technique for revealing suitable genotypes for successful breeding strategies (Nazir et al., 2013). In this study, two of the four principal components were selected with an eigenvalue >1 (Table 5). The contribution of PC-I and PC-II to the total variability was 59.3%, indicating that there is valuable information in the first two components. PC-I contributed the most (32.34%), followed by PC-II (27.03%), PC-III (23.38%) and PC-IV (17.25%).

The scatter plot plotted according to factor scores using principal components (Figure 4) shows that cotton genotypes were distributed in all 4 regions of the plot. This situation reveals the presence of genetic variation among genotypes belonging to different clusters. The genotypes that are close to each other and in the center on the graph are similar to each other in terms of the traits examined, while the genotypes that are far from the center differ in terms of the aforementioned features. A significant genetic diversity was observed among the analyzed commercial Turkish cotton varieties revealed by PCA analysis (Elçi et al., 2014). The same graph shows that there is a close relationship between seed coat resistibility and 100-seed weight.

TABLE 5
PRINCIPAL COMPONENT ANALYSIS OF DIFFERENT TRAITS OF COTTON GENOTYPES

Variable	PCI	PCII	PCIII	PCIV
Eigen value	1.293	1.0811	0.9354	0.6901
% of total variance	32.34	27.03	23.38	17.25
Cumulative variance %	32.34	59.36	82.75	100.00
Factors loading by various characters				
100-Seed weight (g)	0.763	0.163	0.329	-0.531
Seed coat ratio (%)	-0.362	0.533	0.746	0.168
Seed coat thickness (mm)	0.356	-0.729	0.471	0.345
Seed coat resistibility (Newton)	0.673	0.487	-0.221	0.511

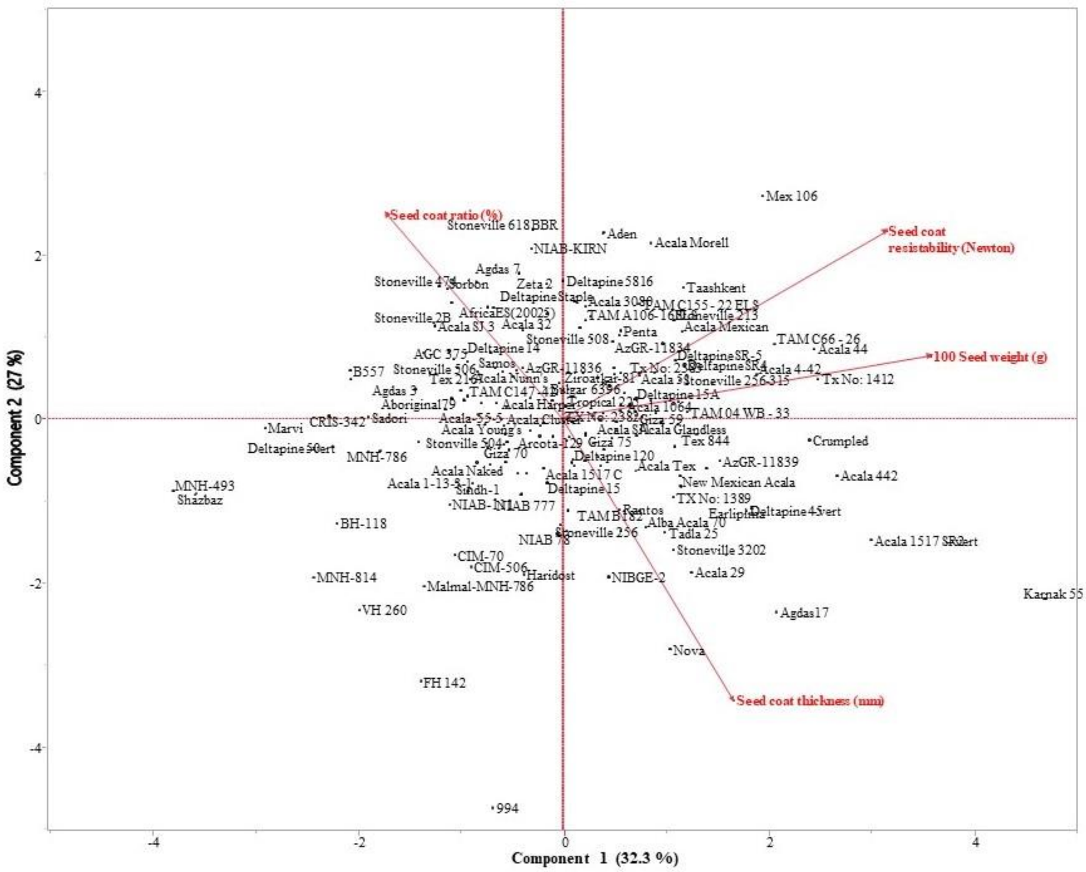

FIGURE 4: Biplot graphical display of the measured traits in 200 cotton (*Gossypium spp*.) genotypes.

3.7 Cluster analysis:

Cluster analysis showed that the 200 cotton genotypes were grouped into 5 clusters (Figure 5). This indicated the presence of disparity among the tested cotton genotypes. The cluster II, being the largest, comprised of 90 genotypes (45%) pursued by cluster V, cluster III, cluster I and cluster IV comprising 54 (27%), 28 (14%), 20 (10%) and 8 (4%) genotypes, respectively (Table 6). As seen in Table 7, cluster V displayed maximum values for all traits. Cluster analysis has been widely used to assess genetic distance, respectively genetic diversity, based on various traits among a given set of genotypes in cotton (Rathinavel, 2018; Jarwar et al., 2019; Sarwar et al., 2021; Valkova and Koleva, 2024). The dendrogram also showed the grouping of genotypes in clusters and sub-clusters (Figure 5). Based on cluster analysis the genotypes in cluster V may be utilized for incorporation of seed coat resistibility traits. The cluster IV may be further exploited in breeding programs for the development of cotton genotypes with high resistant seed coat traits along with desirable 100–seed weight and seed coat thickness.

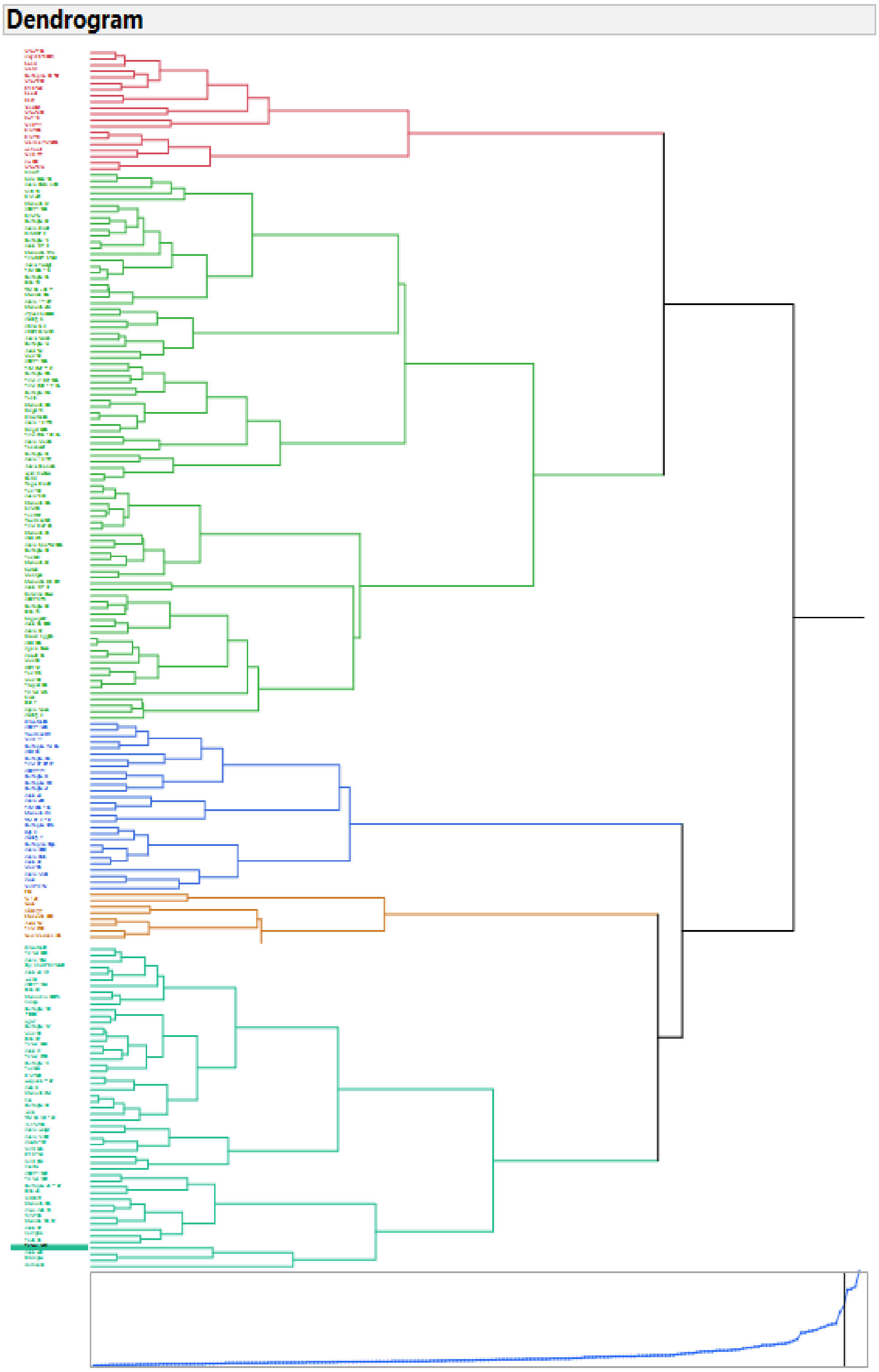

FIGURE 5: A dendrogram showing the position of genotypes in different clusters

TABLE 6
THE DISTRIBUTION OF GENOTYPES INTO 5 CLUSTERS FOR 200 COTTON GENOTYPES

Cluster	No of genotypes	Percentage (%)	Genotypes
I	20	10	1, 2, 9, 10, 11, 13, 15, 17, 23, 24, 28, 32, 33, 80, 81, 91, 92, 93, 108, 168
II	90	45	4, 6, 7, 14, 16, 21, 25, 26, 31, 34, 37, 38, 39, 40, 41, 42, 49, 50, 54, 56, 57, 58, 60, 62, 65, 69, 72, 74, 75, 76, 79, 82, 83, 84, 86, 87, 88, 89, 90, 94, 96, 98, 99, 100, 101, 104, 105, 106, 107, 109, 110, 112, 113, 114, 116, 119, 122, 123, 124, 126, 127, 131, 133, 134, 138, 146, 147, 148, 149, 150, 151, 153, 161, 169, 171, 173, 175, 176, 177, 178, 179, 181, 184, 190, 191, 192, 194, 197, 198, 199, 200
III	28	14	3, 5, 8, 29, 30, 35, 46, 52, 59, 61, 63, 66, 68, 77, 78, 97, 115, 118, 125, 137, 170, 172, 174, 180, 186, 187, 188, 195
IV	8	4	12, 27, 43, 95, 111, 117, 136, 156
V	54	27	18, 19, 20, 22, 36, 44, 45, 47, 48, 51, 53, 55, 64, 67, 70, 71, 73, 85, 102, 103, 120, 121, 128, 129, 130, 132, 135, 139, 140, 141, 142, 143, 144, 145, 152, 154, 155, 157, 158, 159, 160, 162, 163, 164, 165, 166, 167, 182, 183, 185, 189, 193, 196

TABLE 7
MEAN VALUES OF 4 CHARACTERS FOR 5 CLUSTERS OF 200 COTTON GENOTYPES.

Traits	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V
100 Seed weight	8.50	10.39	12.03	13.99	15.43
Seed coat ratio	18.80	23.30	27.80	32.90	37.80
Seed coat thickness	0.48	0.58	0.69	0.81	0.97
Seed coat resistibility	47.36	62.96	75.02	85.70	102.08

IV. CONCLUSIONS AND RECOMMENDATIONS

The analysis of variance revealed that there were sufficient variations among cotton genotypes for seed coat resistibility and its related traits. The results showed the presence of significant differences ($P \leq 0.01$) among the tested genotypes for all traits. Cluster analysis revealed that the 200 cotton genotypes were grouped into 5 clusters. The principal component analysis extracted two principal components PCA1 to PCA2 from the original data having Eigen values greater than one accounting nearly 59.3% of the total variation. Cluster analysis classified the 200 cotton genotypes into five distinct clusters contained 8-90 genotypes. This indicated the presence of diversity among the tested cotton genotypes. The relationships between traits identified through biplot analysis were consistent with Pearson's correlation coefficients, showing positive correlations between 100-seed weight and seed coat resistibility. A significant count of cotton genotypes are used in the study, and this diversity provides the opportunity to select genetic types with desirable seed coat resistibility trait for use in breeding programs.

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