

Analysis of physiological and biochemical parameters with yield components in cotton genotypes under drought stress

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ABSTRACT : Drought stress adversely affects the growth, development and ultimately yield of cotton. The growth and productivity of cotton plants depend largely on their vulnerability to environmental stress. Water deficit is the major constraint that limits agricultural production. Cotton cultivars that can endure and recover from drought are needed to minimize yield loss in dry land areas and to reduce the water needs of irrigated production. Several efforts have been taken to improve cotton production under water limiting conditions through conventional breeding techniques. However, progress in traditional breeding approach has been slow due to limited knowledge on genetics of drought tolerance and involvement of several complex tolerance mechanisms. A study was conducted to determine the association analysis of physiological and biochemical and yield parameters related to water stress in cotton. Genotypic correlation coefficients between different characters were worked out. The present study indicated that seed cotton yield showed significant positive association with photosynthetic rate, NRase activity, SPAD and total chlorophyll content at genotypic level indicating that these characters can be improved simultaneously.

Key Words : Leaf photosynthetic rate, Stomatal diffuse resistance, Soluble protein, Nitrate reductase activity, Total chlorophyll, Yield

How to cite this paper : Ananthi, K., Vijayaraghavan, H., Karuppaiya, M., Gomathy, M., Anand, T. and Senthil Raja, G. (2012). Analysis of physiological and biochemical parameters with yield components in cotton genotypes under drought stress, *Adv. Res. J. Crop Improv.*, **3** (1) : 14-16.

Paper History : Received : 01.12.2011; Revised : 05.04.2012; Accepted : 26.04.2012

Cotton is relatively drought-tolerant, but severe water stress can slow plant development, cause small bolls and squares to shed, and thus reduce the seed cotton yield. This is of agricultural importance since the incidence to stress is unpredictable and plants may be exposed to drought stress at any time during their life cycle under field conditions. Maintenance of adequate soil moisture is essential for successful crop production. Drought endurance recovery needs the special characters to minimize yield loss and reduced water has for irrigated crops. Water stress is considered to be a moderate loss of water, which leads to stomatal closure and limitation of gas exchange. Water stress is characterized by reduction of water content, turgor and total water potential leads to closure of stomata, decrease in cell enlargement and

growth. Severe water stress may result in arrest of photosynthesis, disturbance of metabolism, and finally death (Amarjit *et al.*, 2005). Hsiao (1973) concluded that water stress inhibits cell enlargement more than cell division. It reduces plant-growth inhibition of various physiological and biochemical processes, such as photosynthesis, respiration, ion uptake, carbohydrates translocation, nutrient metabolism and hormones (Bhatt and Srinivasa Rao, 2005).

Correlation coefficients between different characters were worked out as per Falconer (1964). Genotypic correlation coefficients were further portioned into direct and indirect effects by path analysis as suggested by Dewey and Lu (1959).

RESEARCH PROCEDURE

The aim of this experiment was to investigate the responses caused by progressive water stress and the necessary time to have biochemical and physiological changes of *Gossypium* spp. during the vegetative, squaring and boll development stages. For present investigation, four F₃ populations, one F₄ population along with parents were subjected for genetic diversity analysis using physiological features. Three field trails were conducted one at *Kharif* 2008, second in Summer 2009 and another at *Kharif* 2009, at Department of Cotton, Centre for Plant Breeding and Genetics, Tamil Nadu Agricultural University, Coimbatore.

Treatments:

- T₁- Control
- T₂- Stress at vegetative
- T₃- Stress at squaring
- T₄- Stress at boll development

RESEARCH ANALYSIS AND REASONING

Development of more efficient cotton genotypes possessing drought tolerance requires thorough understanding of physiological, biochemical and yield component traits which directly or indirectly plays an important role in influencing the yield. The correlation co-efficient revealed highly significant differences among the genotypes for all the characters studied. The present study indicated that seed cotton yield showed significant positive association with photosynthetic rate, NRase activity, SPAD and total chlorophyll content at genotypic level indicating that these characters can be improved simultaneously (Table 1). The character association revealed that the photosynthetic rate was positively and significantly associated with soluble protein, NRase activity, SPAD and total chlorophyll and negatively associated with stomatal diffusive resistance at vegetative stage.

Among the physiological parameters contributing towards drought tolerance studied photosynthetic rate showed significant positive correlation with soluble protein, SPAD, total

Table 1 : Correlation coefficient (r) among physiochemical traits for the controlled and drought stress conditions in cotton plants

	Photosynthetic rate (μ mol CO ₂ m ⁻² s ⁻¹)	Stomatal diffusive resistance (s cm ⁻¹)	Soluble protein (mg g ⁻¹)	Nitrate reductase activity (μ g of NO ₂ ⁻ g ⁻¹ hr ⁻¹)	SPAD	Total chlorophyll (mg g ⁻¹)	Yield (g/plant)
Vegetative stage							
Photosynthetic rate (μ mol CO ₂ m ⁻² s ⁻¹)	1.00	-0.20	0.63**	0.46**	0.31**	0.56**	0.57**
Stomatal diffusive resistance (s cm ⁻¹)		1.00	0.11	0.11	0.24	-0.14	0.02
Soluble protein (mg g ⁻¹)			1.00	0.28	0.03	0.67**	0.65**
Nitrate reductase activity (μ g of NO ₂ ⁻ g ⁻¹ hr ⁻¹)				1.00	0.27	0.49**	0.52**
SPAD					1.00	-0.09	0.32**
Total chlorophyll (mg g ⁻¹)						1.00	0.79**
Yield (g/plant)							1
Squaring stage							
Photosynthetic rate (μ mol CO ₂ m ⁻² s ⁻¹)	1	-0.15	0.43**	0.22	0.35**	0.11	0.21
Stomatal diffusive resistance (s cm ⁻¹)		1	-0.09	0.16	0.23	-0.01	-0.05
Soluble protein (mg g ⁻¹)			1	0.50**	0.62**	0.77**	0.76**
Nitrate reductase activity (μ g of NO ₂ ⁻ g ⁻¹ hr ⁻¹)				1	0.61	0.34**	0.35**
SPAD					1	0.54**	0.49**
Total chlorophyll (mg g ⁻¹)						1	0.86**
Yield (g/plant)							1
Boll development stage							
Photosynthetic rate (μ mol CO ₂ m ⁻² s ⁻¹)	1	-0.11	0.36**	0.13	0.52**	0.6**1	0.45**
Stomatal diffusive resistance (s cm ⁻¹)		1	0.09	0.08	0.10	-0.03	0.15
Soluble protein (mg g ⁻¹)			1	0.16	0.38**	0.39**	0.35**
Nitrate reductase activity (μ g of NO ₂ ⁻ g ⁻¹ hr ⁻¹)				1	-0.15	0.23	0.32**
SPAD					1	0.46**	0.35**
Total chlorophyll (mg g ⁻¹)						1	0.74**
Yield (g/plant)							1

* and ** indicate significance of values at P=0.05 and 0.01, respectively

chlorophyll and seed cotton yield only at genotypic level and negatively associated with stomatal diffusive resistance. The character stomatal diffusive resistance was negatively associated with soluble protein at squaring stage.

The photosynthetic rate and soluble protein showed considerable positive direct effect resulted in significant positive association with SPAD, total chlorophyll and seed cotton yield per plant. NRase with SPAD showed negative correlation and SDR with SPAD showed indirect effect resulted in negative correlation at boll development stage.

The correlation and path coefficient analysis revealed that the characters photosynthetic rate, soluble protein, NRase, SPAD and total chlorophyll had highly significant positive association with seed cotton yield and also high positive direct as well as indirect effect through many other characters. Hence, simultaneous selection based on photosynthetic rate, soluble protein, NRase, SPAD and total chlorophyll will be promising the seed cotton yield.

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