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Editorial Open Access

Raising Stress Tolerant Rice through Genetic Manipulation of Cyclophilins

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Editorial

Current agricultural productivity will soon be unable to meet the food demands of a continuously increasing population. Agricultural productivity is greatly affected by unfavourable environmental factors, to which crops are exposed. According to FAO, the overall area covering saline and sodic land is about 444 million hectares [1]. Breeders have taken up their approach to coax this situation by their own methods of breeding between the best-suited varieties for generating high-yielding salinity-stress tolerant varieties. On the other hand, crop biotechnologists are engaged in manipulation of different "candidate genes" for producing stress tolerant transgenic plants. Molecular biologists have even taken up an alternative route of gene pyramiding, where more than one transgene, involved in the same or different stress related pathways are introduced and expressed together in plants. Transcript profiling under non-stress and stress conditions using genetically different genotypes (stress sensitive vs. stress tolerant) can also be helpful in identification of the "candidate gene(s)". Xerophytes and prokaryotic extremophiles have also been used as a source of "candidate genes"; as they can survive under the conditions where plants cannot sustain themselves.

Rice is the staple food crop for approximately half the world's population and constitutes approximately 20% of the global daily calorie uptake [2]. Global transcript profiling in rice has shown that salinity stress regulates a large set of genes. One such gene, which showed up-regulation under salinity stress, was cyclophilin, OsCyp2 [3]. Cyclophilins, a subfamily of peptidyl-prolyl isomerases (PPIase), are highly conserved ubiquitous set of proteins, which act as folding catalysts. These proteins were discovered as ligands for immunosuppressive drugs in bovine thymocytes, and later for their PPIase activity [4]. These peptidyl-prolyl cis-trans isomerases catalyze slow conformational change from cis to trans isoforms of Xaa-proline peptide bonds in case of short peptide sequence, which is one of the rate-determining steps in protein folding [5]. Plant Cyclophilins were first identified in 1990 with the isolation of cyclophilin cDNA sequences from tomato (Lycopersicon esculentum), maize (Zea mays), and Brassica napus [6]. In Oryza sativa, we have reported 29 cyclophilin gene members with diverse structure and possibly diverse functions [7].

One of the most notable features of plant cyclophilin genes is their induced expression in response to various stresses which have been reported in several plant species as bean, maize, sorghum, pigeon pea, arabidopsis, tomato, wheat, rice and even the algae [8-16]. Cyclophilins are one of the key groups of stress-induced proteins believed to exert cellular protection, helping the plant to adapt to specific unfavorable changes in environment. A single domain cyclophilin gene, OsCyp2, isolated from rice has shown differential transcript abundance in various abiotic stresses [7]. The rapid increase in the transcript abundance was observed as an early response [7], indicating its role as a stress chaperone in response to multiple stresses. There was a record of 9 OsCYP genes upregulated under salt and desiccation stress, 4 of rice Cyclophilins respond to both salinity and drought stress, while others responded only to salt stress [17]. OsCyp2 transgenic seedlings displayed lower levels of lipid peroxidation products and higher activities of antioxidant enzymes than wild-type seedlings, suggesting that the involvement of OsCyp2 in providing salt tolerance by controlling ROS levels in plants [15]. Heterologous expression of rice cyclophilin gene, OsCyp2, has been shown to enhance stress tolerance in E. coli and S. cereviseae as well [3]. Ectopic expression of this gene in tobacco has also shown its stress mitigating nature by contributing towards ion homeostasis and restricting ROS accumulation [7]. Overexpression of the ThCyp1 in BY2 tobacco cell suspension line and yeast show stress tolerance towards multiple abiotic stresses [18]. AtCyp20-2, which is the ortholog of OsCyp20-2, the only CYP to show PPIase activity in the thylakoid lumen, increased when plants were exposed to strong light or low temperature [19]. Several PPIases have been reported to work in concurrence with different protein kinases to control the activity or stability of key regulatory components and several other transcription factors in stress [20]. Cyclophilins, thus stand out as suitable candidate genes for crop engineering providing multifaceted stress tolerance to plants.

The universal presence and diverse roles of Cyclophilins in plant system serves as an impetus for several studies related to plant Cyclophilins worldwide [21]. A positive correlation between this protein family and stress protection have been deciphered but the exact mechanism which is targeted by cyclophilin proteins to bring about stress protection is yet to be chalked out. A hypothetical model proposing the probable mechanism of function of Cyclophilins in various cellular processes is given in Figure 1. Tracing out their interacting partners as well as experiments on 'loss of function' mutants would provide greater insight into the role of Cyclophilins in abiotic stress tolerance.

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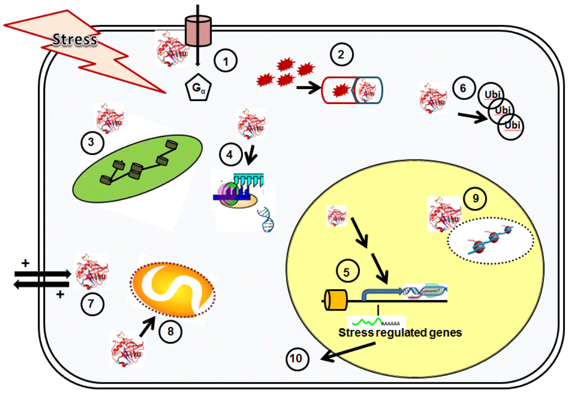

Figure 1: A hypothetical model proposing the diverse functions of cyclophilins operative at cellular level during stress. Cyclophilins possibly operate through diverse strategies to prevent stress-induced injury via its gene regulatory and cellular protection pathways. 1. Signaling via membrane localized receptors, 2. Folding and refolding of aggregated proteins, 3. ROS scavenging, 4. RISC assembly and PTGS of target genes, 5. Transcription and pre mRNA processing, 6. Ubiquitin dependent protein degradation, 7. Ion homeostasis, 8. Mitochondrial protein folding and stabilization, 9. Histone modification and remodeling, 10. Cellular protection and damage repair.

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