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Development of salinity tolerance in wheat

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Abstract
Wheat is the major food source of approximately half of the world population. We have seen enormous growth in population and stagnancy in wheat production in the past decade. Salinity is causing big stress to the plants and hampers healthy growth thus reducing the production. High salt concentration present in the soil causes injury to the internal organs of the plant and affecting its physiology. The present review discusses the role, mechanism, method of producing improved cultivars through molecular breeding and transgenics.

Keywords: salinity, wheat production, QTLs, Na+- K+ concentration, transgenic

Introduction
Wheat is second staple cereal crop after rice in the world providing a daily diet of the 70% population of the world (Tang *et al*., 2011) [25]. Wheat is widely grown under various environmental conditions. In India, the area under wheat is 304.73 lakh hectares with the production of 95.85 million tonnes (Anonymous, 2016) [1]. Cultivated wheat is hexaploid (2n=6x=AABBDD), having the three genomes designated as A, B and D. The size of the wheat genome is large (17Gbp) due to a high content of repeated sequences. For this reason, functional genomic analysis of wheat is difficult. In wheat genome 88,000 genes have been identified (Zhao *et al*., 2011) [31]. Salinity is one of the most effective abiotic stress influenced the early stage growth of crops and decreases the yield at the final stage. The yield loss of wheat cultivars have been considered by Quayyum and Malik, 1988 [20]; Shahbaz *et al*., 2011 under the moderately saline condition and severely affected in the highly saline or salt-affected soil conditions (Perveen *et al*., 2012) [18].
Several varieties/genotypes have been recommended for the salinity affected areas (Table 1). Development of salinity tolerance genotypes of wheat through conventional breeding has been achieved by the several workers of India, Australia and Pakistan (Table 2). In India KRL1-4, KRL19 from CSSRI, Karnal, in Pakistan LU26S, SARC-1 from Saline Agriculture Research Centre (SARC) at University of Agriculture, Faisalabad and Sakha8 in Egypt from the Agricultural Research Centre at, Giza have been successfully released through conventional breeding for the salt tolerance.

Table 1: Crop varieties tolerant to salinity stress recommended for different agro-climatic zones of the country

Stresses	States	Varieties
Sodic Soil	North-western (Punjab, Haryana, Western Uttar Pradesh and Northern Rajasthan)	KRL1-4, KRL19, KRL210, KRL213
	North-Eastern plains (Bihar, Eastern Uttar Pradesh, Bengal Hilly region, Odisha and Assam)	KRL1-4, KRL19, KRL210, KRL213

Table 2: Improvement in salt tolerance of wheat crop using conventional breeding approach

Genotyped Released	Release Source	Performing Ares	References
Indian KRL1-4 and KRL 19	Central Soil Salinity Research Institute (CSSRI) at Karnal, India	Saline soils of northern India	Hollington *et al*., 1994 [9]
LU26S and SARC-1	Saline Agriculture Research Centre (SARC) at University of Agriculture, Faisalabad-Pakistan	All saline soils	Munns *et al*., 2008
Egyptian Sakha 8	Agricultural Research Centre, Giza, Egypt	All saline soils	Munns *et al*., 2008
Kharchia 65	Indian farmers through selection on sodic-saline soils	Kharchi-Pali area of Rajasthan, India	Rana. *et al*, 1980 [21].
Line KTDH 19	Quarrie and Mahmood	Performed well in Spain only	Hollington *et al*., 1994 [9]
S-24	Department of Botany, University of Agriculture, Faisalabad, Pakistan	On all saline soils	Ashraf *et al*., 2002 [2]

Kharchia 65 is one of the salt-tolerant lines of wheat developed by the Indian farmers of Kharchi-Pali area of Rajasthan through selection from the salt-affected field, have been used in the development of the most of the salt-tolerant varieties wheat through conventional breeding in India (Rana, 1980) [21]. KRL1-4 developed from between cross of Karachiya 65/WL711 has well suited to the saline area of north India, while in waterlogged and saline area of Pakistan does not gives a satisfactory performance (Hollington *et al.*, 1994) [9]. Karachia 65 salt tolerant breeding line of India has also been used for the development of salinity tolerance varieties in other countries of the world. In the United Kingdom, Karachia 65/ TW161 (a line identified with exceptional Na+ exclusion) showed remarkable performance in the saline soil of Spain (Hollington *et al*., 1994) [9] but do not give yield advantages in the salt-affected soil of India and Pakistan when compared to local salt tolerant cultivars due to late maturity. To solve the late maturity problem, Mahar *et al.*, (2003) [14] reduced the maturity employing mutation breeding strategy and develop a good line for India and Pakistan along with Na+ exclusion traits (Hollington *et al.*, 2000). Later, salt tolerant line S24 and S36 were developed between the cross of Karachia 65/ LU26S (a salt tolerant and rust susceptible wheat line of Pakistan) (Ashraf and O'Leary, 1996) [3]. According to Ashraf, (2002) [2] the wheat cultivar S24 showed high salt tolerant in comparison to Karachia 65, LU26S and SARC-1 due to the low accumulation of Na+ in leaves with higher yield advantage than many wheat varieties (Ashraf, 2002; Shahbaz *et al*., 2012; Perveen *et al*., 2012) [2, 18, 24].

Table 3: QTLs involved in Salt tolerance mechanism in bread wheat

Trait	QTL	Chr.	Flanking Markers	References
Na+ and K+ accumulation	*Nax1*	-	-	Dubcovskyetal.,1996 [6]
Na+ exclusion	*Q.Na2A & 2B1*			Lindsay *et al*., 2004 [12]
Na+ concentration	*Q.Na2B2*	2A	*wPt-3114/wmc170*	
	Q.Na6A & 7A	2B	*wmc272/barc349*	
	Q.K1D	2B	*wPt-7859/wPt-7161*	
	Q.K3B	6A	*cfd080/barc171*	
	Q.K3D, Q.K4A Q.K4D, Q.K5A Q.K5B, Q.K5D Q.K7A, Q.K7D	7A	*wPt-4744/gwm282*	
K+ concentration	*Nax1*	1D	*wPt-4647/wmc147*	Genc *et al*., 2010 [7]
	Kna1	3B	*gwm299/gwm247*	
		3D	*cfd223/cfd152*	
		4A	*wPt-7919/wPt-0150*	
		4D	*gpw95001/gwm165b*	
		5A	*wPt-1370/Vrn1A*	
		5B	*Vrn1B/wPt-5896*	
		5D	*cfd19a/gwm292a*	
		7A	*wPt-5153/ksm019*	
		7D	*wPt-2258/wPt-3923*	
Na+ exclusion		5AL	*Nax1*	Byrt *et al*., 2007 [4]
Na+ /K+ ratio	QRkn	4D		Gorham *et al*., 1987
Root K?/Na? ratio		4B	Xbarc193-TC246843	Xu *et al*., 2012 [27]
		5B	Xgwm133.2-Xgwm274.2	
		7D	Xgwm44-Xbarc245	
Shoot K+/ Na+ ratio		2D	Xgwm608-wPt-731148	Masoudi *et al*., 2015 [15]
		3B-1	wPt-798970-wPt-8303	
		5A	Xgwm205-wPt-9094	
Root K+ / Na+ ratio		2B-1	wPt-4199-wPt-741382	
		2B-2	wPt-5736-wPt-3949	
		3B-2	wPt-0895-wPt-0013	

Molecular breeding approaches associated to genome mapping, QTLs, linked markers identification and their utilization in marker-assisted backcross breeding have been done successfully by several workers for improving wheat varieties for salinity stress (Ma *et al*. (2007 [13]; Peleg *et al.*, 2008; Genc *et al.*, 2010a [7]; Jing *et al*., 2009 and Ding *et al*., 2011). According to Akbari *et al*. (2006), diversity arrays technology (DArT) is well suited to the hexaploid genome of wheat for QTL mapping study for the various traits. Ghaedrahmat *et al.*, (2014) mapped the QTLs associated with salt tolerance related traits in wheat at seeding stage on a population of 254 RILs derived from Roshan×Sabalan cross developed from single seed descent method, 232 SSR markers were for the parental polymorphism between the parents. His experiments concluded that thirty one QTLs were associated with salinity traits in the RILs population for various salt tolerance associated traits like shoot height (Qsh3A, Qsh5B, Qsh3B, Qsh1D and Qsh2B; on the chromosome 3A, 5B, 3B, 1D and 2B), shoot fresh weight (Q.sfw1D, Q.sfw1A, Q.sfw4B, Q.sfw3B, Q.sfw6B, Q.sfw2A and Q.sfw5B; on chromosomes 1D, 1A, 4B, 3B, 6B, 2A and 5B), shoot dry weight (Q.sdw3B, Q.sdw6A, Q.sdw6B and Q.sdw1A; on chromosomes 3B, 6A, 6B and 1A) and chlorophyll content(Q.chl2B, Q.chl6B, Q.chl7B, Q.chl7D and Q.chl5A; on chromosomes 2B, 6B, 7B, 5A and 7D) under saline and control conditions. A large number of QTLs have also been identified by other workers under saline condition and used in marker-assisted breeding (Genc *et al*., 2010 [7]; Ma *et al.*, 2007 [13]; Mohammadi-Nejad *et al*., 2008 [16]; Tang *et al*., 2011 [25]; Yang *et al*., 2009 [29]; Zhang *et al*., 2010 [30]; Zhou *et al*., 2011). Roshan is a salt-tolerant genotype and Sabalan is breeding lines of (908×FnA12)×1-32-438 of Wheat from Iran (Poustini *et al*., 2004) [19]. Other physiological traits viz. K+, Na+ concentration, K+/Na+ ratio, root-shoot and total dry waits to associated salinity tolerance in wheat have also been examined by Xu *et al* (2013) [26] in a population of RILs derived from a cross a cross Chuan 35050 x Shannong 483. The same kind of experiment has been done related to K+, Na+ concentration, K+/Na+ ratio for salt tolerance in wheat (Xu *et al*., 2012; Munns *et al.*, 2012; Dubcovsky *et al*., 1996; Lindsay *et al*., 2004 ; James *et al*., 2006) [26, 6, 12, 10]. Traits and QTLs associated with salt tolerance in wheat are given in Table 3.

Salinity is the complex trait that cannot be governed by a single gene but scientists have made efforts to develop transgenic salt tolerance wheat cultivars using various genetic engineering tools. In Wheat some genes for over-expression of vacuolar Na+/H+ antiporter gene AtNHX1 isolated from Arabidopsis improve the rate of germination, growth rate, biomass and yield under adverse saline condition (Xue *et al*., 2004) [28]. The excess accumulation of proline under saline condition gives advantages in saline soil. In wheat, Δ1-pyrroline-5-carboxylate synthetase (P5CS) enhanced salt tolerance of wheat by accumulating 2.5-fold higher proline compared to the non-transformed control (Sawahel and Hassan, 2002) [22]. Transgenic wheat plants remained almost unaffected up to 200 mM NaCl and showed a slight reduction at 250 mM NaCl, in comparison with wild-type plants which died or showed low growth at 100 mM NaCl (Table 4).

Table 4: Improvement in salt tolerance of wheat crop using transgenic/genetic engineering approach

Cereal Crop	Gene Engineered	Source Organism	Trait Improved	Growth Improved	References
Wheat	vacuolar Na + /H + antiporter gene *AtNHX1*	*Arabidopsis*	Germination rate, plant biomass and yield. Low leaf Na+ and high leaf K+	Increase in shoot dry weight was 68% and root dry weight 26%	Xue *et al.*, 2004 [28]
	*Δ*_1-pyrroline-5-Carboxylate synthetase (*P5CS*)	Moth bean (*Vigna Aconitifolia*)	Accumulated 2.5-fold more proline as compared to that in wild type	Transgenic plants remained unaffected up to 200 mM and showed slight reduction at 250 mM, while respective wild plants died at 10m*M*	Sawahel and Hassan., 2002 [22]
	Na+/H+ antiporter gene *OsNHX1*	*Oryza sativa*	Yield was improved	Showed higher biomass and yield even at 200 mM NaCl	Chen *et al.*, 2007

Conclusion and future prospectus

Salt stresses are the great threats which influenced wheat crop production. Only a few reports of salt tolerant varieties are available for wheat using conventional, marker-assisted breeding and genetic engineering. Scientists have tried to develop salt-tolerant lines/cultivars of cereal crops through marker-assisted breeding and other approaches but variations in environmental conditions, soil texture and variable salinity levels are the strong barriers which limited the development of cultivars for salinity tolerant. The different developmental phases and complex nature of salt tolerance trait that involves many genes are the other major problem in developing salt tolerant cultivars. The identification of genotypes and traits/QTLs that are tolerant at more than one stage may exist and ideal for multidimensional salinity (Munns and Tester, 2008). However, Identification and pyramiding of the several major and minor traits into the cultivars to achieve durable resistance associated to different developmental phases and various level of salinity could help to improve salinity tolerant beyond seedling to reproductive stages.

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