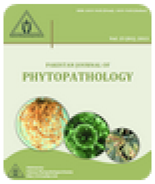
Official publication of Pakistan Phytopathological Society
Pakistan Journal of Phytopathology
ISSN: 1019-763X (Print), 2305-0284 (Online)
http://www.pakps.com



GENETIC POTENTIAL OF COTTON GERMPLASM FOR MANAGEMENT OF BACTERIAL BLIGHT DISEASE

[a]Muhammad Atiq, [a]Waqas Ahmad, [e]Muhammad Rafique, [a]Shahbaz T. Sahi, [b]Abd–ur-Rehman, [a]Muhammad Younis, [a]Muhammad Shafiq, [c]Khalil Ahmad, [a]Tayyaba M. Ahmad, [d]Umar Nawaz
[a] Department of Plant Pathology ,University of Agriculture Faisalabad, Pakistan.
[b] Department of Plant Pathology, University of Poonch, Rawalakot AJK, Pakistan.
[c] Govt, College Satiana Road Faisalabad, Pakistan.
[d] Department of Plant Pathology ,University of Agriculture Faisalabad, Pakistan.
[e] Pest Warning & Quality Control of Pesticides, Ferozwala, Distt. Sheikhupura.

ABSTRACT

In present study fifteen varieties of cotton (FH-114, Bt-121, SLH-336, Kirn, SLH Bt-6, Bt-666, CIM-595, FH-113, Bt-MK2, Bt-222, Bt-457, Bt-7, SLH-317 and Bt-986) were cultivated in research area of the Department of Plant Pathology University of Agriculture Faisalabad during 2012 to determine their genetic response against bacterial blight under randomized complete block design (RCBD). Results showed that none of variety showed immune response against disease while FH-114, Bt-121 and SLH-336 showed moderately resistance to bacterial blight with 15, 17 and 20% disease incidence respectively. While Kirn, SLH Bt-6, Bt-666, CIM-595, FH-113 and Bt-MK2 showed moderately susceptible behavior with (29-38%) disease incidence. The varieties SG-1, Bt-222, Bt-457, Bt-7, SLH-317 and Bt-986 showed highly susceptible response with (41-56%) disease incidence against the disease.

Keywords: Screening, Germplasm, cotton, resistant and *Xanthomonas campestris* pv. *malvacearum*.

INTRODUCTION

Cotton (*Gossipium hirsutum* L.) is the backbone of national economy of Pakistan. It contributes 6.9% to the value added in agriculture and upto1.4 % of GDP (GOP, 2011). Pakistan is the fourth largest cotton producer and is third largest consumer in the world. Cotton yield is influenced by several biological factors which include many diseases of cotton. Among diseases bacterial blight is a potential threat to the cotton caused by *Xanthomonas campestris* pv. *malvacearum (*Vauterin *et al.,* 2000). Yield losses due to bacterial blight of cotton depends upon the type of cultivars and age of the crop plant (Mishra and Krishna, 2001). Although the use of fungicides for the management of disease is superior method but currently it is not successful because of its drawback of pollution and systemic nature of bacterium (Gan *et al*., 2006). Pedley and Martin, (2003) resulted that resistant varieties have been advocated in the past for the management of this disease. It was the most efficient and eco-friendly method for the management of bacterial blight of cotton. Use of resistant varieties is one of the commercial method for the management of disease because it makes possible to avoid other management strategies including acid-delinting seed, sanitary practices during ginning and processing, applying fungicides to seed and the destruction of diseased plant residues followed by tillage operations (Thaxton and El-Zik, 2001; Turkkan and Dolar, 2009). Development of resistant variety is a long-term procedure and short-term solution is the screening of available germplasm of cotton for the source of resistance against bacterial blight of cotton, that's why the present study was designed with the objective to find out source of resistance against bacterial blight disease of cotton.

MATERIALS AND METHODS

Fifteen cotton varieties (Bt-986, CIM-595, Bt-MK2, Bt-7, SLH-336, Bt-121, FH-114, Bt-222, Bt-457, KIRN, Bt-666, SLH Bt-6, SG-1, SLH-317 and FH-113) were collected from Ayub Agriculture Research Institute (AARI) and Cotton Research Institute, Sahiwal. All varieties of cotton

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* Corresponding Author:
Email: atiq1@yahoo.com

were planted in field under RCBD during summer 2011 in Research Area of Plant Pathology, University of Agriculture, Faisalabad, Pakistan Each variety was considered as treatment having three replications with plant to plant (P x P) and row to row (R x R) distance of 20 cm and 60 cm respectively. Seeds of these verities were neither treated with chemical nor given acid delinting to increase chances of primary infection of the disease. The agronomic practices were done properly for the better growth of plants. The data of disease incidence was collected on weekly basis on seedling, flowering and at boll formation by using Sheo Raj disease rating scale of (Sheo Raj, 1988). Scale shows that if disease incidence on a variety is zero to more than 40% then that variety shows different responses i.e. if 0% = immune, 1-10% = highly resistant, 11-20% = moderately resistant, 21-40% = moderately susceptible, > 40% = highly susceptible.

Disease incidence was calculated by using formula (Jagtap *et al*., 2012);

$$Disease\ incidence\ \% = \frac{Total\ infected\ plants\ observed}{Tola\ plants\ observed} \times 100$$

Statistical Analysis: The data obtained with respect to disease incidence was statically analyzed by using SAS/STATE software (SAS Institute, 1990) with least significant design (LSD) at 5% probability level (steel *et al.,* 1997).

RESULTS

Symptoms reveal the clear image of disease incidence by which we can easily recognize the disease. The symptoms appeared in the form of water soaked spots which were formed as a result of pathogen attack. These spots became dark brown with the passage of time and spread on the ventral surface of young leaves. Field screening of cotton germplasm against bacterial blight showed highly significant results. A significant difference was observed among cotton germplasm in terms of disease incidence. Disease incidence ranged from 15 to 56 percent. Among fifteen varieties FH-114, Bt-121 and SLH-336 showed moderately resistance to bacterial blight with disease incidence of 15, 17 and 20% respectively, while Kirn, SLH Bt-6, Bt-666, CIM-595, FH-113 and Bt-MK2 showed moderately susceptible behavior with (29-38%) disease incidence. The varieties SG-1, Bt-222, Bt-457, Bt-7, SLH-317 and Bt-986 showed highly susceptible response with (41-56%) disease incidence against the disease.(Table 1).

Table 1. Response of Fifteen cotton varieties against bacterial blight.

Cultivar/s varieties	Disease incidence (%age)	Rating	Response
FH-114	15 m	2	MR
Bt-121	17 l	2	MR
SLH-336	20 k	2	MR
KIRN	29 j	3	MR
SLH Bt-6	28 i	3	MR
Bt-666	34 h	3	MR
CIM-595	34 h	3	MR
FH-113	35 g	3	MR
Bt-MK2	38 f	3	MR
SG-1	41 e	4	HS
Bt-222	46 c	4	HS
Bt-457	45 d	4	HS
Bt-7	46 c	4	HS
SLH-317	50 b	4	HS
Bt-986	56 a	4	HS
LSD		0.36	

*Means sharing same letters in column are not statistically different at 5% probability.

DISCUSSION

Plant disease resistance is characterized by either partial or complete suppression of pathogen growth or replication at the site of infection **(**Bhuiyan, 2009). There is mechanism behind in each type of resistance which supports the plants population to perform action against a virulent pathogen. When *Xanthomonas campestris* pv. *malvacearum* entered into the mesophyll cells of cotton leaves they showed necrotic lesions which were due to the host cells death response against the bacteria which prevented them from further attack. This type of response is called hypersensitive response (HR). In resistance varieties of cotton the HR mechanism were not compulsory to initiate with the combination of host and pathogen it required a source of energy in the form of ATP which were responsible for efflux of K^+ and influx of H^+ leading to that area where bacteria attacked. Phytoalexins and phenolic compounds (Dihydroxycadalene and Lacinilene) were responsible for induced resistance by phenylpropanoid pathway in varieties of cotton after the attacked of *Xanthomonas campestris* pv.*malvacearum,* while susceptible varieties were failed to produce those types of compounds (Goto, 1992).

The Pathogenesis-Related (PR) Proteins were also accountable for exhibited genetic potential of cotton against the bacterial blight. Metzger *et al*. (1999) reported that most PR proteins in the resistant cotton plant were acid-soluble, low molecular weight and protease-resistant proteins located in the vacuole of plant cells (Van *et al.*, 1999). Cheong *et al*., (2000) identified different types of proteins in resistant cotton plant like peroxidases, ribosome-inactivating proteins, chitinases, defenses, thionins and oxalate oxidase. Among these PR-proteins chitinases was most important because it used to degrading the pathoen cell wall by their mode of action (Li *et al*., 2001).

REFERENCES

GOP. 2011. Pakistan Economic Survey. Economic Advisor's Wing, Finance Division, Islamabad. Government of Pakistan.

Bhuiyan N.H., G. Selvaraj, Y. Wei, and J. King. 2009. Role of lignification in plant defense. Plant Signaling and Behavior 4: 158-159.

Cheong, Y.H., C.Y. Kim, H.J. Chun, B.C. Moon, H.C. Park, J.K. Kim, S.H. Lee, C.D. Han, S.Y. Lee and M.J. Cho. 2000. Molecular cloning of a soybean class III β-1,3-glucanase gene that is regulated both developmentally and in response to pathogen infection. Plant Sci.2000; 154: 71-81.

Gan, Y.T., K.H. M. Siddique, W.J. MacLeod and P. Jayakumar. 2006. Management options for minimizing the damage by Ascochyta blight (*Ascochyta rabiei*) in chickpea (*Cicer arietinum* L.). Field Crops Res. 97: 121-134.

Goto, M. 1992. Fundamentals of Bacterial Plant Pathology, Academic press, New York. Inc. pp.170-172.

Jagtap, G.P., A.M. Jangam and D. Utpal. 2012. Sources of resistance of different cotton genotypes against bacterial blight disease incited by *Xanthomonas axonopodis pv. malvacearum* under natural epiphytotics. Scientific J. Genet.1: 4-9

Li W.L., J.D. Faris, S. Muthukrishnan, D.J. Liu, P.D. Chen and B.S. Gill. 2001. Isolation and characterization of novel cDNA clones of acidic chitinases and β-1,3-glucanases from wheat spikes infected by *Fusarium graminearum*. Theor. Appl. Genet. 102: 353-362.

Metzger, L.G. and F.J. Meins. 1999. Functions and regulation of plant β-1,3-glucanases (PR-2). *In:* Datta, S. K., Muthukrishnan, S. Eds. Pathogenesis-Related Proteins in Plants. CRC Press, Boca Raton, Florida, p. 77-105

Mishra, S.P. and A. Krishna. 2001. Assessment of yield losses due to bacterial blight in cotton. J. Mycol. Pl. Pathol. 31(2): 232-233.

Pedley, K.F. and G.B. Martin. 2003. Molecular basis of Pto-mediated resistance to bacterial speck disease in tomato. Ann. Rev. Phytopathol. 41: 215-243.

SAS Institute Inc., 1990. SAS/STAT User's Guide, Version 6, Cary, NC:SAS Institute Inc.

Sheo Raj. 1988. Grading for cotton disease, Central Inst. *for* Cotton Res., Nagpur Bull., pp. 1-7.

Thaxton, P.M. and K.M. El-Zik. 2001. Bacterial blight. p. 34-35. *In:* T.L. Kirkpatrick and C.S. Rothrock (ed.) Compendium of Cotton Diseases. 2nd Ed. Am. Phytopathol. Soc., St. Paul, MN

Turkkan, M. and F.S. Dolar. 2009. Determination of pathogenic variability of *Didymella rabiei*, the agent of ascochyta blight of chickpea in Turkey. Turkish J. Agric. Forestry 33: 685-591

Steel, R.G., J.H. Torrie and D.A. Dickey. 1997. Principles and Procedures of Statistics. A Biometrical Approach 3rd Edition. McGraw Hill book Co. Inc. New York, U.S.A.

Vauterin, L., J. Rademaker and J. Swings. 2000. Synopsis of the taxonomy of the genus Xanthomonas. Phtyopathol. 90:677-682.

Van Loon L.C. and E.A. Van Strien. 1999. The families of pathogenesis-related proteins, their activities, and comparative analysis of PR-1 type proteins. Physiologic. Mol. Pl. Pathol. 1999; 55: 85-97.