

The Resistance of Bean Yellow Mosaic Virus (BYMV) in Faba bean (*Vicia faba* L.) with Diallel Analysis

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Abstract

Bean yellow mosaic virus (BYMV) has been recognized as one of the major economic disease and reduced a considerable destructive in seed yield, particularly, when plants were infected at the beginning stage of faba bean growing regions of Egypt. Little genetic information is available on the resistance of *Vicia faba* to BYMV disease. Hence, this study was conducted to determine the relative importance of general (GCA) and specific (SCA) combining ability, maternal and non-maternal reciprocal effects on resistance to BYMV in selected faba bean genotypes through mechanical translocation of BYMV. A complete diallel mating scheme including reciprocals of six faba bean genotypes varied in their resistant and susceptible to BYMV were evaluated in the Experimental Farm, Faculty of Agriculture, Suez Canal University, Ismailia, Egypt during two seasons (2008/09 & 2009/10). The results show that the combining ability analysis revealed that both additive and non additive gene effects were present at this juncture and played a major role in the genetic resistance to BYMV. The crosses between the resistant and susceptible faba bean genotypes showed intermediate disease reaction to the BYMV, suggesting a polygenic system of resistance to BYMV. Significant maternal and specific reciprocal differences among the parents and their crosses indicated that maternal inheritance is involved in the reaction of faba bean genotypes to BYMV. Also, significant genotype x years interaction suggested a deficient in stability in the development of virus pathogen on faba bean plants. Therefore, recurrent selection would be appropriate for accumulating genes for resistance to BYMV in *V. faba* and progeny

performance may be based on their parent's performance per se.

Keywords: Bean yellow mosaic virus, BYMV, Combining ability, Diallel, Disease, Faba bean, Resistance.

1. Introduction

Faba bean, *Vicia faba* L., is considered as one of the most important food legumes in Egypt. It is the earliest domesticated food legumes, which believed to be originated in the West Asia Mediterranean region (Bond Et Al. 1994). It plays a major role in the Egyptian diets as a source of protein (Hassan, 1996). *V. faba* is grown mainly by poor farmers, many of them are man and women owner with many children. For these people the crop is vital for both food security and income generation.

In spite of the importance of faba bean crop as a famine and food security plant, it is constantly threatened by production constraints such as drought, low yielding local cultivars, lack of good quality planting materials, land tenure, pests and diseases...etc. (Ibrahim And Nassib, 1979; Hawtin Et Al., 1983; Tivoli Et Al., 1988 and Abdalla & Darwish, 2002). However, under certain environmental conditions, it can improve soil fertility and reduce the incidence of weeds, diseases and pests, when grown in rotation with other field crops (Mwanamwenge Et Al., 1998).

Although of all the constraints, diseases found on faba bean are considered of the most destructive and causes considerable losses in its yield which estimated at over 50%. (El-Hosary Et Al., 1998; Bouhassan Et Al., 2004; Awaad Et Al., 2005; El-Bramawy & Abdul Wahid, 2005 and El-Bramawy & Shaban, 2010). Among these diseases constraints, virus diseases, so many diseases can affect faba bean plants which considered a serious worldwide problem (Jones, 1997 and El-Tahlawy, 2005). Infection by certain viruses causes significant economic losses and yield reduction (estimated by 30% on susceptible cultivars of faba bean cultivars (Khalil & Erskine, 2001). Viral diseases have an important status because they not only cause direct damage to the host, but also predispose the plant to secondary invaders (Beute, 1970 and Mahgoub Et Al., 1997). Among faba bean viruses, bean yellow mosaic virus (BYMV) consider as one of the most devastating viruses affecting faba bean plants in Egypt (Allam Et Al., 1984; Bashir Hmpton, 1996; El-Beshehy, 1999; Khatab, 2002; Elbadry Et Al., 2006 and Radwan Et Al., 2008). BYMV (family Potyviridae, genus Potyvirus) is an aphid transmitted virus in non-persistent mode and has a wide host range (Jones & Mclean, 1989 and Jones, 2004 & 2005). BYMV not only infects legumes causing yield losses, but also affects the horticulture industry by infecting gladiolus, one of the top six flowers of the export market (Anonymous, 1997). Systemic symptoms caused by BYMV infection do not kill faba bean plants, but have the potential to spread faster and further into the crop, causing greater overall yield reduction, despite inducing milder symptoms (Cheng Et Al., 2002 and Sidaros Et Al., 2006).

In spite of all the widespread distribution of bean yellow mosaic virus with a high incidence of the virus (BYMV) across the countries in world wide, the progress made in resistance breeding to BYMV is rarely comparing to other diseases. Therefore, it should be taken into

consideration in the breeding programme (Jones & Mclean, 1989). The spotlight has, therefore, shifted to host plant resistance. It is acknowledged that resistant faba bean varieties could potentially form the basis of sustainable management strategies for faba bean virus diseases (Bashir *Et Al.*, 2002). The selection of faba bean resistant varieties and continuous breeding programme for disease resistance appears to be the efficient means of controlling the disease considering (BYMV).

Although, little work has been done on resistance to BYMV and determination of mode of inheritance. So, it is important to continue in this direction in order to cover and confirm obtaining resistance varieties of faba bean crop. Such studies in these areas will assist the plant breeders in formulating an efficient strategy for incorporating the resistant genes into high yielding improved and stable varieties of the crop considering. Therefore, the overall objective of the present practical work is to contribute to the development of stable bean yellow mosaic virus resistance in faba bean. The specific objective of this study was to evaluate the relative importance of general (GCA) and specific (SCA) combining ability for resistance to BYMV through mechanical transmission of BYMV disease.

2. Materials & Methods

2.1 BYMV isolation and identification

Twenty night samples of faba bean plants exhibiting venial yellowing, followed by obvious faba beans develop veinal yellowing, followed by obvious green or yellow mosaic vein banding with yellowish line patterns. Symptoms which are more prominent on young leaves were collected from eight different fields of Ismailia Governorates. These samples were checked serologically against Bean yellow mosaic virus (BYMV), Alfalfa mosaic virus (AMV), Broad bean mottle virus (BBMV), Broad bean true mosaic virus (BBTMV) and Bean leaf roll virus (BLRV). Plant samples which gave positive reaction in the indirect ELISA test with BYMV as reported by Hobbs *Et Al.*, 1987.

These antibodies were obtained from International Center for Agricultural Research in the Dry Areas (ICARDA). Plant extracts were prepared by grinding thoroughly the tissues (0.5 gm) in the presence of 450 µl extraction buffer to reach a dilution 1/10. The microplates were loaded by 100 µl in each well. Plates were then incubated for 1 hour at 37°C. During incubation cross absorption for the crude primary antiserum was prepared with healthy potato leaves sap according to the dilutions 1/100, 1/5000 and 1/10000.

The microplates were unloaded and washed 3 times with PBS-Tween allowing 3 minutes soaking for each wash. The cross-absorbed 100 µl of antiserum was loaded to each well and the plates were incubated at 37°C. for 90 minutes. The plates were unloaded and washed with PBS-Tween as mentioned above. The secondary antiserum 100 µl (anti rabbit – anti goat enzyme conjugate) diluted 1/1000 was loaded to each well and the plates were incubated at 37°C for 60 minutes. Just before use, 2 tablets of sigma 4-nitrophenylphosphate were dissolved in 21 milliliter of substrate buffer. The colour of the reaction was observed.

Plant samples which gave positive reaction in the indirect ELISA test with BYMV were separated and the extracted diluted sap for sample was used to inoculate the following faba

bean Giza 461 cv. prepared for BYMV. The inoculum was prepared from BYMV infected top faba bean leaves, ground in a mortar containing 0.1 M phosphate buffer, pH 7.0 (1: 2 w: v₁). The homogenate was filtrated through two layers of muslin, and the leaves of healthy plants were dusted with carborundum and rubbed gently with a cotton swab previously dipped into the suspension of virus inoculum. The faba bean plants were kept at 100% water-holding capacity.

2.2 BYMV inoculation with cultivar sours (Giza 461 cv.)

Faba bean of Giza 461 cv. were used as an indicator host cultivar for test inoculum of the BYMV. Giza 461 cv. seeds were sown in a mixture of sand and clay (1: 2 v v₁) in plastic pots (10 cm in diameter) in separated growth chambers under a photoperiod of 12 h (PAR 400 -700 mmolm₂ s₁). Temperatures degree through day and night were 22 and 17°C, respectively and the relative humidity was approximately 70%. The infected faba bean plants were kept at 100% water-holding capacity. This cultivar (Giza 461 cv.) was used in earlier studied as an infected propagative host with BYMV by El-Beshehy (1999) and Radwan *Et Al.* (2008).

Preparation of inoculum of bean yellow mosaic virus was prepared from BYMV infected top faba bean leaves (Giza 461 cv.), ground in a mortar containing 0.1 M phosphate buffer, pH 7.0 (1: 2 wv₁). For artificial mechanical translation (AMT), the homogenate was filtrated through two layers of muslin, and the leaves of healthy plants were dusted with carborundum and rubbed gently with a cotton swab previously dipped into the suspension of virus inoculum.

2.3 Background of parental material

The parents for the current study were selected from previous evaluation which was carried out through a breeding program in the Agronomy Dept, Faculty of Agriculture, Suez Canal University, Ismailia, Egypt. This breeding program was started since few years ago (2003 & 2004) through earlier work which was done by El-Bramawy & Abdul Wahid (2005). Six faba bean parents were selected depend on the earliness, seed yield (g/plant) and degrees of resistance to some diseases at the Experimental field, Fac. of Agric., Suez Canal Univ., Ismailia, Egypt. In addition, some of them (six parents) also evaluated with reaction of BYMV infection previously by El-Beshehy (1999). These parents were chosen as resistant, moderately resistant and susceptible varieties according the former evaluation. Parental names, pedigree, earliness, seed yield (g/plant) and description symptoms were presented in Table (1).

2.4 Parental selection and their crosses

To conform the previous evaluation done in the field, green house experimental at the Agricultural Botany Dept., Fac. of Agric., Suez Canal Univ., Ismailia, Egypt was done to re-evaluate the interaction of the six faba bean parent's plants with BYMV disease under artificial infection conditions of the BYMV considering through season 2007/08. Table (2) shows the obtained results of the interaction between the six faba bean parent's plants with BYMV disease. These results exhibited the main percentage of infection incidence and

severity of the infection for the six faba bean parent's genotypes in comparing to their control.

2.5 Hybridization modeling and obtaining the crosses

According to determination of selected the six faba bean parents, a full diallel mating scheme (6 x 6), where all possible combination in two way among parents was made by hand pollination in season 2007/08 at the Experimental field, Fac. of Agric., Suez Canal Univ., Ismailia, Egypt. The seeds were made available by helping staff technician in Agronomy Dept, of the same University. The crosses obtained through the hybridization model were 30 crosses (hybrids and reciprocal).

2.6 Green house experiment design for interaction between crosses and BYMV

The seeds of faba bean crosses (30) with their respective parents (6) were planted in pots (40 cm in diameter) by rate of 10 seeds per pot. A randomized complete block design (RCBD) with three replicates was used. Each block contained the all pots crosses (30 hybrids and reciprocal) and their parents (six parents). Each plot consisted of one pot with 10 seeds per cross and also one pot per 10 seeds of each parent, for the F₁'s and their respective parents, respectively. This green house experiment was repeated two times through successive seasons 2008/09 and 2009/010 at Agricultural Botany Dept., Fac. of Agric., Suez Canal Univ., Ismailia, Egypt.

2.7 Infection by the inoculum of BYMV

Each of 6 parent and their 30 crosses were evaluated at reaction with BYMV infection using, the interaction faba bean genotypes with BYMV inoculum by artificial mechanical translation (AMT), which mentioned before. Three weeks from the inoculation by BYMV inoculum, leave symptoms were observed. Non-inoculated pots of faba bean generations plants (control) were growth parallel with the inoculated plants of faba bean, where used as a control. Neither fertilizer nor herbicide was applied during the experiment working, where only hand weeding was done when necessary.

2.8 Calculation of BYMV infection percentage and severity of disease

The parents (6) and their F₁'s hybrids and reciprocals (30) were evaluated and examined for disease severity as individual plants in each pot relation to total plants in each one. Table (2) counting and calculating the numbers of infected faba bean plants by BYMV as a percentage of BYMV disease incidences using the parameters rating scale. The disease severity (DS) method was adopted as per Yang *et al.* (1996).

$$DS (\%) = \frac{(\text{disease grade} \times \text{number of plants in each grade})}{(\text{total number of plants} \times \text{highest disease grade})} \times 100$$

2.9 Genetic parameters and Statistical analysis

Faba bean genotypes were partitioned into variations due to parents and crosses using the procedure of Statistical Analysis System (SAS). The analysis of variance for the crosses

was based on Griffing's method 2, model for fixed genotypes (Griffing, 1956) and the linear model (Singh & Chaudhary, 1977). The analysis was performed on individual environments (years/ two seasons) using the diallel-SAS programme written by Kang (1994) and a combined analysis over environments (years) using the diallel-SAS programme written by Zhang & Kang (1997).

The general linear model for individual environments/years was

$$Y_{ijk} = \mu + g_i + g_j + s_{ij} + r_{ij} + b_k + \mu_{ijk}$$

where; Y_{ijk} was the response of the k th observation in the i th environment of the plant; μ was general mean; g_i the general combining ability (GCA) of the i th parent; g_j the general combining ability (SCA) of the j th parent; s_{ij} the specific combining ability associated with the i th and j th cross; r_{ij} the reciprocal effects associated with ij th cross. b_k the effect of the k th replicate and μ_{ijk} is the error associated with each observation.

The general linear model for the combined analysis was

$$Y_{ijkl} = \mu + g_i + g_j + s_{ij} + l_k + b_l (k + g_{lik} + g_{ljk} + s_{lijk} + m_{ijl})$$

In this model, Y_{ijkl} was the observed response to BYMV across the two seasons; μ , g_i , g_j and s_{ij} and its partitions m_i and n_j were for the individual season analysis. The effect k was the effect of the k th season; $b_l (k)$ the effect of the l th replicate within the k th season. The effect g_{lik} was the general combining ability of the i th parent in the season; g_{ljk} the general combining ability of the j th parent in the k th environment and s_{lijk} the specific combining ability associated with the ij th cross in the season. Genetic components of the variation associated with GCA and SCA effects were estimated from their respective expected means squares. The ratio of these components was computed to estimate the relative importance of GCA in predicting progeny performance. The GCA and SCA effects and their standard errors were estimated according to Singh & Chaudary (1977). Pearson correlations using line and top cross means were calculated to compare line and top cross.

3. Results

The analysis variance of the modeling complete diallel fashion scheme (6 x 6), which includes the parental faba bean genotypes (Tribe White, Giza 3, Giza 714, Giza 429, Sakha 1 and BPL 710) shows in Table 3. There were variations ($p < 0.05$) among the tested faba bean genotypes for BYMV disease and seasons or years in the combined analysis. Moreover, the contrast parent x crosses (the test for average heterosis) was significant for both of the individual year/season and combined seasons as presented in Table (3).

Table 3 shows the Griffing analysis of variance for the crosses (hybrids) exhibited significant general combining ability (GCA), specific combining ability (SCA), maternal (M) and specific reciprocal (R) effects in both the individual year/season and in combined.

The ratio $\delta^2\text{GCA}/\delta^2\text{SCA}$ which presented in Table (3) were more than unity (1) for the resistance to bean yellow mosaic virus. On the other side, the combination interaction *i.e.* parents x crosses (P x C), crosses x years (C x Y), general combining ability x years (GCA x

Y), specific combining ability $\times$ years (SCA $\times$ Y), reciprocal, environmental, crosses $\times$ years (REC $\times$ Y), maternal $\times$ year (M $\times$ Y) effects were also significant for the resistance to BYMV disease. While, the maternal effects among the parents were significant just as the specific reciprocal ($p < 0.01$) as shown in Table (3).

Table 4 presents the estimates of GCA effects of each parent for total number of faba bean plants which resistance to bean yellow mosaic virus (BYMV). Sakha 1 cultivar behaved the same trend approximately as the resistant cultivar BPL 710. These both cultivars scored -3.91**, -5.14**, - 4.18** (BPL 710) and -1.64*, -2.16** -3.08** (Sakha 1) in seasons 2008/09, 2009/010 and their combined, respectively. On the other hand, the susceptible cultivar (Giza 2) used in this study exhibited significant and positive GCA in all the conditions, first (2008/09), second (2009/010) season and their respective combined (Table 4). However, the moderately susceptible *i.e.* Giza 429 and Giza 714 had significant and positive GCA effects in the first season, 2008/09 (3.64**) and also in the second season, 2009/010 (1.31*).

Regarding to the estimates of least square mean, table (5) shows the specific combining ability effects and reciprocal effects for 6 $\times$ 6 diallel analysis of resistance to bean yellow mosaic virus (BYMV) of faba bean. The crosses and their reciprocals manifested varying in degree of resistance to BYMV in each of the first, second and the combined season. The crosses *e.i.* $P_1 \times P_6$ (Tribe White $\times$ BPL 710) and $P_3 \times P_6$ (Giza714 $\times$ BPL 710), possessed the negative values and significant SCA effects in both seasons and their combined. The values of these SCA effects were -3.01*, -3.28* -3.89** ($P_1 \times P_6$) and -3.60*, -3.54* -4.18** ($P_3 \times P_6$) in 2008/09, 2009/010 season and their respective combined, in respectively (Table 5). Negative specific reciprocal effects for resistance to BYMV were significant for crosses $P_6 \times P_1$ (BPL 710 $\times$ Tribe White), $P_6 \times P_2$ (BPL 710 $\times$ Giza 3), $P_6 \times P_3$, (BPL 710 $\times$ Giza714), $P_6 \times P_4$ (BPL 710 $\times$ Giza 429) and $P_6 \times P_5$ (BPL 710 $\times$ Sakha 1), in season 2008/09 and 2009/010 and their respective combined (Table 5).

On the other hand, the crosses which used the parent Giza 3 (P_2) as a susceptible cultivar such as $P_1 \times P_2$, $P_2 \times P_3$, $P_2 \times P_4$ and $P_2 \times P_5$ (SCA effects) and $P_3 \times P_2$, $P_4 \times P_2$, and $P_5 \times P_2$ (SCA reciprocal effects) showed positive and significant values of SCA effects and their reciprocal effects, respectively through seasons 2008/09, 2009/010 and their combined. These SCA effects were 6.31**, 3.87*, 5.11** ($P_1 \times P_2$), 6.21**, 8.14**, 4.59** ($P_2 \times P_3$), -1.64, 2.00*, -3.01* ($P_2 \times P_4$) and 4.11**, 6.17**, 5.12** ($P_2 \times P_5$), while SCA reciprocal effects were 2.98*, 1.99, 3.01** ($P_3 \times P_2$), 2.01, 1.38, 1.84 ($P_4 \times P_2$) and 2.58*, 6.07**, 4.36** ($P_5 \times P_2$), respectively through seasons 2008/09, 2009/010 and their combined (Table 5).

In respect of the rest of the crosses which results from hybridization between moderately resistant or moderately susceptible with susceptible or resistance cultivars varied from positive to negative values, where some of these pass the significant level and the other did not reach to the level of significant (Table 5).

4. Discussion

In spite of the importance of the diseases resistance in faba bean crop, the progress made in

resistance breeding to bean yellow mosaic virus (BYMV) disease in *Vicia faba* is rarely and it should be taken into consideration in the future breeding programme. Therefore, it is urgently to shed the light on the faba bean host resistance, since it is acknowledged that, resistant faba bean varieties could potentially form the basis of sustainable management strategies for the diseases (Asiedu, 1998). The selection of resistant varieties and continuous breeding programme for disease resistance appears to be the efficient means of controlling the disease considering (BYMV).

The results of this study clearly indicated that high genetic variation was observed from diallel technique, for bean yellow mosaic virus (BYMV) resistance. Using this technique, we showed that BPL 710 and Sakha 1 were highly resistant for BYMV and possess the highest negative values of GCA. Therefore, they could be considered good combiners for BYMV resistant and showing their aptitude to transmit the resistance trait at any future breeding program. Similar finding was reported in earlier by Shukla *Et Al.* (1978) and MA *Et Al.* (1995).

During survey periods, BYMV genotypes were found widely variations among seasons and locations. Where, genotypes x years interaction were significant, indicating the lack of stability across environments. Hence, this suggests that faba bean parents indicating crosses and also resulted hybrids must be evaluated in more than one year or environment to obtain a precise genetic information.

The ratio $\delta^2\text{GCA}/\delta^2\text{SCA}$ (more than unity) cleared greater role of additive effects in the genetic expressions, which controlling the resistance to bean yellow mosaic virus. However, it should be emphasized that $\delta^2\text{GCA}/\delta^2\text{SCA}$ ratio may not always project the true picture of the gene action for a character. This case is due to the deferential of parental ability to combine well with each other. These findings were so nearly with the results reported by Jones & Smith (2005) during their studies on inheritance of hypersensitive resistance to *Bean yellow mosaic virus* in narrow-leaved lupin (*Lupinus angustifolius*). On the other hand, such combination depends considerably up complex interaction among genes and genotype by environment.

The non-predominance of neither GCA nor SCA was further reflected by non-significant correlation between the parental means and their GCA effects. This indicates that progeny performance cannot be determined from parental performance.

The significant parent female by parent male interaction also confirms the presence of non-additive components in the resistance of crosses/hybrids to bean yellow mosaic virus (BYMV). The ratio of additive variance to total genetic variance in a population is an indication of relative importance of both GCA and SCA in predicting progeny performance in resistance of *Vicia faba* to BYMV. The closer this ratio is to one the greater the chances of predicting progeny performance based on the general combining ability (GCA). Singh (1980) and Shankar *Et Al.* (2002) reported similar finding during their work on *Vigna mungo* and *Lupinus angustifolius*, respectively.

The significance of the contrast, parent vs. crosses justifying the separation of parents and

crosses before the diallel analysis was done. The GCA and SCA sum of squares accounted for 33.14 and 26.46%, respectively of the variation among the faba bean crosses. This demonstrated that both of additive and non-additives gene effects are also important in determining the expression of resistance to BYMV in *Vicia faba* even though the SCA contributed more.

Generally, it is worth to note that Bean yellow mosaic virus (BYMV) was more severe in fields with dense weed populations and it has been associated with other faba bean diseases incidence and severity. Some farmers do not see the need to weeds their faba bean fields, because the highest piece of herbicide and lowest income from the unit area. This leads to spread BYMV and decreases the resistance of cultivars.

From this findings the magnitude and sign of creating new genotypes have resistance genes for BYMV. our results also indicated that initial selection of parents for hybrid combination might probably could be largely be based on the disease reaction of the considering pathogen (BYMV). However, the significance of the maternal and reciprocal effects which detected suggested that the variation were also exhibited.

5. Conclusions

To our knowledge, this is the first study to report on the diallel analysis of bean yellow mosaic virus (BYMV) disease resistance in *Vicia faba* L. Significance implications for faba bean breeding programs that seek to incorporate resistance to bean yellow mosaic virus (BYMV). This is because in the diallel analysis, the additive effects and non-additive genetic effects are so desirable for the resistance to BYMV disease. Hence the progeny performance may be based on the parent performance per se. Therefore, it had emphasized the need to screen parents and crosses before their use in breeding suggesting that combining ability analysis based on progeny test data is useful in faba bean, *Vicia faba* breeding programme.

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Table 1. Faba bean genotypes name, pedigree, earliness (days to 50% flowering), seed yield (g/plant).

No.	Parents Cultivars	Pedigree	Earliness	Seed yield (g/plant)	Description symptoms
P1	Tribe White	Individual plant from sudanese selection	54.26	31.58	Yellow and Leaf roll in upper leaves
P2	Giza 3	Cross (Giza 1 x N A 29)	50.23	23.62	Savers Mosaic, Yellow and Leaf roll in upper leaves
P3	Giza714	Cross (462B1 908/83/503/453/ 83	52.12	31.02	Mosaic, Yellow and Leaf roll in upper leaves
P4	Giza 429	Individual plant selection from Giza 402	52.10	33.98	Light Leaf roll in upper leaves
P5	Sakha 1	Cross(7161924/88 x 620/283/81)	49.21	38.59	Yellow and Leaf roll in upper leaves
P6	BPL 710	NA, Introduce from Clombia.	48.02	37.41	Resistant

Table 2. Interaction between faba bean parental plants and BYMV with scale rating.

No.	Parents Cultivars	S/T * Replicates	Percentage of infection	Percentage of disease severity (DS %).	Interaction Category**
P1	Tribe White	20/30	66.67 %	33.33 %	Moderately Tolerance
P2	Giza 3	25/30	83.33 %	83.33 %	Susceptible
P3	Giza714	22/30	73.33 %	55.00 %	Moderately Tolerance
P4	Giza 429	18/30	60.00 %	15.00 %	Tolerance
P5	Sakha 1	19/30	63.33 %	48.33 %	Moderately Tolerance
P6	BPL 710	-	0.00 %	0.00 %	Resistance

* = Number of symptomatic plant (S) / Total number of tested plants (T).

** 0-10 = Resistance, 10.10 – 30 = Tolerance, 30.10 – 60 = Moderately Tolerance, 60.10 – 90 = Susceptible and 90.10 – 100 = Highly Susceptible.

Table 3. Diallel analysis of variance for bean yellow mosaic virus (BYMV) of faba bean.

Sources of variation	Degree of freedom	Mean squares		
		2008/09	2009/010	combined
Reps	2	9.31*	8.82*	10.30
Years (Y)	1	-	-	24.12**
Reps (R)	4	-	-	15.90*
Genotypes (G)	35	267.11**	149.80**	95.57**
Parent (P)	5	136.23**	102.80**	58.45**
Cross (C)	29	142.84**	150.03**	91.49**
GCA	5	276.71**	229.58**	270.33**
SCA	18	93.17**	110.07*	104.27**
δ^2 GCA/ δ^2 SCA	-	2.97	2.09	2.59
Maternal	5	128.03**	118.95**	107.13**
Reciprocal	18	66.13**	53.43**	21.70**
P x C	1	56.67**	40.27**	26.28*
C x Y	29	-	-	33.03**
GCA x Y	5	-	-	30.40**
SCA x Y	18	-	-	84.38**
REC x Y	18	-	-	16.55*
M x Y	5	-	-	43.15**
Error pooled		11.37	22.62	16.99

*, ** Significantly different from zero at 0.05 and 0.01 probability levels, respectively.

Table 4. Estimates of general combining ability (GCA) effects for 6 x 6 diallel analysis of resistance to bean yellow mosaic virus (BYMV) of faba bean.

No.	Parental	2008/09		2009/010		Combined	
		LSM***	GCA	LSM	GCA	LSM	GCA
P1	Tribe White	9.17	-1.89*	8.99	1.30*	9.08	1.91*
P2	Giza 3	11.6	2.71**	9.89	3.65**	10.75	4.11**
P3	Giza714	18.12	1.09	16.08	1.31*	17.10	0.13
P4	Giza 429	13.28	3.64**	15.09	1.04	15.69	1.11*
P5	Sakha 1	7.12	-1.64*	6.37	-2.16**	6.75	- 3.08**
P6	BPL 710	6.34	-3.91**	5.19	-5.14**	5.77	- 4.18**
SE (gi - gj)		2.95		2.78		2.87	

* Significantly different from zero at 0.05 and 0.01 probability levels, respectively.* ,*

*** LSM = least square means

Table 5. Estimates of specific combining ability (SCA) effects and reciprocal effects for 6 x 6 diallel analysis of Resistance to bean yellow mosaic virus (BYMV) of faba bean.

Crosses	2008/09		2009/010		Combined		Effects
	LSM***	SCA	LSM	SCA	LSM	SCA	
P1 x P2	16.95	6.31**	20.39	3.87*	18.67	5.11**	SCA
P1 x P3	11.32	1.69	14.69	2.19*	13.01	3.00*	SCA
P1 x P4	10.30	2.47*	11.09	1.39	10.69	1.08	SCA
P1 x P5	7.30	4.10**	6.98	5.11**	7.14	7.39**	SCA
P1 x P6	5.21	-3.01*	7.97	-3.28*	6.59	-3.89**	SCA
P2 x P3	19.32	6.21**	22.68	8.14**	21.00	4.59**	SCA
P2 x P4	17.30	-1.64	18.21	2.00*	17.76	-3.01*	SCA
P2 x P5	15.28	4.11**	13.90	6.17**	14.59	5.12**	SCA
P2 x P6	6.31	2.84*	12.01	3.14*	9.16	2.61*	SCA
P3 x P4	9.31	1.36	11.67	1.67	10.49	2.11*	SCA
P3 x P5	7.79	4.09**	7.10	6.33**	7.45	5.29**	SCA
P3 x P6	4.99	-3.60*	6.30	-3.54*	5.65	-4.18**	SCA
P4 x P5	9.79	0.97	12.39	1.22	11.09	0.37	SCA
P4 x P6	5.64	-1.62	5.10	-2.33*	5.37	-2.41*	SCA
P5 x P6	3.68	-1.87	4.23	-1.08	5.96	-1.99	SCA
P2 x P1	20.03	1.61	23.19	2.51*	21.61	-1.87	Recip
P3 x P1	11.63	2.36*	9.36	1.94	10.49	2.23*	Recip
P3 x P2	14.69	2.98*	13.98	1.99	14.34	3.01**	Recip
P4 x P1	8.88	4.32**	7.39	3.68**	8.14	5.06**	Recip
P4 x P2	15.97	2.01	12.98	1.38	14.48	1.84	Recip
P4 x P3	11.10	3.14*	9.89	2.99*	10.49	2.31*	Recip
P5 x P1	7.39	4.98**	6.32	4.19**	6.89	5.16**	Recip
P5 x P2	15.39	2.58*	17.97	6.07**	16.68	4.36**	Recip
P5 x P3	9.07	-1.68	10.20	1.97	9.64	-1.91	Recip
P5 x P4	6.15	0.98	5.38	1.71	5.77	1.67	Recip
P6 x P1	7.19	-6.11**	8.10	-5.98**	8.70	-6.19**	Recip
P6 x P2	8.31	-2.67*	7.08	-3.58**	7.70	-4.42**	Recip
P6 x P3	5.99	-4.32**	4.29	-6.87**	5.14	-10.18**	Recip
P6 x P4	6.13	-3.91**	5.33	-5.48**	5.73	-6.11**	Recip
P6 x P5	4.21	-6.68**	3.94	-4.69**	4.08	-5.67**	Recip
SE (sii)	-	4.31	-	3.76	-	2.61	-
SE (sij)	-	2.01	-	1.59	-	1.69	-
SE (sii-sjj)	-	4.26	-	4.65	-	3.91	-
SE (ii-skj)	-	4.96	-	5.14	-	4.11	-
SE (ij-skj)	-	5.24	-	4.96	-	3.79	-

P1= Tribe White, P2= Giza 3, P3= Giza714, P4 = Giza 429, P5 = Sakha I and P6 = BPL 710

*, **Significantly different from zero at 0.05 and 0.01 probability levels, respectively.

*** LSM = least square means.