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Antioxidative defense response of selenium by hyper accumulator plant *Brassica rapa* var. Ps66 and *Toria* towards phytoremediation

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Natural processes such as volcanic eruptions, anthropogenic activities lead to emission of heavy metals in ecosystem. *Brassica* species have competency to absorb and sequester Se and harness to manage environmental Se contamination via phytoremediation. All the test species of *Brassica* (*Brassica juncea*, *Brassica carinata*, *Brassica rapa* PS66, *Brassica rapa* *Toria*, *Brassica rapa* KBS, *Eruca sativa*) were found to respond to Se by registering changes in the expression of antioxidative enzymes and tolerance level showed significant inhibition at higher concentration. The raised value of oxidative stress determinants-lipid peroxidation and hydrogen peroxide, near 100 μ M signified build up of stress at this concentration. *Brassica rapa* showed greater Se tolerance as was evident from the increased expression of glutathione peroxidase (GPX) in the treated plants, results corroborated with in gel assays for the enzymes, whereas little or no basal activity was found in the control plants. The positive correlation between Se concentration and GPX activity is suggestive for the presence of Se-dependent GPX despite the fact that most plant GPX studied so far have not been reported to require Se for their function. 2D analysis under regular and selenium stress of *Brassica rapa* PS66 have revealed the presence of fructose bisphosphate aldolase, GRF-1 interacting factor-3, ribulose bisphosphate carboxylase proteins. One special attribute of *Brassica rapa* PS66 and *Toria* is their ability to convert inorganic Se to volatile forms predominantly dimethylselenide (DMSe) which is 500-600 times less toxic than the available form of selenium in the environment, thus a potential benefit for selenium phytoremediation.

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Analysis of internal transcribed spacer region of *Ilex khasiana* Purk and *Ilex venulosa* Linn, two species endemic to Meghalaya

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The genus *Ilex* is the only living genus of family *Aquifoliaceae*. Sequence variation in the internal transcribed spacer (ITS) region of nuclear DNA was used to assess inter and intra-specific relationship *Ilex khasiana* and *Ilex venulosa*, two endemic tree species of Meghalaya. The nucleotide sequences of whole ITS region of *I. khasiana* and *I. venulosa* ranged between 695-697 base pairs. While ITS1 revealed highest G+C content of 60.979% and 94.75% conserved sites, ITS2 showed 29.68% variable sites with a ti/tv value of 0.51 and sequence divergence value of 11.009. The 5.8S region of nrITS was found to be the most conserved region with 99.73% conserved sites. Nucleotide sequence representing whole ITS region of *I. khasiana* revealed higher sequence divergence value (10.009%) than *I. venulosa* (5.034%). A comparative study of ITS sequences was done for the individuals representing three populations of *I. venulosa*. While nucleotide sequence of ITS representing individuals of population Lad-Mawphlang (E 91°44.974'/N 25°22.491') revealed higher G+C% content of 57.020 with ti/tv value of 1.00, population Mawkajem (E 91°53'30.95''/N 25°20'46.41'') showed highest sequence divergence with a value of 7.286%. The neighbor-joining phylogenetic tree generated from the multiple sequence alignment of nrITS region form two separate clusters. While individuals representing *I. venulosa* grouped as Cluster I, individuals representing *I. khasiana* formed cluster II. However, one individual of *I. venulosa* collected from Mawkajem clustered separately as a subgroup within cluster II.

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