TÜBİTAK

Turkish Journal of Agriculture and Forestry

http://journals.tubitak.gov.tr/agriculture/

Research Article

Turk J Agric For
(2015) 39: 212-226
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doi:10.3906/tar-1406-3

Moth bean germplasm screening against yellow mosaic virus, II. Development of moth bean high-yielding seed and fodder cultivars

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Received: 01.06.2014 • **Accepted:** 29.10.2014 • **Published Online:** 06.04.2015 • **Printed:** 30.04.2015

Abstract: Moth bean [*Vigna aconitifolia* (Jacq.) Marechal] susceptibility to yellow mosaic virus (YMV) purged the crop from the farming system. Therefore, genotype-by-environment interaction (GEI) and biplot studies were undertaken to develop YMV-resistant moth bean cultivars from the germplasm. The germplasm was acquired from the National Agricultural Research Centre (NARC), Islamabad and from the farm fields in two provinces, Punjab and Sindh, Pakistan. Two different groups of moth bean genotypes were screened for YMV versus seed yield (11 genotypes) and YMV versus fodder yield (10 genotypes) over three years (2006–2008) in three locations in Pakistan [D.I.Khan Agriculture Research Station (ARS), Serai Naurang ARS, and Karak ARS]. In all germplasm, four moth bean lines were identified as highly resistant to YMV with maximum grain (013393-C, 013388) and fodder (DMB-118-E, DMB-118-A) yields across all years and locations. Genotype, environment, GEI, and biplot analysis revealed that two moth bean lines (013393-C and DMB-118-E) showed the lowest YMV scoring (1) and maximum grain (33.40, 29.70, and 33.98 g plant^{-1}) and fodder yields (15.30, 17.40, and 15.35 t ha^{-1}) compared with susceptible checks, respectively. Keeping in view the genetic potential of YMV-resistance and the high grain and fodder yields of two moth bean lines (013393-C, DMB-118-E), the Provincial Seed Council (PSC) of Khyber Pakhtunkhwa, Pakistan approved the two lines with the highest grain and fodder yields as new moth bean cultivars, naming them Dera Moth and Green Moth, respectively.

Key words: Moth bean [Vigna aconitifolia (Jacq.) Marechal] germplasm, yellow mosaic virus (YMV), genotype-by-environment interaction, biplot analysis, cultivar development

1. Introduction

Moth bean [*Vigna aconitifolia* (Jacq.) Marechal], also called Turkish gram, is native to India, Pakistan, and Myanmar, where it grows both wild and as a cultivated plant. It is also grown in other parts of Asia, Africa, the United States, and Cuba. As a pulse, it is mostly grown in India and Thailand; elsewhere it is mostly grown as forage, green manure, or a cover crop. In tropical Africa, it has been recorded from Sudan, Eritrea, Somalia, Kenya, and Botswana (Brink and Jansen, 2006). Raw and uncooked moth bean seeds (100 g) contain 343 calories, 23 g of protein, 62 g of carbohydrates, and 1.6 g of fat (USDA, 2013). Moth bean seed is a rich source of protein, and in Pakistan and India it is generally used as human food by low-income consumers in rural areas and as a forage crop. The seed is cooked whole or split, and the green pods can be cooked and eaten as vegetables. Seeds are also processed in dhal (a sprouted bean paste) or bhujia (a salted snack). Currently in Pakistan and India, moth bean is grown on its own or intercropped with other cereals, such as pearl millet, and it is also grown in rotation with cotton as a forage crop (Brink and Jansen, 2006). Due to its drought-resistant qualities, its ability to combat soil erosion, and its high protein content, moth bean has been identified as a potentially significant food source for developing countries (Adsule, 1996).

Due its susceptibility to yellow mosaic virus (YMV), the moth bean crop has been eliminated from the farming system of Pakistan. Moth bean is one of the crops targeted by YMV which causes severe damage to grain and fodder yields and their quality. YMV is a geminivirus and is the most vital and common diseases of beans and other field/vegetable crops. YMV is transmitted through the vector white fly, *Bemisia tabaci* Genn., a devastating biotic stress that can cause up to 100% damage to a large number of leguminous crops. The disease causes yellow coloration/patches on leaves, while in severe form the entire leaf becomes yellow and shows complete chlorosis, which is an indication of disease severity, restricted photosynthesis, and impact on

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the pods. The affected plants produce fewer flowers, pods, and seeds, resulting in low grain and fodder yields.

In the neighboring country, India, YMV disease was first noticed during the early seventies in Uttar Pradesh and Rajasthan (Tyagi and Mathur, 1978); however, some say it was first reported in 1955 in India and transmitted through whitefly (Shad et al., 2006). In Pakistan, Hussain et al. (2004) concluded the first report on mungbean yellow mosaic India virus, also reported by Qazi et al. (2006). It is not spread by mechanical inoculation or by seed (Shad et al., 2005): however, the strain of mungbean yellow mosaic virus (MYMV) in Thailand is reported to be mechanically transmitted (Honda et al., 1983). A good deal of research efforts have been directed towards screening mungbean and moth bean germplasm against YMV for identification of resistant sources under diverse environmental conditions, and a number of resistant lines have been reported (Bashir and Zubair, 2002; Yogeesh et al., 2012a). Although chemical control of white flies may limit the local spread of YMV, genetic resistance and the use of YMV-resistant crop cultivars are the only economically viable methods of disease control. Despite the severity of damage caused by YMV, information on the inheritance patterns of the resistance gene controlling this disease is limited (Yogeesh et al., 2012b). Yellow mosaic resistance cultivars can be developed either through direct selection of YMV-resistant lines or by involving the resistant lines in hybridization. However, identification of resistant sources against YMV is a prerequisite for this approach.

Moth bean is an excellent food legume and a best fodder for livestock; however, its area of cultivation has decreased to a great extent in Pakistan. During 2006–2007 the average harvested area was 1.48 million ha occupied by dry beans including moth bean (Ahmad, 2007). According to the GenBank status of plant genetic resources (PGR) in Pakistan, 66 different accessions of moth bean have been collected and preserved for future use (Ahmad, 2007). The major reasons for reduction in crop area are the susceptibility of indigenous cultivars to YMV, nonavailability of resistant cultivars, and low yield. Therefore, moth bean has become a less common crop. Unfortunately, until now no research institute has taken up this crop in its mandate, and that is why no resistant cultivar has been developed in Pakistan. In the wake of moth bean eradication from the cropping system, farmers have been deprived of a valuable dual-purpose crop. Therefore, there is a dire need to develop high-yielding YMV-resistant cultivars of moth bean.

Moth bean genotypes were evaluated for various morpho-physiological, growth, and yield-related traits, and significant variations were observed among genotypes for various traits (Kumar, 2008; Yogeesh et al., 2012a, 2012b). Moth bean genetic accessions were studied for genetic variability and heritability, and maximum range of variation was recorded for yield and fodder traits (Sihag et al., 2004). Surveys of the spread of YMV disease and the extent of damage in moth bean revealed that YMV was the most important disease of moth bean during 2001, and the disease was noted mainly in local cultivars; however, improved cultivars had 0%–10% disease intensity (Khatri et al., 2003). Due to different planting dates, the resistant and susceptible moth bean genotypes performed differently in the presence of YMV and showed varied performance regarding biochemical constituents (Mali et al., 2000; Arora et al., 2009).

Selection of disease-resistant lines for the development of high-yielding cultivars has already been reported in different pulse crops and resulted in the development of two new high-yielding lentil cultivars, Masoor-2004 and Ratta Kulachi-2004 (Yaqoob et al., 2005). High-yielding disease-resistant cultivars of chickpea: Karak-1, Karak-2, Karak-3, and Lawagher-2000 (Ahmad et al., 2006a, 2006b) and Dahst (Bakhsh et al., 2005) were developed through hybridization and selection. A high-yielding and YMV-resistant cultivar was developed in mungbean, Karak Mung-1 (Ahmad et al., 2006e). In screening against MYMV, 110 mungbean genotypes and 134 mashbean lines were found with ratios of 85:43, 14:28, 5:8, and 6:45 (highly resistant, resistant, moderately resistant, and susceptible/highly susceptible, respectively) (Bashir et al., 2006a; Khanzada et al., 2006). In 108 mungbean accessions screened for YMV, all entries showed the highest susceptibility, and YMV was a considerable factor to be included in breeding programs to develop high-yielding cultivars of *V. radiata* L. (Habib et al., 2007). Resistance against YMV in moth bean suggested that single plant selection is more reliable then mass selection when developing disease-resistant lines in field crops (Yaqoob, 2007; Yaqoob et al., 2007a, 2007b, 2010).

In mungbean yellow mosaic India virus (MYMIV), using whitefly as vector, 164 mungbean genotypes were screened; all genotypes were systemically infected with virus, significant variations were observed in responses among genotypes, and 35 genotypes were moderately resistant to the virus showing significant differences for yield contributing traits (Akhtar et al., 2011). The differential response of 100 accessions of mungbean to MYMV was determined and used to categorize mungbean into resistant and susceptible depending upon severity of infection. None of the genotypes were highly resistant; however, four, eight, and thirty genotypes were resistant, moderately resistant, and moderately susceptible to MYMV, respectively (Iqbal et al., 2011). Before the present study, initial screening studies of moth bean germplasm were reported by Yaqoob (2007) and Yaqoob et al. (2007a, 2007b). Thirty F_1's of Indian bean (*Lablab purpureus*) were screened against YMV under field conditions; only five F_1's were symptomless against YMV and these may be utilized for good segregates to YMV resistance in Indian bean breeding (Singh et al., 2012). In a survey based on field observations, the incidence of YMV ranged from 4% to 40% in mungbean depending upon crop cultivar and location, while in mashbean the MYMV incidence was 5%–100% (Bashir et al., 2006b). When 254 lines of mungbean were evaluated against MYMV under natural field conditions conducive to the development of disease, including whitefly virus vector population, the majority of the lines were infected (seven lines were classified as susceptible and 247 as highly susceptible) (Shad et al., 2006). Khan et al. (2012) concluded that none of the mungbean cultivars/lines was immune to MBYMV; however, the cultivars Aari-2006 and NM-2006 were resistant and moderately resistant, respectively, and Mung-97001 and M-6 showed moderate susceptibility. Therefore, the present study was planned to screen moth bean germplasm against YMV under natural environmental conditions where a large population of viruliferous white fly is always present. The study looks at the YMV effect on grain and fodder yields and will contribute to the development of new high-yielding moth bean cultivars in Pakistan.

2. Materials and methods

2.1. Experimental design and procedure

The present investigation includes two different groups of moth bean genotypes screened for YMV versus seed yield (11 genotypes) and YMV versus fodder yield (10 genotypes) (Table 1) in a series of experiments over three years (2006–2008) at three different agricultural research stations (ARS): D.I.Khan ARS, Serai Naurang ARS, and Karak ARS, Khyber Pakhtunkhwa, Pakistan. In all experiments sowing took place during the month of May. Plots were laid out in randomized complete block (RCB) design with three replications. Each plot comprised six rows measuring 5 m in length. Row-to-row and plant-to-plant spacing was 30 cm and 10 cm, respectively. The space between subplots and blocks was 100 cm. The genotypes highly susceptible to YMV belonging to the first group (013393-A, 013425-B) and the second group (DMB-108-A, DMB-118-D) were randomly planted after every two test entries in control and disease-spreader rows in

Table 1. Moth bean genotypes used in the studies.

S. no.	Name of accession	Procured
	Group-1, 11 moth bean genotypes studied for YMV vs. seed yield	
G1	013388	IABGR, NARC, Islamabad, Pak.
G2	013392	IABGR, NARC, Islamabad, Pak.
G3	013393-A	IABGR, NARC, Islamabad, Pak.
G4	013393-B	IABGR, NARC, Islamabad, Pak.
G5	013393-C	IABGR, NARC, Islamabad, Pak.
G6	0134012-A	IABGR, NARC, Islamabad, Pak.
G7	0134012-B	IABGR, NARC, Islamabad, Pak.
G8	013416-A	IABGR, NARC, Islamabad, Pak.
G9	013416-B	IABGR, NARC, Islamabad, Pak.
G10	013425-A	IABGR, NARC, Islamabad, Pak.
G11	013425-B	IABGR, NARC, Islamabad, Pak.
	Group-2, 10 moth bean genotypes studied for YMV vs. fodder yield	
G1	DMB-107-A	Farmer’s field of District Sialkot, Punjab, Pak.
G2	DMB-107-B	Farmer’s field of District Sialkot, Punjab, Pak.
G3	DMB-107-C	Farmer’s field of District Sialkot, Punjab, Pak.
G4	DMB-108-A	Farmer’s field of District Layyah, Punjab, Pak.
G5	DMB-108-B	Farmer’s field of District Layyah, Punjab, Pak.
G6	DMB-118-A	Farmer’s field of Tando Jam, District Hyderabad, Sindh, Pak.
G7	DMB-118-B	Farmer’s field of Tando Jam, District Hyderabad, Sindh, Pak.
G8	DMB-118-C	Farmer’s field of Tando Jam, District Hyderabad, Sindh, Pak.
G9	DMB-118-D	Farmer’s field of Tando Jam, District Hyderabad, Sindh, Pak.
G10	DMB-118-E	Farmer’s field of Tando Jam, District Hyderabad, Sindh, Pak.

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their relevant group of genotypes. The germplasm in all experiments and all environments (years and locations) were kept pesticide free (with no insecticide spray) in order to build up and maintain a high population of vector, the whitefly (*Bemisia tabaci* Genn.), for the development of high disease pressure. A basal dose of N:P_2O_5 fertilizers at 50:125 kg ha^{-1} was applied at the time of sowing. The soil was loamy clay with pH 8.0 at D.I.Khan ARS, sandy clay with pH 7.5 at Serai Naurang ARS, and loamy sand with pH 7.4 at Karak ARS. Conventional agronomic practices were employed to keep the crop in good condition.

The data regarding maximum and minimum temperatures and rainfall during the crop seasons (May–August, 2006–2008) are provided in Figures 1 and 2. The temperature was highest at D.I.Khan ARS followed by Serai Naurang ARS, while at Karak the temperature was low compared to the other agriculture research stations (Figure 1). The low temperature at Karak ARS may be due to the higher rainfall at Karak (Figure 2). During our previous moth bean germplasm studies regarding response to YMV disease across locations (Yaqoob, 2007; Yaqoob et al., 2007a, 2007b), the current resistant/susceptible accessions were selected for further studies after affirmative selection in an observatory.

2.2. Trait measurement and analyses

In all experiments after germination, genotypes were regularly monitored for the presence of white fly and development of YMV disease on a single-plant basis. In both groups of genotypes, observations of YMV infection were recorded on a single-plant basis when 100% of the plants in the spreader lines were infected with YMV. Relevant data on YMV disease incidence (on a 1–9 rating scale) was recorded on single-plant basis (Table 2), means were calculated to generate the corresponding values for each genotype (Shukla et al., 1978; Muniyappa et al., 1987; Bashir and Zubair, 2002, 2005; Sadiq et al., 2007; Yogeesh et al., 2012a), and the grain and fodder yields were also measured. These experiments were repeated for three years in three locations. Data were subjected to G × E interactions (Gomez and Gomez, 1984) and analyzed through the program MstatC. After obtaining significant variations through G × E analysis, various means for all traits were discussed. For confirmation of these results biplot analysis was carried out on the same data (Yan, 2001; Yan and Hunt, 2002).

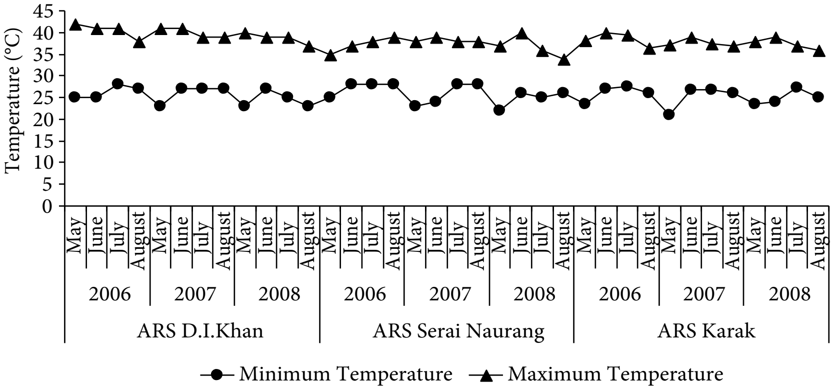

Figure 1. Maximum and minimum temperatures (°C) for moth bean crop season at three locations during 2006, 2007, and 2008.

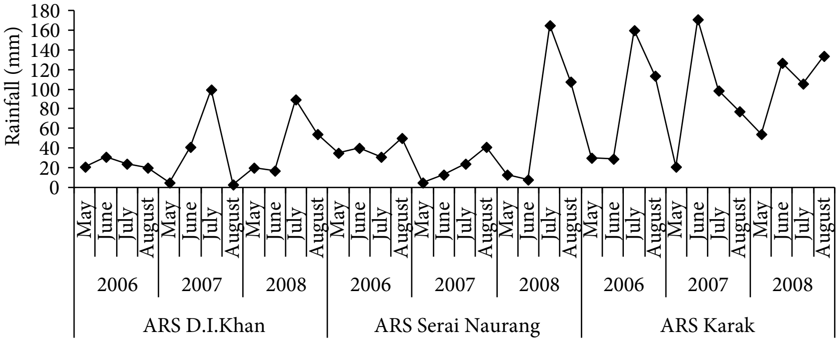

Figure 2. Rainfall data for moth bean crop season at three locations during 2006, 2007, and 2008.

Table 2. Standard procedure adopted for recording YMV incidence in moth bean genotypes.

Score	Category	Plant infestation (%)
1	Highly resistant	0%–5%
3	Resistant	6%–10%
5	Moderately resistant	21%–40%
7	Susceptible	61%–80%
9	Highly susceptible	100%

3. Results

For YMV, both groups of genotypes and genotype-by-environment (location) interaction revealed significant (P ≤ 0.01) differences; however, the locations revealed nonsignificant mean values. For seed and fodder yields, the genotypes, locations, and G × E interactions revealed significant (P ≤ 0.01) variations (data not shown). The extent of this performance depended on the magnitude of genetic variability found in genotypes, and the genotype × environment interaction effects that occur when genotypes differ in their relative performance across environments.

3.1. Moth bean accessions (group-1) screened for YMV and seed yield

The first group, with 11 moth bean genotypes, was screened for YMV incidence and seed yield per plant. The YMV rating ranged from 1.00 to 7.67 among genotypes, 3.55 to 3.73 for locations, and a 1 to 8 rating for genotype × location interactions (Table 3). In moth bean genotypes, the accessions 013393-C (1.00 rating) and 013388 (1.33 rating) showed the least incidence of YMV and were highly resistant to YMV, followed by six other genotypes (013392, 013393-B, 0134012-A, 0134012-B, 013416-B, and 013425-A) with YMV incidences 2.00–2.67. The moth bean genotypes 013393-A, 013416-A, and 013425-B revealed maximum YMV attack and were highly susceptible to YMV (7.00–7.67). The location means were nonsignificant for YMV; however, on average the genotypes had minimum YMV incidence at Karak ARS (3.27 rating) followed by D.I.Khan (3.55 rating), and Serai Naurang (3.73 rating). In genotype × location interaction, the lowest YMV incidence was observed for moth bean accession 013393-C (1 rating) at all locations, accession 013388 with rating of 1 at D.I.Khan ARS and Karak and a rating of 2 at Serai Naurang, and genotype 013425-A with rating of 2 at all locations and authenticated to be highly resistant to YMV at all locations. Maximum YMV incidence (7–8 rating) was observed in accessions 013393-A, 013416-A, and 013425-B at all locations, and these were

Table 3. Moth bean genotype performance against YMV incidence (1–9 rating) across locations.

Accessions	ARS D.I.Khan	ARS Serai Naurang	ARS Karak	Means (1–9 rating)
013388	1	2	1	1.33
013392	2	3	2	2.33
013393-A	8	8	7	7.67
013393-B	3	3	2	2.67
013393-C	1	1	1	1.00
0134012-A	3	3	2	2.67
0134012-B	3	3	2	2.67
013416-A	7	7	8	7.33
013416-B	2	2	2	2.00
013425-A	2	2	2	2.00
013425-B	7	7	7	7.00
Means (1–9 rating)	3.55	3.73	3.27	-

highly susceptible to YMV. Other interactions also showed YMV with a rating of 2 to 3. On average, moth bean accessions 013393-C and 013388 exhibited minimum and at par YMV incidence for genotype and G × E interactions and were highly resistant to YMV.

Regarding seed yield per plant, in the first group of moth bean genotypes moth bean accessions varied from 4.56 to 32.36 g per plant and location means ranged from 9.86 to 13.89 g per plant, while in genotype × location interactions the seed yield ranged from 3.40 to 33.98 g per plant (Table 4). Moth bean genotype 013393-C had maximum seed yield per plant (32.36 g), followed by 013416-B, 013392, and 01325-A, which ranged from 14.33 to 15.93 g per plant and had less than half the seed yield of the promising genotype (013393-C). In location means, all accessions produced maximum seed yield per plant at D.I.Khan ARS (13.89 g), followed by Karak (12.40 g) and Serai Naurang (9.86 g). In G × E interactions, accession 013393-C had maximum seed yield per plant at the three locations (29.70–33.98 g). It was followed by two other accessions, 013392 and 013416-B, with seed yields of 22.15 and 20.10 g per plant, respectively. The minimum values for seed yield per plant were in genotypes 013388 at D.I.Khan ARS and Serai Naurang (3.40 and 4.40 g plant^{-1}), 0134012 at Serai Naurang (3.99 g plant^{-1}), and 013425 at D.I.Khan (4.40 g plant^{-1}). All other interactions revealed medium seed yield per plant. Overall, the moth bean accession 013393-C, being highly resistant to YMV, had maximum seed yield per plant for genotype and G × E interactions.

3.2. Moth bean accessions (group-2) screened for YMV and fodder yield

The second group of moth bean genotypes (10 accessions) were studied for YMV incidence and fodder yield. For YMV incidence, accessions ranged from 1.00 to 7.67 and locations ranged from 4.00 to 4.60, while the YMV rating for genotype × location interaction was 1–8 (Table 5). In moth bean genotype means, accessions DMB-118-E (1.00) and DMB-118-A (1.33) showed the lowest level of YMV incidence, followed by DMB-107-C (2.33), and were highly resistant. Accessions DMB-118-D, DMB-118-C, DMB-108-A, DMB-107-A, and DMB-107-B had the maximum YMV rating (5.33–7.67) and were highly susceptible. Other accessions showed a medium rating for YMV. The location means were nonsignificant for YMV; however, on average the genotypes produced minimum YMV rating (4.00) at Serai Naurang ARS, followed by Karak, and D.I.Khan with ratings of 4.20 and 4.60, respectively. In genotype × location interactions, moth bean accessions DMB-118-E (1) and DMB-118-A (1-2) revealed the lowest YMV incidence at all locations and were highly resistant. These were followed by three other genotypes: DMB-107-C, BMB-108-B, and DMB-118-B with YMV ratings of 2–3 at the majority of locations. Maximum YMV incidence (7–8 rating) was observed in moth bean accessions DMB-118-D at all locations and in DMB-118-C at Serai Naurang ARS, and both were highly susceptible to YMV. All other interactions revealed medium ratings for YMV. On average, moth bean accessions DMB-118-E and DMB-118-A exhibited minimum YMV incidence for

Table 4. Moth bean genotype performance for seed yield per plant across locations.

Accessions	ARS D.I.Khan	ARS Serai Naurang	ARS Karak	Means (g)
013388	3.40	4.40	5.88	4.56
013392	22.15	10.15	12.78	15.03
013393-A	8.40	8.21	10.10	8.90
013393-B	15.81	4.77	6.20	8.93
013393-C	33.40	29.70	33.98	32.36
0134012-A	13.40	3.99	5.19	7.53
0134012-B	19.10	7.20	9.30	11.87
013416-A	8.25	4.79	6.90	6.65
013416-B	12.80	14.90	20.10	15.93
013425-A	11.68	13.80	17.50	14.33
013425-B	4.40	6.60	8.50	6.50
Means (g)	13.89	9.86	12.40	-

Table 5. Moth bean genotype performance against YMV incidence (1–9 rating) across locations.

Accessions	ARS D.I.Khan	ARS Serai Naurang	ARS Karak	Means (1–9 rating)
DMB-107-A	6	5	6	5.67
DMB-107-B	6	5	5	5.33
DMB-107-C	2	2	3	2.33
DMB-108-A	9	6	5	6.67
DMB-108-B	5	2	3	3.33
DMB-118-A	1	1	2	1.33
DMB-118-B	2	3	6	3.67
DMB-118-C	6	8	3	5.67
DMB-118-D	8	7	8	7.67
DMB-118-E	1	1	1	1.00
Means (1–9 rating)	4.60	4.00	4.20	-

genotype and G × E interactions and were highly resistant.

Regarding fodder yield in the second group of moth bean genotypes, accessions varied from 3.39 to 16.02 t ha^{-1}, location means ranged from 6.91 to 8.04 t ha^{-1}, while genotype × location interactions ranged from 1.94 to 20.20 t ha^{-1} (Table 6). In genotype means, accession DMB-118-E obtained the highest fodder yield (16.02 t ha^{-1}) followed DMB-118-A (14.10 t ha^{-1}). Four other genotypes, i.e. DMB-107-A, DMB-107-B, DMB-107-C, and DMB-118-B, also produced medium and comparable fodder yield ranging from 6.40 to 8.52 t ha^{-1}, while other genotypes had the lowest fodder yield. In location means, overall the accessions produced maximum fodder yield at D.I.Khan ARS (8.04 t ha^{-1}) followed by Serai Naurang (7.91 t ha^{-1}) and Karak (6.91 t ha^{-1}). In G × E interactions, genotype DMB-118-A produced maximum fodder yield at D.I.Khan ARS (20.20 t ha^{-1}) followed by DMB-118-E with the highest fodder yield at three locations ranging from 15.30 to 17.40 t ha^{-1}. Minimum fodder yield was recorded in accessions in DMB-108-A at Serai Naurang ARS (1.94 t ha^{-1}), DMB-

Table 6. Moth bean genotype performance for fodder yield across locations.

Accessions	ARS D.I.Khan	ARS Serai Naurang	ARS Karak	Means (t ha^{-1})
DMB-107-A	7.9	7.30	7.92	7.71
DMB-107-B	12.20	8.00	5.35	8.52
DMB-107-C	6.12	7.80	6.80	6.91
DMB-108-A	3.68	1.94	5.41	3.68
DMB-108-B	4.00	3.95	2.21	3.39
DMB-118-A	20.20	12.00	10.10	14.10
DMB-118-B	4.02	9.30	5.88	6.40
DMB-118-C	2.10	6.50	5.15	4.58
DMB-118-D	4.87	4.90	4.93	4.90
DMB-118-E	15.30	17.40	15.35	16.02
Means (t ha^{-1})	8.04	7.91	6.91	-

118-C at D.I.Khan (2.10 t ha^{-1}), and DMB-108-B at Karak (2.21 t ha^{-1}). All other interactions revealed medium values for fodder yield. Overall, accessions DMB-118-E and DMB-118-A, being resistant to YMV, produced the highest fodder yield for genotype and G × E interactions.

3.3. Biplot analysis over years and locations

The results through biplot are presented in two sections: a) section one represents the results of "which-won-where" to identify the best genotypes for each environment, b) section two shows genotype performance and stability results (Figures 3–6). Group-1 moth bean genotypes are indicated with a letter 'G' (genotype) followed by a number, viz., G1 (13388), G2 (13392), G3 (013393-A), G4 (013393-B), G5 (013393-C), G6 (0134012-A), G7 (0134012-B), G8 (013416-A), G9 (013416-B), G10 (013425-A), and G11 (013425-B) (Figures 3 and 4). Group-2 moth bean genotypes were also designated with a letter: G1 (DMB-107-A), G2 (DMB-107-B), G3 (DMB-107-C), G4 (DMB-108-A), G5 (DMB-108-B), G6 (DMB-118-A), G7 (DMB-118-B), G8 (DMB-118-C), G9 (DMB-118-D), and G10 (DMB-118-E) (Figures 5 and 6) to accommodate and make visible the genotypes in the graphs and avoid overlapping. The environments are abbreviated and followed by year, viz., DIK06/07/08 (D.I.Khan ARS 06/07/08), SN06/07/08 (Serai Naurang ARS 06/07/08), and KK06/07/08 (Karak ARS 06/07/08).

3.4. Group-1: moth bean genotypes with YMV disease scoring

The first two principal components (PCs) explain 94% (PC1 = 90.6%, PC2 = 3.4%) of total GGE variation.

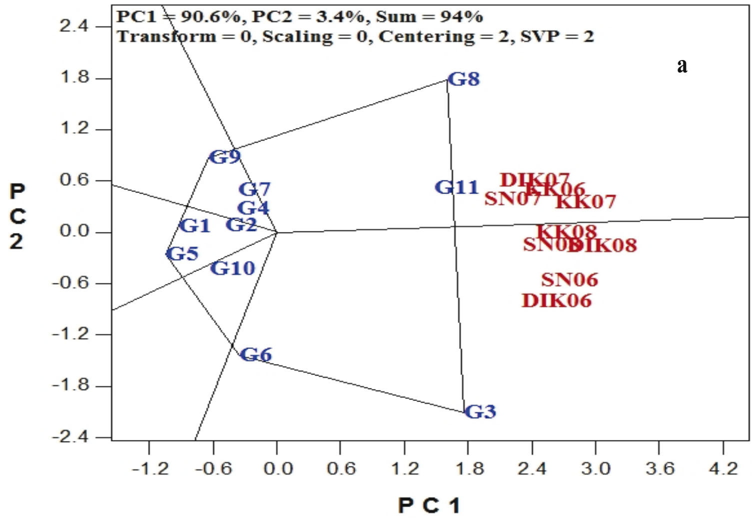

Figure 3a. Polygon view of the biplot for winning genotypes in the tested environments.

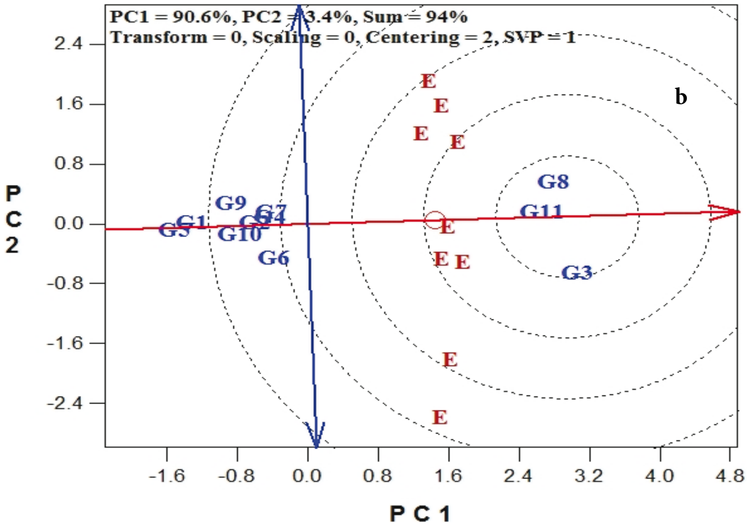

Figure 3b. Ranking of genotypes for both disease scoring and stability.

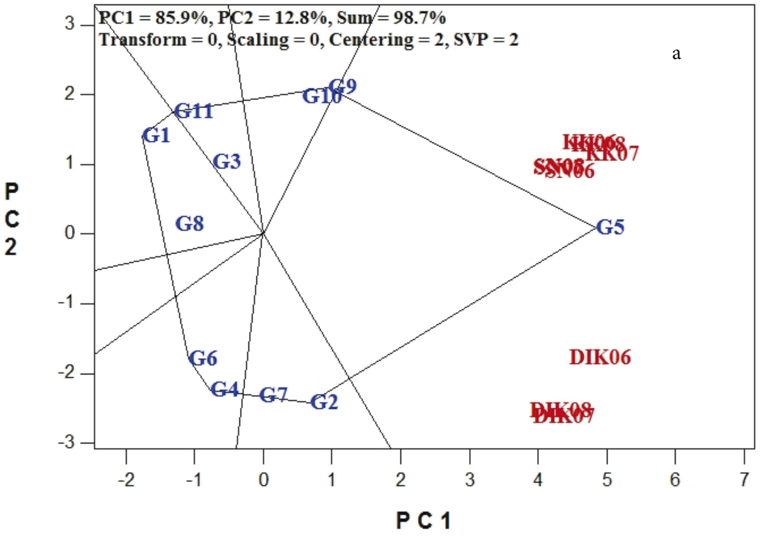

Figure 4a. Polygon view of the biplot for winning genotypes in the tested environments.

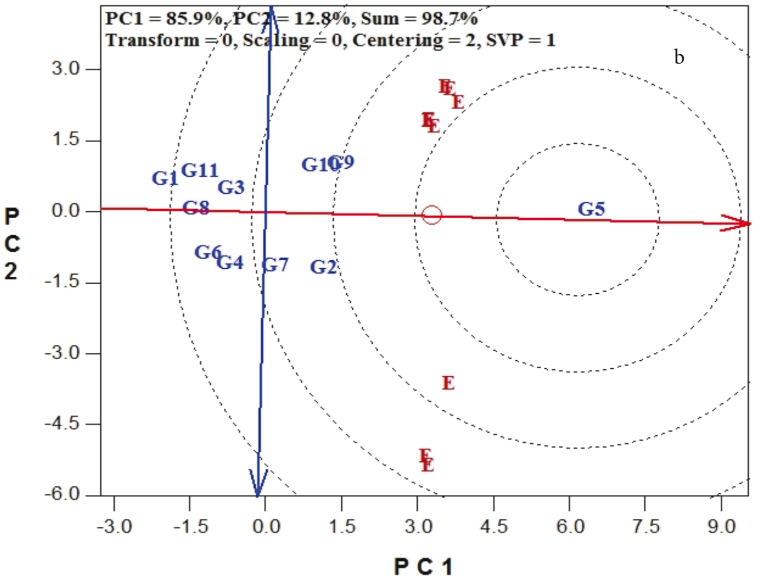

Figure 4b. Ranking of genotypes for both yield and stability in performance.

3.4.1. The "which-won-where" patterns

The polygon view of the GGE biplot indicates the best genotypes in each environment and group of environments (Figure 3a). The polygon was drawn by connecting the markers of the most responsive genotypes (i.e. those furthest away from the biplot origin) in such a way that all other genotypes are contained in the polygon. All the genotypes were divided into six sectors; however, environments fell into only two sectors (Figure 3a). Minimum disease scoring was recorded for G5 (013393-C) and G1 (13388) over all environments. In the first sector where the vertex genotype is G8 (013416-A), four environments were grouped together (DIK07, KK06, KK07, and SN07), whereas the second sector containing vertex genotype G3 (013393-A) occupies the remaining five environments (DIK07, DIK08, KK08, SN06, and SN08). It clearly exhibits that both vertex genotypes G8 (013416-A) and G3 (013393-A) were heavily infested with disease in their respective environments that fall within their quadrants. On the other hand, those genotypes that occupied positions opposite these two sectors exhibited resistance against disease.

3.4.2. Genotype means, YMV disease, and their stability

Figure 3b shows the ranking of 11 genotypes for average disease score and stability in performance. The line with a single arrow head passing through the origin is known

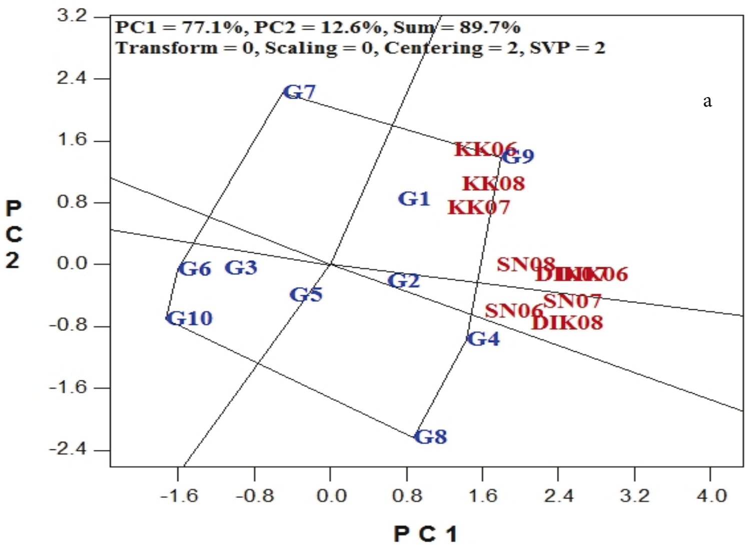

Figure 5a. Polygon view of the biplot for winning genotypes in the tested environments.

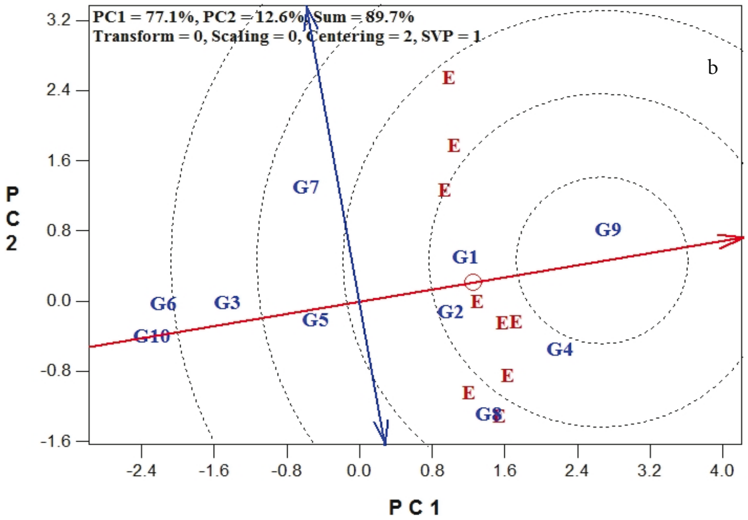

Figure 5b. Ranking of genotypes for both disease scoring and stability.

as the average environment axis (AEC) or, simply, the performance line. Genotypes closer to the concentric circles indicate higher mean disease scoring. The line with double arrow heads passing through the origin and perpendicular to the AEC represents the stability of genotypes. In either direction away from the biplot origin on this axis, are greater G × E interactions and reduced stability. As low disease incidence is required for selecting resistant genotypes, the ideal genotypes are those having low disease scoring and high stability. Since G5 (013393-C) and G1 (13388) showed low disease scores coupled with higher stability in performance they were marked for selection (Figure 3b). Three genotypes, G3 (013393-A), G8 (013416-A), and G11 (013425-B), showed maximum consistent disease scoring across environments (Figure 3b).

3.5. Group-1: moth bean genotypes with seed yield

The first two PCs explain 98.7% (PC1 = 85.9%, PC2 = 12.8%) of total GGE variation.

3.5.1. The "which-won-where" patterns

The "which-won-where" pattern of the GGE biplot (Figure 4a) indicated the best genotype in each environment and group of environments. In Figure 4a, only one sector was identified as important where the vertex genotype is G5 (013393-C), and all environments occupied a position in the same sector. It clearly exhibited that the vertex genotype G5 (013393-C) produced maximum average

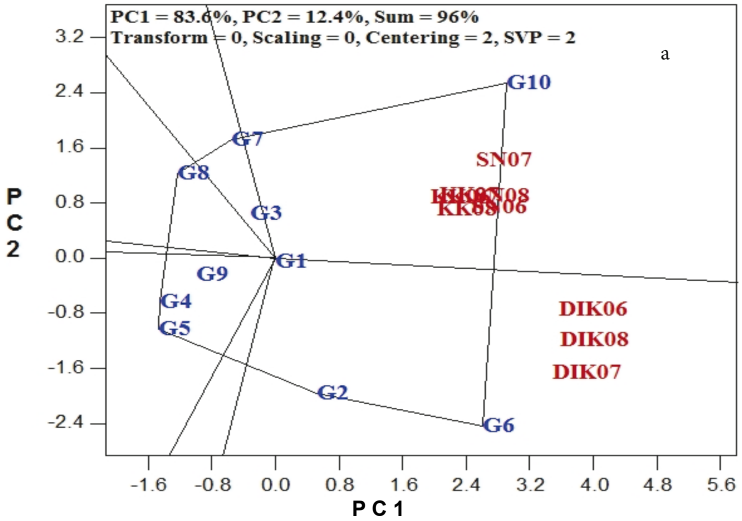

Figure 6a. Polygon view of the biplot for winning genotypes in the tested environments.

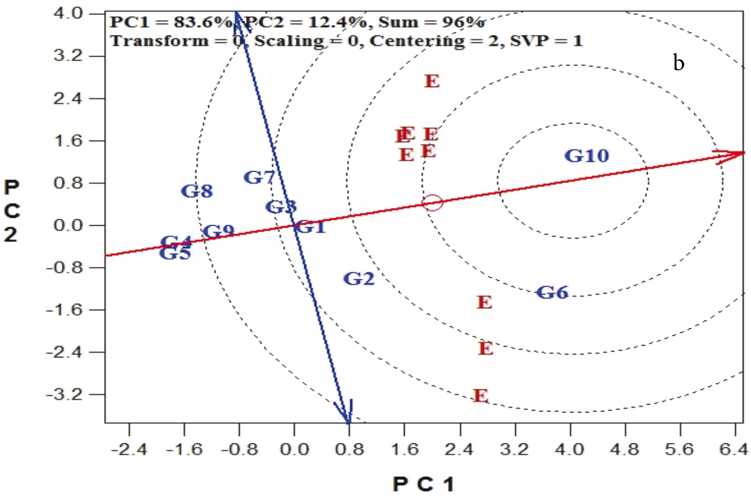

Figure 6b. Ranking of genotypes for both yield and stability in performance.

yields across all environments (Figure 4a). The remaining genotypes present in sectors with no environment in their quadrants showed poor performance in all environments.

3.5.2. Genotype means, seed yield, and their stability

Figure 4b shows the ranking of 11 genotypes for average yield and stability in performance across environments. Based on the ranking of genotypes with ideal entry, the most promising genotype was G5 (013393-C), as it was present in the center of the concentric circles (Figure 4b). Since higher average yield and high stability in performance are required for genotype selection, G5 (013393-C) outclassed all other genotypes regarding average yield and stability in performance.

3.6. Group-2: moth bean genotypes with YMV disease scoring

The first two PCs explain 89.7% (PC1 = 71.1%, PC2 = 12.6%) of total GGE variation.

3.6.1. The "which-won-where" patterns

Figure 5a indicates the best genotypes in each environment and group of environments. In polygon view three important sectors were drawn. All environments fell into two sectors. Genotypes G10 (DMB-118-E) and G6 (DMB-118-A) exhibited resistance against disease across all environments. In the first sector where the vertex genotypes are G9 (DMB-118-D) and G1 (DMB-107-A), most environments were grouped together (i.e. DIK06, DIK07, KK06, KK07, KK08, and SN08), whereas in the second sector, genotype G2 (DMB-107-B) occupies the position into which the remaining environments were grouped (i.e. DIK08, SN06, and SN07) (Figure 5a). These three genotypes, G1 (DMB-107-A), G2 (DMB-107-B), and G9 (DMB-118-D), were heavily infested with disease in their respective environments that fell within their quadrants.

3.6.2. Genotype means, YMV disease, and their stability

The ranking of 11 genotypes for their average disease score and stability in performance is shown in Figure 5b. Since low disease infestation is required for selecting resistant genotypes, the ideal genotypes were G10 (DMB-118-E) and G6 (DMB-118-A), which had low disease scoring, high stability, and were far away from the center of the concentric circle (Figure 5b). Genotypes closer to the concentric circles indicate higher mean disease scoring. Only one genotype, G9 (DMB-118-D), showed maximum consistent disease scoring across environments, followed by G4 (DMB-108-A).

3.7. Group-2: moth bean genotypes with fodder yield

The first two PCs explain 96% (PC1 = 83.6%, PC2 = 12.4%) of total GGE variation.

3.7.1. The “which-won-where” patterns

The “which-won-where” pattern of the GGE biplot indicated the best genotype in each environment and group of environments (Figure 6a). The two sectors were identified as important sectors, and the vertex genotypes are G10 (DMB-118-E) and G6 (DMB-118-A). Genotype G6 (DMB-118-A) was followed by G2 (DMB-107-B) in producing maximum yield in three environments (i.e. DIK06, DIK07, and DIK08) (Figure 6a). However, genotype G10 (DMB-118-E) outclassed all other genotypes in six environments (i.e. KK06, KK07, KK08, SN06, SN07, and SN08). The remaining genotypes present in sectors with no environment in their quadrants showed poor performance across all environments.

3.7.2. Genotype means, fodder yield, and their stability

The average yield and stability in performance of 11 genotypes across environments is presented in Figure 6b. Based on ranking of genotypes with ideal entry, the most promising genotype was G6 (DMB-118-A) as it was present in the center of the concentric circles, and thus exhibited high mean yield coupled with high stable performance across environments. Genotype G10 (DMB-118-E) ranked second for average yield and stability in performance.

After GEI and biplot analyses, moth bean accessions 013393-C and 013388 selected from group-1 exhibited minimum and at par YMV incidence and maximum seed yield for genotype and G × E interactions and were highly resistant to YMV. In the second group of moth bean genotypes, accessions DMB-118-E and DMB-118-A were resistant to YMV and produced the highest fodder yield for genotype and G × E interactions.

4. Discussion

Crop growth, yield, its components, and biomass yield are under the control of genes, which are modulated by continuous interaction with the environment. Among the environmental variables, temperature strongly influences branching, plant height, and length of the vegetative period. In the present GEI and biplot studies, a differential response was observed for the first group of moth bean genotypes regarding YMV and seed yield across locations. The yields of YMV-resistant and susceptible moth bean lines were quite divergent within and across locations. The moth bean lines showing resistance against YMV at one location remained unchanged with the same excellence of resistance at other locations, and the same pattern was followed by highly susceptible accessions. In our previous studies, out of 66 collections two accessions, 013388-A and 013393-C, were highly resistant to YMV, and six (013392-A, 013393-A, 013393-B, 013416-A, 013416-B, and 013425-A) were resistant to YMV, and response of germplasm to YMV revealed distinct variation (Yaqoob, 2007). In past studies, 18 moth bean genotypes were evaluated during two different seasons for YMV and various morpho-physiological, growth, and yield-related traits, and significant differences were observed in the genotypes for all traits (Kumar, 2008). Moth bean genotype 013393-C remained highly resistant to YMV coupled with the highest seed yield in all environments (locations and years). However, moth bean lines 013393-A, 013416-A, and 013425-B had maximum disease scoring in all environments and highest susceptibility to YMV. The susceptible moth bean control had the highest disease scoring and also produced low yield at various research stations. Moth bean germplasm collected from different geographical regions revealed significant genetic variability among genotypes regarding YMV and scope for improvement in yield and fodder traits through simple selection (Yogeesh et al., 2012b). The effect of MYMV disease varies cultivar to cultivar which might be due to the genetic make-up of the mungbean genotypes (Sadiq et al., 2007). The incidence of YMV ranged from 4% to 40% in mungbean, depending upon crop cultivar and location, while in mashbean the MYMV incidence range was 5%–100% under field conditions (Bashir et al., 2006a). None of the mungbean lines were immune to MYMV; however, the cultivars Aari-2006 and NM-2006 had resistance and moderate resistance, respectively, and Mung-97001 and M-6 showed moderate susceptibility (Khan et al., 2012). Out of 132 urdbean lines, 53, 32, and 11 genotypes were highly resistant, resistant, and moderately resistant against

MYMV, respectively, while other lines were moderate-to-highly susceptible (Bashir and Zubair, 2002).

The observed harmony among selected (resistant/susceptible) moth bean lines regarding their response to YMV disease across locations clearly showed the affirmative selection response of our previous studies (Yaqoob, 2007; Yaqoob et al., 2007a, 2007b). In 62 moth bean genetic accessions studied for genetic variability, maximum range of variation was recorded for yield and fodder traits and genetic stocks; MH-65, MH-34, MH-66, and MH-45 were the most promising and reserved for further improvement (Sihag et al., 2004). Moth bean genotypes exhibited significant differences for yield and fodder traits, indicating the presence of greater genetic variability, and the breeding material was appropriate for the investigations (Yogeesh et al., 2012b). Mungbean germplasm was screened against MYMV under field conditions, and revealed four genotypes resistant, eight moderately resistant, and 30 moderately susceptible to MYMV (Iqbal et al., 2011). Mungbean genotypes were studied against YMV, and 35 lines were found moderately resistant to YMV with significant variability in yield-contributing traits (Akhtar et al., 2011). However, the YMV resistance/tolerance was studied in mungbean germplasm, and some of the genotypes also produced a good yield despite being highly susceptible to YMV disease (Habib et al., 2007), which might be due to low disease pressure.

In the case of the second group of moth bean genotypes studied for YMV and fodder yield, two out of ten moth bean lines (DMB-118-E and DMB-118-A) showed the lowest scoring for YMV, followed by DMB-107-C, while the rest of the accessions remained highly susceptible, susceptible, and moderately susceptible to YMV. In previous studies, genetic resistance against YMV was found in land races of moth bean that could be exploited directly and/or through hybridization for evolving high-yielding, resistant moth bean cultivars (Yaqoob, 2007). In our own past studies (Yaqoob et al., 2007b), most indigenous moth bean genotypes were highly susceptible to YMV disease; however, the resistant lines (DMB-107C, DMB-107E, DMB-108B, and DMB-118-A) were quite divergent for almost all traits examined in the present study, and two new moth bean cultivars with resistance to YMV and good seed and fodder yields were developed. In 121 moth bean accessions screened for YMV 64 genotypes were resistant, one moderately resistant, and all remaining types were susceptible (Yogeesh et al., 2012a). However, the F_1 and F_2 populations phenotyped for YMV under natural conditions revealed a monogenic dominant control of YMV-resistance in F_2 populations with ratio of 3:1 (resistant:susceptible). Out of 36 moth bean genotypes, 10 accessions (DMB-107-E, DMB-107-F, DMB-108-D, DMB-118-A, MB-1118-C, 013393, 013412-A, 013412-B, 012425-B, and 013388) were highly resistant to YMV (1 rating), while 13 lines were resistant to YMV (3 rating) (Yaqoob et al., 2007a). The mungbean and mashbean lines screened against MYMV showed ratios of 85:43, 14:28, 5:8, and 6:45 (highly resistant, resistant, moderately resistant, and susceptible/highly susceptible) (Bashir et al., 2006b; Khanzada et al., 2006).

In the present GEI and biplot study, moth bean lines DMB-118-E and DMB-118-A produced the highest fodder yield and excelled over all other lines in all environments (years and locations). The response of various moth bean lines to YMV was almost analogous, corresponding to all locations and years. For instance, the moth bean lines DMB-118-E and DMB-118-A remained highly resistant and showed the highest fodder yield in all environments. Similarly, lines DMB-107-A, DMB-107-B, DMB-108-A, and DMB-118-D remained susceptible to YMV disease and had poor fodder yield in all environments. Moth bean lines DMB-108-A, DMB-118-C, and DMB-118-D were completely destroyed due to severe infestation and had the highest YMV scoring. These three moth bean lines could be used as disease spreaders in future field screening programs. Surveys of the spread of YMV disease and the extent of damage in moth bean revealed that YMV was the most important disease of moth bean in the region and had a higher incidence in 2001 than in 2000. The disease was noted mainly in local cultivars, while the improved cultivars RMO-40, RMO-257, RMO-435, and Jwala had 0%–10% disease intensity (Khatri et al., 2003). Due to different planting dates, moth bean resistant and susceptible genotypes performed differently in the presence of YMV and showed varied performances for biochemical constituents (Mali et al., 2000; Arora et al., 2009), However, YMV causes a greater loss of electrolytes from the infected leaf tissues of highly susceptible moth bean genotypes (Gour, 1989). Previous findings reported by Mahar et al. (2002), Bakhsh et al. (2005), and Ahmad et al. (2006c, 2006d) revealed varied responses to YMV disease in mungbean and chickpea genotypes, and significant variation was observed for yield-related traits. Similarly, Bashir et al. (2006a), Khanzada et al. (2006), and Yaqoob et al. (2005, 2007a, 2007b) successfully screened the mungbean, mashbean, and moth bean genotypes regarding YMV and reported their varied responses to viral disease.

The GEI (Gomez and Gomez, 1984) and biplot analyses (Yan, 2001; Yan and Hunt, 2002) revealed that lines 013393-C and DMB-118-E selected from group-1 and group-2 moth bean genotypes, respectively, were highly resistant against YMV as well as high yielding (grain and fodder). The seeds were multiplied and submitted for varietal approval as new cultivars to the Provincial Seed Council (PSC) Khyber Pakhtunkhwa, Pakistan. The PSC approved line 013393-C as Green Moth and line DMB-118-E as Dera Moth, two new YMV-resistant and high-yielding moth bean cultivars for grain and fodder purposes, during 2009. The two new moth bean cultivars Dera Moth and Green Moth were developed from lines 013393-C and DMB-118-E, respectively, and possess the genetic potential for YMV resistance and high grain and fodder yields.

Acknowledgments

The authors are grateful for the financial support of the Pakistan Agricultural Research Council (PARC), Islamabad, Pakistan, through the Agricultural Linkages Program (ALP), which was used to study the development of YMV-resistant and high grain and fodder yield moth bean cultivars.

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