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**W**heat (*Triticum* sp.) stands as the second largest staple crop of the world with 17% of the total cultivatable land under wheat production. Global annual wheat production needs to be increased at quantum leaps from the present production of more than 650 million metric tons so as to feed the ever burgeoning world population. Unfortunately, with the changing global climate, various abiotic stresses further hamper the wheat productivity. Development of abiotic stress tolerant cultivars is necessary to achieve the goal of enhanced wheat productivity. With the available gene pool within a species becoming limited, it becomes imperative that we search genes responsible for abiotic stress tolerance across the, genus, species and even kingdom and using rDNA technology develop transgenic wheat tolerant to abiotic stresses. The present study involved identification of abiotic stress responsive genes from tolerant plant systems *Pennisetum glaucum*, *Triticum aestivum*, *Ziziphus nummularia* and *Prosopis cineraria* using Roche 454 and Illumina sequencing platforms. De novo assembly and transcriptome annotations were performed to have insight about genes, gene family and transcriptional factors related to abiotic stress. Further analysis for

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