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Supplementary Table 1

Stress	Name of the system	Gene	Gene origin	Recipient plant	Effects	Reference
Heavy metals	Copper-resistant protein (Cop)	*copC*	*Pseudomonas sp*. Az13	*Arabidopsis thaliana*	Enhanced Cu accumulation in the plant body	(329)
		copC	*Pseudomonas fluorescens*	*Nicotiana tabacum* (cv. Wisconsin)	Compared to the control, transgenic plants accumulated twice as much Cu.	(330)
	The copper efflux (cus) system	*CusF*	*Escherichia coli*	*Arabidopsis thaliana*	In comparison to untransformed plants, Cu accumulation in the roots of $CusF_{cw}$ (Cell wall CusF) transgenic lines was up to two times higher.	(331)
	Ⱥ-glutamylcysteine synthetase-glutathione synthetase (StGCS-GS)	Glutathione *StGCS-GS*	*Streptococcus thermophilus*	*Beta vulgaris*	Greater absorption of HMs in the shoots	(332)
	Cadmium factor1	*ScYCF1*	*Saccharomyces cerevisiae*	*Populus alba* X *P. tremula* var. *glandulosa*	Elevated Cd levels in aerial tissues. The plants' roots accumulated higher levels of Cd, Zn and Pb.	(333)

	Bacterial gene encoding organomercurial lyase	*MerB*	*Escherichia coli*	*Arabidopsis*	A potential candidate for degradation of organomercury Even at the lowest levels of merBpe expression, transgenic lines expressed merBpe mRNA and MerB protein at levels that fluctuated over a 10- to 15-fold range, conferring resistance to organomercurials.	(334)
			Escherichia coli XL1-Blue	*Nicotiana tabacum*	Enhanced tolerance towards methyl Hg and more accumulation of Hg	(335)
	Bacterial heavy metal resistance system	*MerC*	*Escherichia coli*	*Arabidopsis thaliana*	Greater accumulation of Cd than the wild type	(336)
			Acidithiobacillus ferrooxidans	*Arabidopsis thaliana*	Twice the accumulation of mercuric ions as compared to the control	(337)
	Transmembrane mercury transport protein	*merT*	*Pseudomonas alcaligenes*	*Arabidopsis*	Enhanced tolerance of mercuric chloride and decreased oxidative stress.	(338)
			Pseudomonas K-62	*Nicotiana tabacum*	More uptake of Hg.	(339)
Hydrocarbons and chlorinated compounds	naphthalene dioxygenase system	*Naphthalene dioxygenase(N*	*Pseudomonas*	*Arabidopsis* sp. and *Oryza sativa*	Enhanced phenanthrene uptake from the environment compared to wild-type plants.	(340)

		ahAc and *NahAd)*				
	Glutathione transferases	Glutathione transferases (*GST*)	*Trichoderma virens*	*Nicotiana tabacum*	Enhanced tolerance towards anthracene. Higher remediation of anthracene as compared to the control plant.	(341)
	The rhamnosyltransferase gene	*rhlA*	*Pseudomonas aeruginosa*	*Medicago sativa*	Rhamnolipids generated in greater quantities by transgenic plants as compared to the control plants probably solubilized oil hydrocarbons, making them more accessible to organisms that degrade the oil.	(342)
	The chlorocatechol dioxygenase gene	*cbnA*	*Ralstonia eutropha NH9*	*Oryza sativa*	Efficient conversion of 3-chlorocatechol to 2- chloromucote by the transgenic plants thereby further facilitating further degradation of the contaminants,	(343)
Water Logging	Hemoglobin	*VHb*	*Vitreoscilla*	*Arabidopsis* and *Zea mays*	Transgenic *Arabidopsis* remained green after 14 days of waterlogging treatment. In *Zea mays*, in response to waterlogging stress, the introduction of *VHb* dramatically improved plant growth parameters such as seedling height, main	(344)

					root length, lateral root number, root dry weight, and shoot dry weight.	
Cold stress	acyl-lipid Delta12-desaturase	*desA*	*Synechocystis* sp. *PCC6803*	*Solanum tuberosum*	Greater content of unsaturated fatty acids in the lipids in transgenic plants thereby conferring protection from cold stress.	(345)
Drought stress	Cold shock proteins	*CspA* and *CspB*	*Escherichia coli*	*Triticum aestivum*	Increased 1000-grain weight and grain yield as compared to control plants under drought stress.	(346)
	Maltooligosyltrehalose synthase	*BvMTS*	*Brevibacterium helvolum*	*Oryza sativa*	Enhanced drought tolerance without retardation of growth.	(347)
Salt Stress	Choline oxidase	*codA*	*Arthrobacter globiformis*	*Lycopersicon esculentum*	Compared to wild-type plants, *codA*-transgenic plants demonstrated better resistance to salt stress during seed germination and subsequent growth of young seedlings. Leaves of *codA*-transgenic plants showed increased levels of relative water content, chlorophyll content and proline content.	(348)

			Agrobacterium, pBI121 derived from Ti-plasmid and *Hsp terminator*	*Eucalyptus camaldulensis*	The transcription level of *codA* was higher with Hsp terminator. Higher content of glycine betaine in transgenic plant	(349)
			Arthrobacter globiformis	*Solanum lycopersicum* cv. *'Moneymaker'*	Accumulation of glycine betaine in the transformed plant. When exposed to salt stress, transgenic lines demonstrated noticeably better rates of photosynthetic activity, antioxidant enzyme activities and less ROS buildup in the leaves than wild-type plants. In transformed plants, there was a decrease in K+ efflux and an increase in Na+ efflux in the roots as compared to transformed plants.	(350)
	glyceraldehyde-3-phosphate dehydrogenase	*PsGPD*	*Pleurotus sajor-caju*	*Oryza sativa*	Transgenic lines had increased biomass and relative water content. Higher stomatal conductance and osmotic potential were also observed.	(351)