

Evaluation of genetically engineered crops using transcriptomic, proteomic, and metabolomic profiling techniques.

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Supplemental Table 3: Comparison of GE varieties with altered metabolic traits with non-GE varieties.

Species	Techniques : T , transcriptomics P , proteomics ; M, metabolomics	References	Varieties or traits	Differences in GE with respect to control	Differences between non-GE lines, timepoints or link to environment
Barley	T	Hansen et al. (2007)	C-Hordein anti-sense in Golden Promise background (greenhouse-grown plants)	In seeds, C-Hordein decreased and sulphur-rich Hordein increased, increasing the demand for sulphur and S-aminoacids resulting in an upregulation of key genes. In total 139 genes up or down regulated. Changes in amino acid content (up to 18 % for cystein)	
Grapevine	T	Cutanda-Perez et al. (2009)	Constitutive ectopic expression of VlmybA1-2 (regulatory gene) into hairy roots and plants. VvMYBA1 transcription factor controls the expression of UDP-glucose:flavonoid 3-O-glucosyltransferase	*De novo* production of anthocyanins in all transgenic vegetative organs. Activation of only few genes, most involved in both proanthocyanidin and anthocyanin biosynthesis.	
	P	Sauvage et al. (2007)	Modified levels of alcohol dehydrogenase activity. Control, sense, and antisense	Changes in carbon metabolism-associated proteins in leaves	

			lines grown in greenhouse		
Potato	T	Baroja-Fernández et al. (2009)	Sucrose synthase overexpressed and antisensed in tuber	Antisense line: 186 genes down-regulated and 171 genes upregulated. Overexpressing line: 60 genes down-regulated and 58 genes up-regulated	
	P	Lehesranta et al. (2005)	Range of diverse varieties, landraces and GE lines (empty vector or potato sense and antisence Mal1 gene or antisense S-adenosylmethionine decarboxylase (SamDC) gene	No new protein; differences in a total of 9 proteins out of 730	Qualitative and quantitative differences in 1077 out of 1111 proteins when comparing varieties and landraces
	M	Defernez et al. (2004)	Same as Lehesranta et al. (2005), plus sense and antisense fructokinase gene (40 GE lines and controls)	GE with modified polyamine content: significant differences in proline, trigonelline and numerous phenolics. Certain other GE lines: several compounds in higher or lower amounts (no more than 2−3x)	Important variability in the whole data set
	M	Catchpole et al. (2005)	Expression of globe artichoke sucrose:sucrose 1-fructosyltransferase, or this gene together with 1-fructan:fructan 1-fructosyltransferase	Composition of GE within the natural metabolite range and very similar to the progenitor line, with the exception of the predictable up-regulation	A large variation in metabolite profile was found between the conventional cultivars

				of some fructans and their expected derivatives	
	M	Kim et al. (2009)	Constitutively expression of human beta amyloid, curdlan synthase or glycogen synthase	Neither quantitative nor qualitative differences found between GE and controls	One week of storage significantly modified tuber metabolite patterns
	Targeted compositional analysis	Shepherd et al. (2006)	Same as Defernez et al. (2004)	Some differences but not consistent in soluble carbohydrates, glycoalkaloids, vitamin C, total nitrogen and fatty acids	Most obvious differences found between two non-GE varieties (cv. Record and cv. Desiree)
Rice	T	Dubouzet et al. (2007)	Feedback-insensitive alpha subunit of rice anthranilate synthase leading to high tryptophan content in seeds	In 8-day-old seedlings: higher levels of anthranilate, tryptamine, and serotonin; about 12 out of 21,500 genes showed significant differential expression	
	T	Beatty et al.(2009)	Over-expression of alanine aminotransferase to obtain a strong nitrogen use efficiency phenotype. Plants grown hydroponically	0.11% and 0.07% differentially regulated genes in roots and shoots	
	P	Islam et al. (2005)	Seed expression of a sunflower seed albumin gene	Lower amounts (21% to 68%) of 4 glutelin and 1 globulin in GE mature seeds. varied from, suggesting re-allocation of sulfur reserves from endogenous proteins to	

				the sulfur sink in transgenic grain	
	M	Wakasa et al. (2006)	Feedback-insensitive alpha subunit of rice anthranilate synthase leading to high tryptophan content in seeds	164-265x increase in free tryptophan, predicable 2x increase in the amount of indole acetic acid, increase in other free amino acids (up to 5.2x for alanine), no substantial change in the amount of other phenolic compounds	
	P,M	Takahashi et al. (2005)	Expression of YK1, a homolog of maize HC-toxin reductase, conferring tolerance to several stresses	Slight differences in metabolites content between control and *YK1* callus, but nearly identical in leaf and panicle (greenhouse). Proteome of cultured cells: higher levels for 5 spots out of 668	
Tomato	T, M	Enfissi et al. (2010)	Down-regulation of DE-ETIOLATED-1 to improve nutritional antioxidant content	Widespread effects on diverse sectors of metabolism	
	T, M	Matto and Handa 2007 (review)	Fruit-specific expression of a yeast S-adenosylmethionine decarboxylase gene leading to high spermidine and spermine levels	One-quarter of 1067 genes differentially regulated during fruit ripening. Multiple metabolic pathways influenced and prominently : levels of choline, Glu, Gln,	

				Asn, citrate, malate and fumarate increased ; Asp,Thr, Val, glucose and sucrose decreased.	
	M	Le Gall et al. (2003)	Maize transcription factors LC and C1 were simultaneously overexpressed with the aim of increasing amounts of flavonols in ripe fruit	Significantly increase for 6 main flavonoid glycosides, differences for at least 15 other metabolites including citric acid, sucrose, phenylalanine, and trigonelline	Changes in GE line were less than 3x and within the natural variation of field-grown crops
	M	Long et al. (2006) See also Bino et al. (2005) for non-GE mutant hp-2dg	Carotenoid mutants: Og, rr, hp; GE over-expressing phytoene desaturase or 1-deoxyxylulose-5-phosphate synthase; Antisense ferulate 5-hydroxylase	Metabolic changes limited to modified pathways for GE lines	Several metabolisms altered (elevated chlorogenic acid, rutin and carotenoid content) in high-pigment (hp) mutant
	M	Fraser et al. (2007)	Over-expression of a phytoene synthase gene increasing carotenoid content	Specific sectors of metabolism altered in green fruit, levels of 43% of the metabolites significantly altered in ripe fruit (elevation in amino acid and fatty acid content)	
	M	Giliberto et al. (2005)	GE lines up-regulating the cryptochrome-2 gene	Overproduction of anthocyanins and chlorophyll in leaves and of flavonoids and	

				lycopene in fruits	
Wheat	T	Baudo et al. (2006, 2009) See also Shewry et al. (2007) for a review	GE and conventionally-bred lines expressing in endosperm a set of genes encoding subunits of glutenin. GE also express bar gene in leaves	Differently expressed genes between GE and parent in endosperm: 0.02-0.05% (depending on development stage), leaves: 0.06%. Differently expressed genes between GE and non-GE (with same set of glutenins) in endosperm: 1.6-1.3%, leaves: 0.04%.	Differently expressed genes between conventially-bred lines in endosperm: 5,7-1%, leaves: 0.27%
	M	Baker et al. (2006), Beale et al. (2009) See also Shewry et al. (2007) for a review	GE and conventionally-bred lines expressing in endosperm a set of genes encoding subunits of glutenin	Polar metabolites studied. Differences in aminoacid composition generally within the same range as the one between control lines grown on different sites and in different years	Stronger influence of site and year than of genotype
	M	Stamova et al. (2009)	Dx5 glutenin subunit expressing lines (+ bar gene) compared to lines with bar gene alone. Developing grain studied in greenhouse	Most metabolic changes were transient during development. Only 3 metabolite changes validated (guanine, 4-hydroxycinnamic acid and unknown)	

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