The Journal of Animal & Plant Sciences, 27(1): 2017, Page: 175-185
ISSN: 1018-7081

DETERMINATION OF THE ANTHRACNOSE (*COLLETOTRICHUM LINDEMUTHIANUM* (SACC. AND MAGN.) LAMBS. SCRIB.) RESISTANCE IN SOME TURKISH BEAN GENOTYPES BY ARTIFICIAL INOCULATION AND MOLECULAR METHODS

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ABSTRACT

A total of 123 bean genotypes collected from different regions of Turkey and 7 foreign anthracnose-resistant varieties were evaluated for resistance to anthracnose disease caused by the fungal pathogen *Colletotrichum lindemuthianum* (Sacc. and Magn.) Lambs. Scrib. Analysis was conducted using artificial inoculation as well as resistance-linked molecular markers. Artificial inoculation was performed in a growth chamber using Race 55. Molecular markers were obtained from SCAR [SAS13 (950 bp, *Co-4*^{2}), SC08 (910 bp, *Co-4*), SF10 (1072 bp, *Co-10*), SZ04 (567 bp, *Co-6*)] and RAPD ($OA18_{1500}$ (1500 bp, *Co-1*^{5}) primers associated with resistant genes. Results of artificial inoculation showed that in addition to the 7 foreign varieties, 21 Turkish bean genotypes were anthracnose-resistant, while the remaining 102 Turkish genotypes were not. Moreover, results of molecular-marker screening indicated the presence of one or more amplicons associated with resistant-gene markers (*Co-4*^{2}, *Co-4*, *Co-6*, *Co-10* and Co-*1*^{5}) in the majority of resistant genotypes. Only one accession (G89) had all 5 amplicons, and 6 accessions (G19, G20, G34, G93, G97 and Jaguar) had no amplicons. The present study discovered Turkish bean germplasm of both Andean and Mesoamerican source to have a high level of resistance against anthracnose Race 55. In addition, amplicons connected with several resistance genes were found in this broad bean germplasm. Bean genotypes distinguished in the present study as anthracnose resistant could be utilized in future reproducing programs.

Keywords: Anthracnose (*Colletotrichum lindemuthianum*), artificial inoculation, common bean (*Phaseolus vulgaris* L.), disease resistance, RAPD, SCAR.

INTRODUCTION

The common bean (*Phaseolus vulgaris* L.) is an important source of protein, carbohydrates and minerals and is widely produced throughout the world (Gonçalves-Vidigal *et al*. 2013). Cultivated races include diverse bean germplasm originating from both the Andean and Mesoamerica (Logozzo *et al*. 2007; Erdinç *et al*. 2013). *Colletotrichum lindemuthianum* (Sacc. et. Magn.) Lambs. Scrib, the agent of anthracnose disease, spreads mostly in cool and moist areas and leads to major economic losses in common bean production (Nkalubo *et al*. 2007; Geetha *et al*. 2013; Madakbas *et al*. 2013a).

Anthracnose races in Turkey were first identified by Alam and Rudolph (1993), who noted the presence of this agent not only in the Central Black Sea Region, where fresh bean is most commonly produced, but in other regions of Turkey as well (Madakbas *et al*. 2011). Various studies have been conducted examining the genetic characteristics of the disease in Turkey (Madakbas and Ellialtioglu 2005; Madakbas *et al*. 2006, 2009, 2011 & 2013a,b). Improving anthracnose resistance in bean cultivars represents a challenge because of the high genetic variation of the disease agent (Balardin *et al*. 1997; Sicard *et al*. 1997a, b; Young *et al*. 1998; Sharma *et al*. 1999; Melotto and Kelly 2001; Ansari *et al*. 2004; Talamini *et al*. 2006; Bardas *et al*. 2007; Damasceno e Silva *et al*. 2007; Ishikawa *et al*. 2008; Pereira *et al*. 2010).

To date, a number of anthracnose-resistant genes found in common bean cultivars have been characterized. These include genes from cultivars of both Andean (*Co-1*, *Co-1*^{2}, *Co-1*^{3}, *Co-1*^{4}, *Co*-1^5, *Co-12*, *Co-13*, *Co-14*, *Co-15*) and Mesoamerican (*Co-2*, *Co-3*, *Co-3*^{2}, *Co-4*, *Co-4*^{2}, *Co-4*^{3}, *Co-5*, *Co-6*, *Co-7*, *co-8*, *Co-9*, *Co-10*, *Co-11*) origins; moreover, with the exception of *Co-8*, all the aforementioned genes are dominant genes (Kelly and Vallejo 2004; Gonçalves-Vidigal *et al*. 2009; Gonçalves *et al*. 2010).

Molecular markers have been used in molecular marker assisted selection studies for disease resistance breeding programs in plants about more than a decade (Sensoy *et al*, 2007). Due to the inefficient utilization of artificial inoculation in anthracnose resistance levels of bean germplasm evaluation (Mesquita *et al*. 1998), molecular markers have been developed as a more

reliable method of determining anthracnose resistance levels of bean germplasm (Young *et al*. 1998; Alzate-Marin *et al*. 2003; Queiroz *et al*. 2004; Gonçalves-Vidigal and Kelly 2006).

In Turkey, where anthracnose presents a serious problem for bean production, identifying bean germplasm that is resistant to this pathogen is crucial for future breeding programs. Therefore, this study aimed to determine anthracnose resistance levels in 123 Turkish bean genotypes as well as 7 foreign genotypes using both artificial inoculation and molecular markers.

MATERIALS AND METHODS

A total of 122 common bean (*P. vulgaris* L.) accessions, 1 runner bean (*P. coccineus* L.) accession (G121) (Table 1) and 7 known anthracnose-resistant foreign bean varieties [Michigan State University Varieties: Isles, Blackhawk, Chinook, Jaguar, Phantom, Newport and Mackinac (http://bean.css.msu.edu/Variety.cfm)] were analyzed for anthracnose resistance using artificial inoculation and molecular markers. Bean seeds were sown in pots containing a 1:1 mixture of peat:perlite and grown in a growth chamber at 20±2ºC and 100% humidity with a 12 h photoperiod, with 3 replicates of 10 plants per pot per accession in a completely randomized experimental design.

Artificial inoculation: Anthracnose Race 55 *C. lindemuthianum* was used for artificial inoculation. Race 55 was incubated in petri dishes containing Potato Dextrose Agar (PDA) at 25ºC for 14 days. Spore suspensions were prepared by scraping spores with a brush, adding 10 ml of distilled water and filtering through cheesecloth. Fungi spore concentrations of $1.2x10^6$ were established using a heamocytometer, and Tween-20 was added (10 drops per 100 ml) to the prepared suspension (Madakbas 2007).

After reaching the fully developed trifoliate leaf stage (about 14 days after germination), bean seedlings were spray-inoculated with the Race 55 spore suspension and placed in a growth chamber at 20±2ºC and 100% humidity with a 12 h photoperiod (Gonçalves-Vidigal and Kelly 2006). Fourteen days after inoculation, disease reaction was scored visually using a 0-9 scale, with scores of 0-3 considered to indicate resistance and scores of 4-9 to indicate susceptibility (Alzate-Marin *et al*. 2001; Madakbaş *et al*. 2013a). After completing artificial inoculation procedures, anthracnose reagent was collected from necrotic regions of diseased plants, re-isolated in PDA medium and examined under a microscope for verification.

SCAR and RAPD Amplification: Genomic DNA was isolated according to a modified CTAB procedure (Doyle and Doyle 1987). DNA quantification was performed using a Biotech UV 1101 photometer. Bean genotypes were analyzed using SCAR [SW12 (*Co-3/Co-9*, 700 bp), SC08 (*Co-4*, 910 bp), SAS13 (*Co-4*^{2}, 950 bp), SAB3 (*Co-5*, 400 bp), SZ04 (*Co-6*, 567 bp), SZ20 (*Co-6*, 845 bp), SB12 (*Co-9*, 350 bp), SF10 (1072 bp)] (BIC, 2009) and RAPD [$OA18_{1500}$ (1500 bp)] (Gonçalves-Vidigal and Kelly 2006) primers. PCR amplification was performed in a 20 µl reaction system containing 30 ng genomic DNA, 1.5 mM $MgCl_2$, 0.2 µM primer, 0.2 mM each dNTPs, 1x PCR buffer (100 mM Tris-HCl, pH 8.8, 50 mM KCl) and 1 unit *Taq* DNA polymerase. PCR was performed separately for each SCAR (BIC 2009) and RAPD (Gonçalves-Vidigal and Kelly 2006) primer. Amplification products were fractionated on 15 g/l agarose gel in 1X TAE buffer at 90 V for 2 h and markers associated with resistance genes identified according to band width.

RESULTS AND DISCUSSION

Artificial inoculation: The results of artificial inoculation indicating the classification of bean accessions according to their reaction to anthracnose Race 55. While the majority of accessions tested were classified as susceptible to anthracnose Race 55, 20 Turkish common bean genotypes (G5, G19, G29, G38, G66, G73, G75, G76, G77, G81, G88, G91, G92, G93, G95, G106, G107, G114, G119, and G155), 1 Turkish runner bean genotype (G121) and 7 foreign known resistant varieties (Michigan State University Varieties: Isles, Blackhawk, Chinook, Jaguar, Phantom, Newport and Mackinac) were classified as resistant to anthracnose Race 55 (Table 2).

Molecular marker results: The results of molecular marker analysis. Nine SCAR primers [SW12 (*Co-3/Co-9*, 700 bp), SC08 (*Co-4*, 910 bp), SAS13 (*Co-4*^{2}, 950 bp), SAB3 (*Co-5*, 400 bp), SZ04 (*Co-6*, 567 bp) SZ20 (*Co-6*, 845 bp), SB12 (*Co-9*, 350 bp), SF10 (1072 bp) (BIC, 2009)] and 1 RAPD primer [$OA18_{1500}$ (1500 bp)] (Gonçalves-Vidigal and Kelly, 2006) were used to analyze bean genotypes. No amplification was found by the SW12, SAB3, SZ20 and SB12 SCAR primers or by the $OA18_{1500}$ RAPD marker for *Co-1*$^{5.}$ Amplicons linked to gene *Co-4*^{2}, which were identified in 110 genotypes, were found to be the most widespread among Turkish bean accessions, followed by amplicons for *Co-4* (92 genotypes), *Co-10* (27 genotypes), *Co-6* (74 genotypes) and *Co-1*^{5} (6 genotypes) (Table 3).

In 5 Turkish accessions (G19, G20, G34, G93, G97), no molecular markers linked to resistance genes could be identified; in 13 accessions (G2, G5, G9, G10, G15, G21, G33, G35, G70, G75 G110, G116, G117), only the SAS 13 marker for *Co-4*^{2} was identified; in 5 accessions (G14, G25, G32, G80, G128), only the SC08 SCAR marker for *Co-4* was identified; in 2 accessions (G13 and G27), only the SZ04 marker for *Co-6* was

identified, and in 1 accession (G73), only the SF10 marker for *Co-10* was identified.

G89 had all the observed amplicons of the studied markers associated with anthracnose-resistance genes. Moreover, the accessions G4, G8, G18, G42, G52, G64, G118, G121, G122, G127, G129, and G130 had all the observed amplicons of the markers associated with *Co-4*, *Co-4*^{2}, *Co-6* and *Co-10* genes.

Among the Turkish bean varieties found to be resistant, 5 had amplicons for the *Co-4*^{2} marker, 3 for the *Co-6* marker, 2 for the *Co-4* marker, 2 for the *Co-10* marker and 1 for the *Co-1*^{5} marker. In contrast, no amplicons for any of the studied markers were found in one of the known-resistant varieties (Jaguar).

Turkey is a leading green-bean producer, accounting for approximately 3% of production worldwide. Moreover, variations in climate and geography that include a number of different ecogeographic regions suitable for bean production, along with the preservation of diverse bean genotypes by farmers and seed exchange among regions, has meant that Turkey possesses significant genetic diversity for the common bean (Ekincialp and Sensoy 2013; Erdinc *et al.* 2013). At the same time, anthracnose, a bean disease caused by the fungal pathogen *Colletotrichum lindemuthianum* (Sacc. and Magn.) Lambs. Scrib.), has also spread throughout the country. Turkey's Central Black Sea Region has the most appropriate ecological factors to support anthracnose disease, and some of these factors are also present in certain parts of the Central Anatolian Region (Madakbaş *et al*. 2013a, b). Anthracnose races have been isolated and identified from both these regions. Race 55, the isolate used in this study, was obtained from the province of Samsun (Madakbaş *et al*. 2013a), which is responsible for the majority of fresh bean cultivation in Turkey (Anonymous 2012).

Artificial inoculation showed 20 local common bean genotypes and 1 local scarlet runner bean genotypes to be resistant to anthracnose Race 55 and 102 common bean genotypes to be susceptible to the disease. Moreover, no symptoms of the disease were observed on the 7 known anthracnose-resistant foreign common-bean varieties, including the Isles, Blackhawk and Newport varieties, which have been previously shown to have high levels of resistance to both Andean and Mesoamerican anthracnose races (Balardin and Kelly 1998; del Rio *et al*. 2003).

Combating anthracnose and developing resistant varieties is complicated by the pathogen's large number of races. At the same time, the multitude of races prompts variations in plant response to the disease. A study by Vidigal Filho *et al*. (2007) found a high genetic diversity in the response of 26 bean genotypes to 3 Andean races (7, 19 and 55) and 9 Mesoamerican races (9, 31, 65, 69, 73, 81, 89, 95 and 453), with reported Pathogenicity Index (PI) values, i.e. the ratio of susceptible genotypes to total genotypes, of 89 for Andean bean genotypes and 6 for Mesoamerican genotypes. Moreover, about 65% of bean genotypes had developed some degree of resistance to anthracnose Andean Race 55. By comparison, the present study found an overall resistance rate of 82.9%, with PI values of 98.08 for Andean bean genotypes and 71.83 for Mesoamerican bean genotypes. In this context, the anthracnose Race 55 had the largest effect on Andean bean genotypes, and it had also a high rate of infection in Mesoamerican bean genotypes. Even so, Mesoamerican bean genotypes were found to have relatively high levels of resistance against anthracnose Race 55. Various studies have shown Andean Race 55 capable of infecting genotypes from both Andean and Mesoamerican bean gene pools (Balardin *et al*. 1997; Madakbaş *et al*. 2013a). Balardin and Kelly (1998) found PI values to be higher for Andean anthracnose races than for Mesoamerican anthracnose races. The authors also reported Andean bean genotypes to have higher PI values than Mesoamerican bean genotypes against Race 55. The differences in resistance levels observed in connection with bean genotype and pathogen race suggest that Mesoamerican anthracnose races could play important roles in breeding programs for Andean bean genotypes, and, conversely, Andean anthracnose races could play important roles in Mesoamerican bean-breeding programs.

Bigirimana and Höfte (2001) reported that results of artificial inoculation for anthracnose resistance varied among bean plants according to plant-development stage. Various factors including number of spores and environment and incubation conditions have also been shown to affect the results of artificial inoculation used to test anthracnose resistance (Mesquita *et al*. 1998). For this reason, researchers have looked into the molecular methods for determining resistance. Numerous studies (Mendez-Vigo *et al*. 2005; de Melo *et al*. 2005; Gonçalves-Vidigal and Kelly 2006; Dongfang *et al*. 2007; Rodriguez-Suarez *et al*. 2007; Ragagnin *et al*. 2009) reported RAPD and SCAR primers to bind to genes resistant to anthracnose. Associations have been reported between the following markers and genes: $OA18_{1500}$ (*Co-1*^{5})- 1.2 cM; SC08 (*Co-4*)- 7.8 cM; SAS13 (*Co-4*^{2})- 0.01 cM; SZ04 (*Co-6*)- 2.9 cM; and SF10 (*Co-10*)-12.3 cM (Young *et al*. 1998; Alzate-Marin *et al*. 2003; Queiroz *et al*. 2004; Gonçalves-Vidigal and Kelly 2006).

In the present study, resistant bean genotypes were most likely to carry the amplicons associated with the genes *Co-4*, *Co-4*^{2} and *Co-6*, although the amplicon associated with the gene *Co-10* was also found in some resistant Turkish genotypes of Mesoamerican origin and the amplicon associated with the gene *Co-1*^{5} in some resistant Turkish genotypes of Andean origin as well as the known anthracnose-resistant variety Chinook, also of Andean origin. Gonçalves-Vidigal *et al*. (2009)

emphasized the importance of the *Co-1* gene and its alleles as a resource for improving anthracnose resistance in Mesoamerican bean varieties and resistance genes of Mesoamerican origin, such as *Co-2*, *Co-3*, *Co-4*, *Co-4^2* and *Co-6*, for ensuring anthracnose resistance in Andean bean genotypes. A study by Madakbaş *et al*. (2009) examining SCAR markers for anthracnose resistance in 53 green bean genotypes identified markers associated with the genes *Co-1*, *Co-2*, *Co-4*, *Co-4^2*, and *co-8*; the authors reported that all anthracnose-resistant green bean genotypes had the markers associated with the genes *Co-2*, *Co-4*, and *Co-4^2*, whereas the markers associated with the gene *Co-1* presented in only the bean genotype KO and cv. Yalova-5. Using the SAS13 primer, Dongfang *et al*. (2008) found the presence of markers associated with the gene *Co-4^2* to be present in a number of bean genotypes.

Several studies have also reported gene pyramiding, a method that transfers multiple disease-resistant genes into a single cultivar, to be effective in increasing anthracnose resistance (Geffroy *et al*. 1998; Alzate-Marin *et al*. 2001; Madakbaş and Ellialtioğlu 2005; Ragagnin *et al*. 2009). In this regard, many researchers have pointed out the value of the genes *Co-1* and *Co-4* (Madakbaş *et al*. 2013 a, b). In the present study, the vast majority of resistant bean genotypes were shown to have the amplicons associated with the gene *Co-4^2*, suggesting that these genotypes could play important roles in transferring anthracnose-resistance to bean genotypes of Andean origin.

Four of the SCAR primers used in the present study were able to successfully detect amplicons responsible for anthracnose resistance [SC08 (*Co-4*, 910 bp), SAS13 (*Co-4^2*, 950 bp), SZ04 (*Co-6*, 567 bp), and SF10 (1072 bp)]. Geetha *et al*. (2013) also reported that some of these markers were tightly linked to the genes associated with anthracnose resistance and could be used effectively in their detection. In addition, Gonçalves-Vidigal and Kelly (2006) reported the RAPD marker $OA18_{1500}$ to be tightly linked to and thus important in detecting the *Co-1^5* gene.

Table 1. Some distinguished traits of the common bean accessions used in the present study.

Acc. #	Grow Habit	Seed color	Pods length (cm)	# of pods per plant	100 seed weight (g)	Acc. #	Grow Habit	Seed color	Pods length (cm)	# of pods per plant	100 seed weight (g)	Acc. #	Grow Habit	Seed color	Pods length (cm)	# of pods per plant	100 seed weight (g)
G1	Pole	White	13.22	16.50	36.00	G43	Pole	Black	11.79	26.67	31.87	G95	Bush	Black	9.34	31.00	18.73
G2	Pole	White	10.43	26.00	25.10	G45	Pole	White	13.09	23.00	42.60	G96	Pole	Brown-White	13.18	10.00	40.35
G3	Pole	White	12.31	15.25	28.45	G46	Pole	White	14.32	23.67	54.65	G97	Pole	White	21.75	16.50	39.75
G4	Pole	White	12.32	20.33	35.15	G47	Pole	White	14.80	21.67	48.15	G98	Bush	Black	11.67	18.75	33.20
G5	Pole	Brown-Dark Brown	9.93	35.33	27.27	G48	Pole	White	14.88	7.00	35.30	G99	Pole	White	19.44	11.50	41.31
G6	Pole	Black	11.43	32.34	31.13	G49	Pole	White-Brown-Violet	12.03	15.34	43.00	G100	Pole	Brown-Red	11.54	15.17	59.83
G7	Pole	White	12.17	55.50	29.97	G50	Pole	White	14.60	16.00	44.98	G101	Pole	White	14.13	20.94	36.80
G8	Pole	Brown-Dark Brown	12.71	23.75	50.30	G52	Pole	White	11.64	38.00	36.25	G102	Pole	White	21.78	11.67	42.23
G9	Pole	White	9.68	28.25	25.00	G54	Pole	Cream-Red	13.28	20.22	40.90	G103	Bush	Brown	10.41	11.67	37.89
G10	Pole	White	11.42	34.50	31.75	G55	Pole	Cream-Violet	15.02	35.50	55.05	G104	Bush	Brown	10.69	16.50	18.61
G11	Pole	White	13.24	14.22	33.10	G56	Pole	White	11.38	15.67	51.59	G105	Pole	Brown-Dark Brown	9.31	22.17	44.80
G12	Pole	White	12.14	17.06	30.55	G57	Pole	Brown-Dark Brown	12.18	14.67	46.90	G106	Bush	Black	9.42	20.33	18.10
G13	Pole	White	9.63	44.50	26.80	G58	Pole	Cream-Red	13.26	16.50	36.00	G107	Bush	Brown	8.70	15.00	27.78
G14	Pole	White	10.83	10.83	40.73	G59	Pole	Brown	14.54	18.75	41.55	G108	Pole	Cream-Red	10.03	20.00	42.35
G15	Pole	Black	12.35	20.00	31.05	G60	Pole	Brown-Violet	13.19	12.00	41.47	G109	Pole	Brown-Dark Brown	13.90	8.94	52.50
G16	Pole	White	13.05	78.00	45.90	G62	Pole	Cream-Red	9.84	20.17	33.53	G110	Pole	Brown	11.66	23.33	25.90
G17	Pole	White	10.37	48.00	26.75	G63	Pole	Cream-Red	10.42	18.50	31.15	G111	Pole	Brown-Dark Brown	14.71	13.00	52.60
G18	Pole	White	13.19	13.33	45.00	G64	Pole	White	11.81	22.50	34.30	G112	Bush	Black	13.91	22.50	35.33
G19	Pole	White	11.42	27.83	15.83	G65	Pole	White	13.78	26.33	37.05	G113	Pole	Red-White	10.79	21.00	43.48
G20	Pole	White	10.30	12.94	29.80	G66	Pole	Black	8.82	10.25	44.80	G114	Bush	Black	9.37	35.00	17.13
G21	Pole	White	9.89	16.40	26.86	G70	Bush	Black	11.86	32.17	32.54	G115	Pole	White	13.60	13.00	27.40
G22	Pole	White	7.58	5.00	20.55	G71	Bush	White	8.44	11.00	47.20	G116	Pole	White	9.81	4.67	24.15
G23	Pole	White	12.83	29.09	33.05	G72	Bush	Black	10.07	16.33	33.06	G117	Pole	White	11.91	21.00	22.96
G24	Pole	White	12.90	38.39	26.03	G73	Bush	White	13.32	32.33	23.50	G118	Pole	White	10.98	28.75	40.13
G25	Pole	White	11.44	32.17	44.50	G74	Bush	White	15.57	20.83	48.70	G119	Pole	White	13.14	10.50	29.54
G26	Pole	Brown	9.12	40.50	23.55	G75	Bush	White	10.33	18.50	31.02	G120	Bush	Brown	12.88	21.00	39.63
G27	Pole	White	11.15	25.38	27.30	G76	Bush	White	12.61	27.00	26.60	G121	Pole	White	11.38	17.22	88.73
G28	Pole	White	9.46	11.00	37.83	G77	Bush	White	13.22	12.00	26.70	G122	Pole	White	21.90	13.00	43.39
G29	Pole	White	10.93	23.67	18.83	G78	Bush	White	11.43	20.00	35.56	G123	Pole	Cream-Red	16.99	8.00	65.69
G30	Pole	Red	16.84	9.00	44.20	G79	Bush	White	11.72	29.50	48.28	G124	Pole	Cream-Red	14.95	14.50	54.51
G32	Pole	Brown-	17.31	12.67	62.68	G80	Bush	Brown	17.37	18.50	44.59	G125	Bush	Cream-Red	12.05	10.00	48.35

G33	Pole	Black Brown-Dark Brown	13.39	30.00	31.56	G81	Bush	Black	9.04	37.67	16.93	G127	Pole	White	16.29	5.00	44.15
G34	Pole	Red	10.63	22.39	30.15	G82	Bush	Light red	12.78	18.00	46.57	G128	Bush	Brown	20.36	21.83	42.45
G35	Pole	Brown-Dark Brown	13.56	23.83	34.93	G84	Bush	Light brown	15.06	25.23	41.50	G129	Pole	White	11.50	18.33	42.15
G36	Pole	Brown-White	12.82	11.39	50.10	G88	Bush	White	14.19	18.00	17.79	G130	Bush	Cream-Red	13.82	23.50	47.00
G37	Pole	Brown-Dark Brown	13.72	15.25	58.60	G89	Bush	Brown-Red	12.07	11.33	40.38	G131	Pole	Cream-Red	14.02	20.75	50.60
G38	Pole	Brown	18.01	8.45	33.35	G90	Bush	Brown	12.28	24.00	41.30	G151	Pole	Brown-Violet	14.47	24.00	54.97
G39	Pole	Black	10.89	7.33	38.73	G91	Bush	White	13.45	5.83	38.21	G152	Pole	Brown-Violet	11.27	18.67	53.50
G40	Pole	Brown-Dark Brown	13.93	14.17	55.10	G92	Bush	White	13.95	15.17	30.19	G153	Pole	Brown-Dark Brown	13.75	24.00	40.40
G41	Pole	Cream-Violet	10.81	22.39	35.80	G93	Bush	Black	8.93	41.44	17.57	G154	Pole	Brown	18.09	13.67	39.65
G42	Pole	White	11.62	19.94	23.05	G94	Bush	Black	9.33	19.00	34.51	G155	Pole	Black	11.43	13.00	52.60

Table 2. Reactions of common bean accessions based on 0-9 scale in artificial inoculation method for race 55

Ac.#	Org.*	Scale value	Ac.#	Org.	Scale value	Ac.#	Org.	Scale value	Ac.#	Org.	Scale value
G1	MA	7.26	G35	MA	6.54	*G75*	*MA*	*0.00*	G112	MA	3.85
G2	MA	6.27	G36	A	8.20	*G76*	*MA*	*0.17*	G113	A	8.33
G3	MA	6.02	G37	A	7.30	*G77*	*MA*	*0.11*	*G114*	*MA*	*1.29*
G4	MA	8.22	*G38*	*MA*	*1.46*	G78	MA	8.38	G115	MA	5.02
G5	*MA*	*2.77*	G39	MA	7.72	G79	A	8.63	G116	MA	5.34
G6	MA	7.40	G40	A	8.39	G80	A	8.37	G117	MA	5.06
G7	MA	7.21	G41	MA	5.77	*G81*	*MA*	*0.81*	G118	A	5.34
G8	A	7.18	G42	MA	6.94	G82	A	6.05	*G119*	*MA*	*3.11*
G9	MA	7.71	G43	MA	6.19	G84	A	5.56	G120	MA	6.27
G10	MA	6.16	G45	MA	6.90	*G88*	*MA*	*0.00*	*G121*	*A*	*0.00*
G11	MA	6.03	G46	A	6.19	G89	A	7.25	G122	A	6.04
G12	MA	6.71	G47	A	6.06	G90	A	5.89	G123	A	8.89
G13	MA	6.60	G48	MA	7.90	*G91*	*MA*	*0.20*	G124	A	5.04
G14	A	8.74	G49	A	8.37	*G92*	*MA*	*0.20*	G125	A	8.69
G15	MA	7.07	G50	A	5.71	*G93*	*MA*	*0.90*	G127	MA	5.55

G16	A	7.39	G52	MA	4.27	G94	MA	6.96	G128	A	8.67
G17	MA	5.50	G54	A	7.20	*G95*	*MA*	*0.69*	G129	A	6.44
G18	A	8.15	G55	A	8.93	G96	A	8.08	G130	A	7.67
G19	*MA*	*0.15*	G56	A	6.75	G97	MA	5.97	G131	A	8.38
G20	MA	7.46	G57	A	8.37	G98	MA	7.76	G151	A	5.99
G21	MA	4.64	G58	A	9.00	G99	A	5.50	G152	A	6.86
G22	MA	6.76	G59	A	7.82	G100	A	7.59	G153	A	8.03
G23	MA	4.39	G60	A	8.63	G101	MA	7.27	G154	A	7.48
G24	MA	3.82	G62	MA	8.38	G102	A	5.90	*G155*	*MA*	*1.52*
G25	A	5.73	G63	MA	8.00	G103	MA	7.89	*Isles*	*MA*	*0.00*
G26	MA	7.75	G64	MA	5.07	G104	MA	6.40	*Black Hawk*	*MA*	*0.00*
G27	MA	6.85	G65	MA	6.12	G105	A	7.96	*Chinook*	*A*	*0.00*
G28	MA	7.43	*G66*	*A*	*2.71*	*G106*	*MA*	*0.51*	*Jaguar*	*MA*	*0.00*
G29	*MA*	*0.00*	G70	MA	8.00	*G107*	*MA*	*1.72*	*Phantom*	*MA*	*0.00*
G30	A	8.02	G71	A	8.50	G108	A	8.51	*Newport*	*MA*	*0.33*
G32	A	6.08	G72	MA	8.63	G109	A	8.41	*Mackinac*	*MA*	*0.00*
G33	MA	6.47	*G73*	*MA*	*0.00*	G110	MA	6.19			
G34	MA	8.71	G74	A	5.92	G111	A	6.86			

*Origin: MA: Mesoamerican, A: Andean

Table 3. Specific marker amplifications and gene linked to marker in common bean accessions.

Ac.#	Marker	Gene	Ac.#	Marker	Gene	Ac.#	Marker	Gene
G1	SAS13, SC08	Co-4^2, Co-4	G47	SAS13, SC08, SZ04	Co-4^2, Co-4, Co-6	G101	SAS13, SC08, SZ04	Co-4^2, Co-4, Co-6
G2	SAS13	Co-4^2	G48	SAS13, SC08	Co-4^2, Co-4	G102	SAS13, SC08, SF10	Co-4^2, Co-4, Co-10
G3	SAS13, SC08, SZ04	Co-4^2, Co-4, Co-6	G49	SAS13, SC08, SZ04	Co-4^2, Co-4, Co-6	G103	SAS13, SC08	Co-4^2, Co-4
G4	SAS13, SC08, SF10, SZ04	Co-4^2, Co-4, Co-10, Co-6	G50	SAS13, SC08, SZ04	Co-4^2, Co-4, Co-6	G104	SAS13, SC08	Co-4^2, Co-4
G5	SAS13	Co-4^2	G52	SAS13, SC08, SF10, SZ04	Co-4^2, Co-4, Co-10, Co-6	G105	SAS13, SC08, SZ04	Co-4^2, Co-4, Co-6
G6	SAS13, SC08, SF10	Co-4^2, Co-4, Co-10	G54	SAS13, SC08, SZ04, $OA18_{1500}$	Co-4^2, Co-4, Co-6, Co-1^5	G106	SAS13, SZ04	Co-4^2, Co-6
G7	SAS13, SC08	Co-4^2, Co-4	G55	SAS13, SC08, SZ04	Co-4^2, Co-4, Co-6	G107	SAS13, SC08, SF10	Co-4^2, Co-4, Co-10
G8	SAS13, SC08, SF10, SZ04	Co-4^2, Co-4, Co-10, Co-6	G56	SAS13, SC08, SZ04	Co-4^2, Co-4, Co-6	G108	SAS13, SC08, SZ04	Co-4^2, Co-4, Co-6
G9	SAS13	Co-4^2	G57	SAS13, SC08, SZ04, $OA18_{1500}$	Co-4^2, Co-4, Co-6, Co-1^5	G109	SAS13, SZ04	Co-4^2, Co-6
G10	SAS13	Co-4^2	G58	SAS13, SC08, SZ04	Co-4^2, Co-4, Co-6	G110	SAS13	Co-4^2
G11	SAS13, SF10	Co-4^2, Co-10	G59	SAS13, SC08, SZ04	Co-4^2, Co-4, Co-6	G111	SAS13, SC08, SZ04	Co-4^2, Co-4, Co-6
G12	SAS13, SF10, SZ04	Co-4^2, Co-10, Co-6	G60	SAS13, SC08, SZ04	Co-4^2, Co-4, Co-6	G112	SAS13, SC08, SZ04	Co-4^2, Co-4, Co-6
G13	SZ04	Co-6	G62	SAS13, SC08, SZ04	Co-4^2, Co-4, Co-6	G113	SAS13, SC08, SZ04	Co-4^2, Co-4, Co-6
G14	SC08	Co-4	G63	SAS13, SC08, SZ04	Co-4^2, Co-4, Co-6	G114	SAS13, SC08, SZ04	Co-4^2, Co-4, Co-6

G15	SAS13	Co-4[2]	G64	SAS13, SC08, SF10, SZ04	Co-4[2], Co-4, Co-10, Co-6	G115	SAS13, SC08	Co-4[2], Co-4
G16	SAS13, SC08	Co-4[2], Co-4	G65	SAS13, SC08, SZ04	Co-4[2], Co-4, Co-6	G116	SAS13	Co-4[2]
G17	SAS13, SC08	Co-4[2], Co-4	G66	SAS13, SC08, SZ04	Co-4[2], Co-4, Co-6	G117	SAS13	Co-4[2]
G18	SAS13, SC08, SF10, SZ04	Co-4[2], Co-4, Co-10, Co-6	G70	SAS13	Co-4[2]	G118	SAS13, SC08, SF10, SZ04	Co-4[2], Co-4, Co-10, Co-6
G19	-	-	G71	SAS13, SC08	Co-4[2], Co-4	G119	SAS13, SC08	Co-4[2], Co-4
G20	-	-	G72	SAS13, SZ04	Co-4[2], Co-6	G120	SAS13, SC08, SZ04	Co-4[2], Co-4, Co-6
G21	SAS13	Co-4[2]	G73	SF10	Co-10	G121	SAS13, SC08, SF10, SZ04	Co-4[2], Co-4, Co-10, Co-6
G22	SAS13, SC08	Co-4[2], Co-4	G74	SAS13, SC08, SZ04, $OA18_{1500}$	Co-4[2], Co-4, Co-6, Co-1[5]	G122	SAS13, SC08, SF10, SZ04	Co-4[2], Co-4, Co-10, Co-6
G23	SAS13, SZ04	Co-4[2], Co-6	G75	SAS13	Co-4[2]	G123	SAS13, SC08, SF10	Co-4[2], Co-4, Co-10
G24	SAS13, SC08, SF10	Co-4[2], Co-4, Co-10	G76	SAS13, SC08	Co-4[2], Co-4	G124	SAS13, SC08, SF10, SZ04	Co-4[2], Co-4, Co-10, Co-6
G25	SC08	Co-4	G77	SAS13, SC08	Co-4[2], Co-4	G125	SAS13, SC08, SZ04	Co-4[2], Co-4, Co-6
G26	SAS13, SC08, SF10	Co-4[2], Co-4, Co-10	G78	SAS13, SC08, SZ04	Co-4[2], Co-4, Co-6	G127	SAS13, SC08, SF10, SZ04	Co-4[2], Co-4, Co-10, Co-6
G27	SZ04	Co-6	G79	SAS13, SC08, SZ04, $OA18_{1500}$	Co-4[2], Co-4, Co-6, Co-1[5]	G128	SC08	Co-4
G28	SAS13, SC08, SZ04	Co-4[2], Co-4, Co-6	G80	SC08	Co-4	G129	SAS13, SC08, SF10, SZ04	Co-4[2], Co-4, Co-10, Co-6
G29	SAS13, SF10, SZ04	Co-4[2], Co-10, Co-6	G81	SAS13, SZ04	Co-4[2], Co-6	G130	SAS13, SC08, SF10, SZ04	Co-4[2], Co-4, Co-10, Co-6
G30	SAS13, SC08, SZ04	Co-4[2], Co-4, Co-6	G82	SAS13, SC08, SZ04	Co-4[2], Co-4, Co-6	G131	SAS13, SC08, SZ04	Co-4[2], Co-4, Co-6
G32	SC08	Co-4	G84	SAS13, SC08, SZ04	Co-4[2], Co-4, Co-6	G151	SAS13, SC08, SZ04	Co-4[2], Co-4, Co-6
G33	SAS13	Co-4[2]	G88	SAS13, SC08, SZ04	Co-4[2], Co-4, Co-6	G152	SAS13, SC08, SZ04	Co-4[2], Co-4, Co-6
G34	-	-	G89	SAS13, SC08, SF10, SZ04, $OA18_{1500}$	Co-4[2], Co-4, Co-10, Co-6, Co-1[5]	G153	SAS13, SC08, SZ04	Co-4[2], Co-4, Co-6
G35	SAS13	Co-4[2]	G90	SAS13, SC08, SZ04, $OA18_{1500}$	Co-4[2], Co-4, Co-6, Co-1[5]	G154	SAS13, SC08, SZ04	Co-4[2], Co-4, Co-6
G36	SAS13, SC08, SZ04	Co-4[2], Co-4, Co-6	G91	SAS13, SC08	Co-4[2], Co-4	G155	SAS13, SC08, SZ04	Co-4[2], Co-4, Co-6
G37	SAS13, SC08, SZ04	Co-4[2], Co-4, Co-6	G92	SAS13, SC08	Co-4[2], Co-4	Isles	SC08	Co-4
G38	SAS13, SC08, SZ04	Co-4[2], Co-4, Co-6	G93	-	-	Black Hawk	SAS13	Co-4[2]
G39	SAS13, SC08, SZ04	Co-4[2], Co-4, Co-6	G94	SAS13, SC08, SZ04	Co-4[2], Co-4, Co-6	Chinook	SAS13, SC08, SZ04, $OA18_{1500}$	Co-4[2], Co-4, Co-6, Co-1[5]
G40	SAS13, SC08, SZ04	Co-4[2], Co-4, Co-6	G95	SAS13, SC08, SZ04	Co-4[2], Co-4, Co-6	Jaguar	-	-
G41	SAS13, SC08, SZ04	Co-4[2], Co-4, Co-6	G96	SAS13, SC08, SZ04	Co-4[2], Co-4, Co-6	Phantom	SAS13, SF10	Co-4[2], Co-10
G42	SAS13, SC08, SF10, SZ04	Co-4[2], Co-4, Co-10, Co-6	G97	-	-	Newport	SAS13, SZ04	Co-4[2], Co-6
G43	SAS13, SF10,	Co-4[2], Co-10	G98	SAS13, SC08, SZ04	Co-4[2], Co-4, Co-6	Mackinac	SAS13, SF10, SZ04	Co-4[2], Co-10, Co-6
G45	SAS13, SC08, SZ04	Co-4[2], Co-4, Co-6	G99	SAS13, SF10	Co-4[2], Co-10,			
G46	SAS13, SC08, SZ04	Co-4[2], Co-4, Co-6	G100	SAS13, SC08, SF10	Co-4[2], Co-4, Co-10,			

Conclusion: In conclusion, the vast number of pathogen races is one factor limiting the fight against anthracnose disease, making identification of the source of disease resistance an important element of cultivar-improvement efforts. Despite Turkey's importance as a bean-producing country and the highly diverse bean germplasm it possesses, studies on bean anthracnose in Turkey are limited. The present study found Turkish bean germplasm of both Andean and Mesoamerican origin to possess a high degree of resistance against anthracnose Race 55. Moreover, amplicons associated with several resistance genes were found in this extensive bean germplasm. Bean genotypes identified in the present study as anthracnose resistant could be employed in future breeding programs utilizing gene pyramiding to increase anthracnose resistance.

Acknowledgements: This study was a part of PhD thesis of the first author and was funded by the project # 2008-FBE-D002 of Scientific Research Projects Council of Yuzuncu Yil University. We would like to thank Dr. J. Kelly and Dr. S. Y. Madakbaş for their material supply.

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