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Short Communication

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Screening and cross-compatibility of various *Vigna* species for yellow mosaic virus resistance

Nirmala Sehrawat,[1*] Mukesh Yadav[2]

[1]Centre for Biotechnology, Maharshi Dayanand University, Rohtak, Harayna, India
[2]Department of Biotechnology, Maharishi Markandeshwar University, Mullana, Ambala, India

Abstract: Seven *Vigna* species were studied for yellow mosaic virus resistance during rainy season. The YMV resistant species *V. umbellata* was attempted to cross with the YMV susceptible species in line x tester fashion using hand emasculation and pollination technique. The results demonstrated that severe infection of yellow mosaic virus at early seedling growth stage up to maturity produced less pods and those produced are either empty or with infected seeds. Different combining compatibilities were also observed among the studied *Vigna* species. Ricebean exhibited more compatability with *V. mungo* followed by *V. sublobata*. The genotypes of *V. luteola*, *V. trilobata*, *V. aconitifolia* and *V. unguiculata* were found incompatible in present investigation. The number of F_1 seeds in the crossed pod ranged from 1 to 3. Immature or shriveled seeds of crossed pods revealed integrity of the various *Vigna* species. Present investigations suggests ricebean as a potential natural resource for YMV resistance and this trait can be introduced in agriculturally important but YMV susceptible crops through breeding. In near future, improved varieties of food grain legumes may surplus the sustainable agriculture production in biotic stress prone areas.

Keywords: Legumes, yellow mosaic virus, screening, crossing, cross-compatibility

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Legumes are an imperative, environment-friendly food grain crops with rich source of proteins, minerals and vitamins. Legumes may surmount the rising problem of protein malnutrition which is a major nutrition problem in Asia and affects children most rigorously (Graham and Vance, 2003). These crops are important part of sustainable agriculture production. Legumes play critical role in restoration of soil fertility by atmospheric nitrogen fixation in symbiosis with *Rhizobium* species. Rapid growth, early maturity and easily digestibility without flatulence further add their value in various cropping systems (EL-Karamany, 2006). Legumes are utilized in several ways, where seeds, sprouts and young pods are consumed as sources of protein, amino acids, vitamins and minerals, and plant parts are used as fodder and green manure.

The major yield limiting factors in legumes includes susceptibility to various biotic (viral, fungal, bacterial pathogens and insects) and abiotic (temperature, drought, salinity, water -logging etc.) stresses (Sahoo et l. 2002). Among various biotic restraints, yellow mosaic virus is the major threat for huge economical losses in the Indian subcontinent (Nene, 1973). The disease is caused by begomoviruses with bipartite genomes (Karthikeyan et al. 2004). Begomoviruses are a large group of white fly-transmitted plant viruses containing single-stranded circular DNA encapsidated in geminate particles (Khattak et al. 2000). Initial symptoms of the disease appear as small yellow specks along the veins which spread over the leaf. In severe infections the entire leaf may become chlorotic which later turns in to necrotic regions (Qazi et al. 2007).

Breeding has appeared as a feasible alternate for overcoming limitations of stable and efficient transformation system for legume improvement. However, efforts have been made with limited success to augment the tolerance against yellow mosaic disease through this approach. Lack of inherent variability, low harvest index and absence of appropriate ideotypes for different cropping systems further make vulnerable the crop improvement. New sources of resistance to YMV (including inter-specific

Corresponding Author:
Sehrawat N. (✉) Center for Biotechnology, Maharshi Dayanad University, Rohtak-124001, India
Email: nirmalasehrawat@gmail.com

sources) have been identified and molecular markers linked to resistance genes become available (Maiti et al. 2011; Chen et al. 2012). Unfortunately, none of the known variety of legumes is fully resistant to YMV infection (Seo et al. 2004).

The wild relatives of crop species possess greater genetic diversity and resistance than their related cultigens and are considered as source of important genes for the genetic improvement of weak crops (Pandiyan et al. 2010). According to Polhill and van der Maesen (1985), the genus *Vigna* consists of more than 150 species originating mainly from Africa and Asia which includes seven cultivated species namely cowpea (*Vigna unguiculata* (L.) Walp.), bambara groundnuts (*Vigna subterranea* (L.) Verdc.), mungbean (*Vigna radiata* (L.) Wilczek), urdbean (*Vigna mungo* (L.) Hepper), adzuki bean (*Vigna angularis* (Willd.) Ohwi & Ohashi), moth bean (*Vigna aconitifolia* (Jacq.) Marechal), and rice bean (*Vigna umbellata* (Thunb.) Ohwi & Ohashi). Rice bean is an important crop of South-east Asia. Its centre of origin, genetic diversity and its wild form has dispersed across a wide area of the tropical monsoon forest climatic zone from eastern India, Nepal, Myanmar, Thailand, Laos and southern China to East Timor (Tomooka, 2009). It has many valuable characters as bruchid resistance, disease resistance particularly to yellow mosaic virus and bacterial leaf spot along with the highest potential grain yield among Ceratotropis species (Tomooka et al. 2000b; Kashiwaba et al. 2003; Somta et al. 2006). However; rice bean has not been subjected to efficient breeding and it is described as a scientifically ignored crop with immense potential.

The present study has been carried out to screen the *Vigna* species of different origin for yellow mosaic virus resistance. Their inter-specific combining ability has also been studied to improve the weak crops via breeding approach.

MATERIAL AND METHODOLOGY

Plant material

Seeds of 7 *Vigna* species i.e. *V. mungo, V. sublobata, V. unguiculata, V. aconotifolia, V. trilobata, V. luteola,* and *V. umbellata* were procured from National Bureau of Plant Genetic Resources, New Delhi and Division of Genetics, Indian Agricultural Research Institute, New Delhi.

Screening for yellow mosaic virus symptoms

Seeds of all *Vigna* species were sown in separate rows with proper spacing in experimental field plot (20'x30') during rainy season at Herbal Garden, Maharshi Dayanand University, Rohtak, Haryana. The plant leaves were observed for the development of yellow mosaic disease symptoms throughout the crop growth period and photographs were taken regularly.

Crossing of YMV resistant and susceptible genotypes

The identified YMV resistant *Vigna* species was used as source of yellow mosaic virus resistance and considered as male parent (♂) while YMV susceptible *Vigna* species was taken as female parent (♀) for breeding purpose. Seeds of parental lines were sown in separate rows with proper spacing in field plot (20'x20') at Herbal Garden, M.D.U., Rohtak. The YMV resistant and susceptible genotypes were tried to cross in line x tester fashion using hand emasculation and polllination technique in early morning hours as reported by Boling et al. (1961). Significant numbers of flowers were crossed to obtain higher number of hybrid pods.

RESULTS

Screening of *Vigna* species for YMV symptoms

The field evaluation of different *Vigna* species showed that yellow mosaic virus drastically infected plants of *V. mungo, V. sublobata, V. unguiculata, V. aconotifolia, V. trilobata* and *V. luteola* at late vegetative stage (Fig.1A, 1B, 1C and 1D). YMV infection at reproductive stage produced either empty pods or yellow color pods with in-viable/infected seeds (Fig.1E). However, the plants of *V. umbellata* did not show any YMV symptoms throughout the growth period and this species was considered as resistant against yellow mosaic disease (Fig.1F).

Cross-compatibility of *Vigna* species

The out crossing rate of different *Vigna* species showed useful variations. The pollen grains of YMV resistant ricebean showed significant compatibility with YMV susceptible *V. mungo* followed by *V. sublobata*. However, *V. umbellata* was non-compatible with other wild *Vigna* species i.e. *V. unguiculata, V. aconotifolia, V. trilobata* and *V. luteola* in this study. The crossed pods obtained enclosed 1 to 3 F_1 healthy seeds (Fig. 1G) but some successful crosses also showed poor seed filling or immature or shriveled seeds.

DISCUSSION

The results revealed that crossing technique reported by Boling et al. (1961) produced successful pod set with good seed filling in *V. mungo* and *V. sublobata* (Fig. 1). Variations in origin and reproductive hurdles produced hybrid pods with immature seeds or caused hybrid abort. These mechanisms prevail for maintaining the integrity of related species (Adinarayanamurthy et al. 1993). Results also suggested that *V. mungo* is highly crossable with *V. umbellata.* The findings of present investigations corroborates with earlier reports in other *Vigna* species (Khattak et al. 2006; Pandiyan et al. 2012). The F_1 hybrids can be screened further for YMV resistance (in rainy season), for their morphology, growth habit, flowering, along with seed size with respect to their respective progenitors. Morphological characteristics of hybrid mature plants help in testing of genetic purity of hybrid

Figure 1 Different *Vigna* species showing YMV susceptibility (A, B, C, and D), production of yellow pods, YMV resistant ricebean (F) and crossed pod with single seed (G).

seeds for the desired trait (Dongre et al. 2011). Evaluation of hybrids in disease will certainly lead to the development of stable and improved variety for yellow mosaic disease resistance.

Conclusion

Most of studied *Vigna* species (except *V. umbellata*) are sensitive towards yellow mosaic virus particularly in rainy and humid season. The infection of YMV at initial growth stage caused complete loss of the crop results in zero grain yields. However; ricebean plants exhibited high resistance for YMV throughout the crop season. All *Vigna* species also showed different cross-compatibility. Therefore, this study suggests that ricebean can be used as a source of YMV resistance that can be introduce in YMV susceptible crops through breeding. Improved varieties of nutritious grain legumes for biotic stress tolerance will significantly add to the sustainable agriculture production in disease prone areas in near future.

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