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Metabolome variability in crop plant species – When, where, how much and so what?

Howard V. Davies [a,*], Louise V.T. Shepherd [a], Derek Stewart [a], Thomas Frank [b], Richard M. Röhlig [b], Karl-Heinz Engel [b]

[a] Plant Products and Food Quality Programme, Scottish Crop Research Institute, Invergowrie, Dundee DD2 5DA, Scotland, UK
[b] Technische Universität München, Lehrstuhl für Allgemeine Lebensmitteltechnologie, Maximus-von-Imhof-Forum 2, D-85350 Freising-Weihenstephan, Germany

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ABSTRACT

"Omics" technologies provide coverage of gene, protein and metabolite analysis that is unsurpassed compared with traditional targeted approaches. There are a growing number of examples indicating that profiling approaches can be used to expose significant sources of variation in the composition of crop and model plants caused by genetic background, breeding method, growing environment (site, season), genotype × environment interactions and crop cultural practices to name but a few. Whilst breeders have long been aware of such variation from tried and tested targeted analytical approaches, the broad-scale, so called "unbiased" analysis of the metabolome now possible, offers a major upside to our understanding of the true extent of variation in a plethora of metabolites relevant to human and animal health and nutrition. Metabolomics is helping to provide targets for plant breeding by linking gene expression, and allelic variation to variation in metabolite complement (functional genomics), and is also being deployed to better assess the potential impacts of climate change and reduced input agricultural systems on crop composition. This review will provide examples of the factors driving variation in the metabolomes of crop species.

1. Introduction

Plant breeding in its many guises, be it conventional, marker assisted, or genetically modified (GM) drives the production of new varieties required to compete successfully in the complex global agricultural marketplace, with increasing emphasis on the use of early landrace varieties and wild species to introduce the new genes and alleles required to improve pest and disease resistance, quality and yield (Fernie et al., 2006 and references therein). There are also growing demands for germplasm adapted to deal with changing climates and which are effective under a range of cultural practices including low input and organic systems. In addition, there are clearly demands from the market for foods with higher nutritional value and which do not compromise high safety standards present in the current food chain.

Targeted analysis of specific key compounds, using well established and validated protocols, has provided the cornerstone for assessing the nutritional value and safety of cultivated crop species. A significant body of data on the targeted analysis of GM crop composition has already been developed (see International Life Science Institute (ILSI) at http://www.cropcomposition.org; Ridley et al., 2004). Such information provides a benchmark against which the new generations of crops and advances in production systems can be evaluated. Genetic background, growing environment (geographical, seasonal) and crop management practices are major factors underpinning this variation. Genetic changes induced by selective breeding are such that major domesticated crops are typically represented by hundreds, even thousands, of unique cultivars specialised for production in a wide variety of geographic regions. Thus databases will be representative and never complete.

2. Non-targeted approaches and detection of unintended effects

A fuller evaluation of the compositional variation of raw agricultural commodities and downstream products will emerge through the development of comparative metabolomics databases that can be expanded and modified by the international community. This information can be used to benchmark any measured differences between a particular crop against the extent of "acceptable" variation within the framework of a history of safe use of the crop species in question. There is an ongoing debate over the potential value of much broader scale, more unbiased analytical approaches including metabolomics in risk assessment which, through the quantity of data they generate, may help to identify effects which could stimulate the need for further risk assessment,

* Corresponding author. Fax: +44 1382 568503.
E-mail address: howard.davies@scri.ac.uk (H.V. Davies).

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and reduce the level of uncertainty that unintended effects have occurred. Most of this debate has clearly focused on GM crops but it is already clear from metabolomic analyses that significant natural variation exists within crop gene pools, accentuated by interactions with the prevailing environment.

Metabolomics clearly has much to offer in developing new insights into the regulation of plant metabolism but it must be recognised that the technology has limitations. The plant kingdom may contain between 90,000 and 200,000 metabolites (Dixon and Strack, 2003), although for a single species the number may approach a few thousand (the estimate for Arabidopsis is ca. 5000). Thus full coverage of the metabolome is a real challenge. Analysis is also challenging as the technology produces vast amounts of data. Various data mining approaches are being used to analyze these large data sets (e.g. cluster analysis, principal component analysis [PCA]). PCA can be used to assist the researcher in identifying non-random patterns that can be further explored (possibly using targeted analytical approaches). A number of initiatives have looked towards developing standards for metabolomics data in addition to a range of technology-specific and general data formats (see Hardy and Taylor, 2007; Davies, 2009 and references therein).

This paper reviews the use of metabolomics to assess natural variation and also focuses on some case studies in more detail. The review includes reference to the use of metabolomics to compare GM crops with their conventional comparators as this is an important debating point. The review will not cover the various metabolomic technologies and the reader is referred to Schauer and Fernie (2006), Hall (2006) and Davies (2009).

3. General observations – the UK Food Standards Agency (FSA) GO2 programme

Probably one of the largest publically funded programmes commissioned to assess the potential use of "omics" approaches in comparative analysis and their relevance to risk assessment was the GO2 programmed launched by the UK Food Standards Agency. The full report can be found at http://www.food.gov.uk/multimedia/pdfs/g02report. This three-year research programme was launched in September 2001, with funding of £5.5 M provided by the UK Treasury Department, focusing on the applicability and practicality of a variety of existing and emerging techniques for the safety assessment procedures for the next generation of GM foods. The programme examined the use of transcriptomic, proteomic and metabolomic techniques in a number of different plant species including potato, barley, tomato and Arabidopsis.

With regard to metabolomics, Nuclear Magnetic Resonance (NMR) spectroscopy proved to be a rapid, reproducible and robust technique for metabolite profiling and detected one unidentified, possibly novel, metabolite in barley which was increased in all five transgenic lines studied. However, there were fewer overall changes seen in the metabolome of GM wheat than of GM barley. It was considered unlikely that this level of difference would be detected with targeted analytical methods. One research group identified a number of metabolites in non-GM potatoes that had not previously been described in crop plants, indicating the potential value of untargeted metabolomic analysis (Parr et al., 2005). Metabolomics publications arising from the FSA projects observed that the differences between conventional varieties were always significantly greater than the differences between the wild-types and their respective transgenics (Defernez et al., 2004; Catchpole et al., 2005); this despite the fact that some GM lines had very distinct morphological phenotypes.

The review concluded that methods developed in this extensive research programme were successful at detecting unintended changes resulting from transgene insertion into plants However, the vast majority of these changes were small (ca. 2-fold or less) with evidence provided that at least some of these changes may be due to somaclonal variation resulting from the *in vitro* manipulation of plants rather than the presence of an inserted transgene *per se.* It is also clear that differences in the metabolome between plants grown in different environments, and even different cultivars of the same species grown in the same environment, were of greater significance and variation than the effect of the transgene itself. However, the studies focused on transgenic plants with specific genes and modified traits, and one cannot generalise about the potential for unintended effects in all GM organisms (GMOs). A case-by-case approach remains pragmatic.

4. Specific case studies

4.1. Maize

Targeted studies of maize kernels have demonstrated the impact of factors such as developmental stage (Seebauer et al., 2004), environment and farming practice (Harrigan et al., 2007a,b), and genetic background and growing seasons (Reynolds et al., 2005; Ridley et al., 2004) on the natural variability of metabolites. In addition to the targeted analyses of individual compounds, metabolite profiling techniques have been shown to be useful tools for the investigation of complex plant matrices (Lozovaya et al., 2006; Castro and Manetti, 2007). More recently, the EU project SAFEFOODS (http://www.safefoods.nl) has used maize as one target species to assess the use of metabolomics to assess the major drivers of natural variation. Some of the data arising from this project are provided below.

4.1.1. Differentiation of maize varieties

Metabolites from four maize cultivars (cv. Flavi, Lukas, Pontos and Shorty), grown over three seasons (2004, 2005 and 2006) at one location (Frankendorf) in Bavaria (Germany), were profiled using the methodology described by Röhlig et al. (2009). This procedure results in four fractions containing fatty acid methyl esters and hydrocarbons (fraction I), free fatty acids, alcohols and sterols (fraction II), sugars and sugar alcohols (fraction III), acids, amino acids and amines (fraction IV). Metabolite profiling data from the combined four fractions I–IV obtained for the four cultivars were statistically assessed via PCA to determine the major sources of variation within the dataset (Fig. 1). On the basis of the data from all four fractions, each genotype could be clearly distinguished in 2004 (Fig. 1A) but in subsequent years cv. Pontos was not easily discriminated (Fig. 1B and C). The combined data from all three growing seasons (2004–2006) did not allow a separation of cultivars (Fig. 1D) but revealed a clear clustering according to growing season (Fig. 1E). The data therefore indicate a more pronounced impact of growing season than of genetic background on the natural variability of metabolites.

The metabolic variability, expressed by the number of statistically significant ($p < 0.05$) differences in metabolite levels between the four cultivars (20% in 2004, 15% in 2005 and 25% in 2006) was in the same order of magnitude as observed for low phytic acid maize mutants. Application of a Gas Chromatography-Mass Spectrometry (GC-MS) metabolite profiling approach revealed 11–30% of the detected compounds to be statistically significantly different ($p < 0.05$) between wild-type maize and low phytic acid maize mutants (Hazebroek et al., 2007). A study investigating the nutritional and metabolic profiles of different maize hybrids via targeted analyses of 47 analytes revealed statistically significant differences ranging from 33% to 47% of total comparisons (Reynolds et al., 2005).

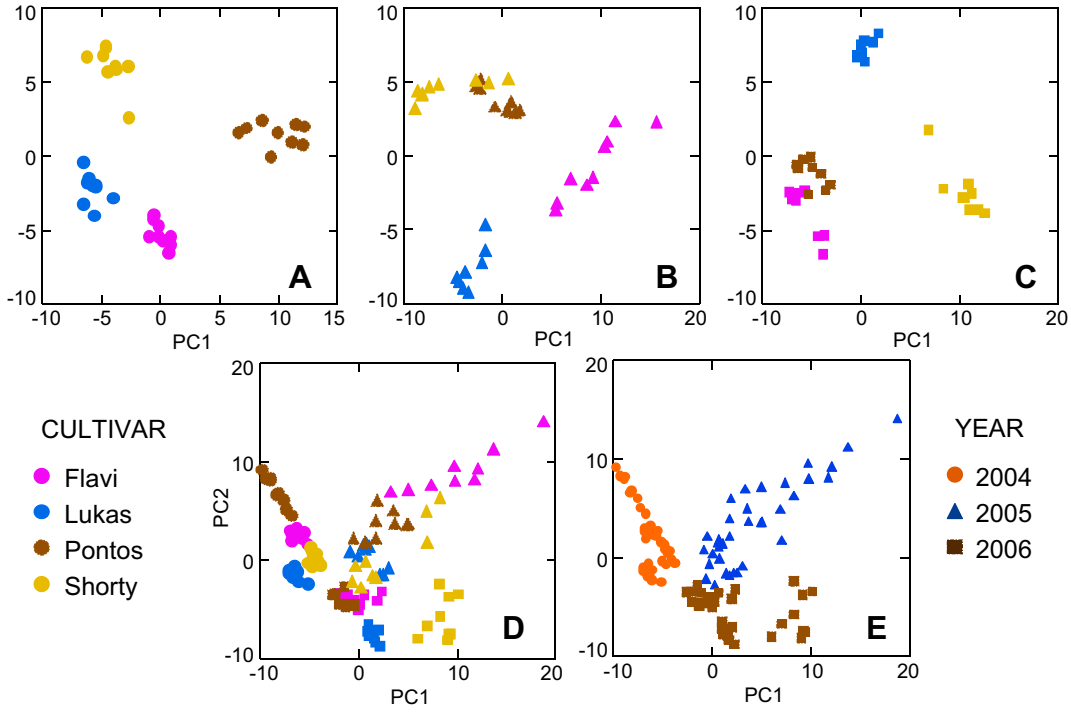

Fig. 1. Principal components analysis of metabolite profiling data from fractions I to IV in growing seasons 2004 (A), 2005 (B), 2006 (C) and from combined data of 2004–2006 (D and E) at farming location Frankendorf, Bavaria.

4.1.2. Influence of growing location

Scores plots of principal component analyses of GC-MS metabolite data obtained for one maize variety (Amadeo) cultivated over three consecutive years at four locations in Bavaria (Mittich, Reith, Strassmoos and Thann) are shown in Fig. 2. In 2004 maize grown at Strassmoos was easily separated from the other sites on the first principal component (PC) with Mittich differentiated on the second PC (Fig. 2A). In 2005 location Strassmoos was again clearly separated from the other growing locations (Fig. 2B). However, in 2006 no obvious separation occurred for any of the sites

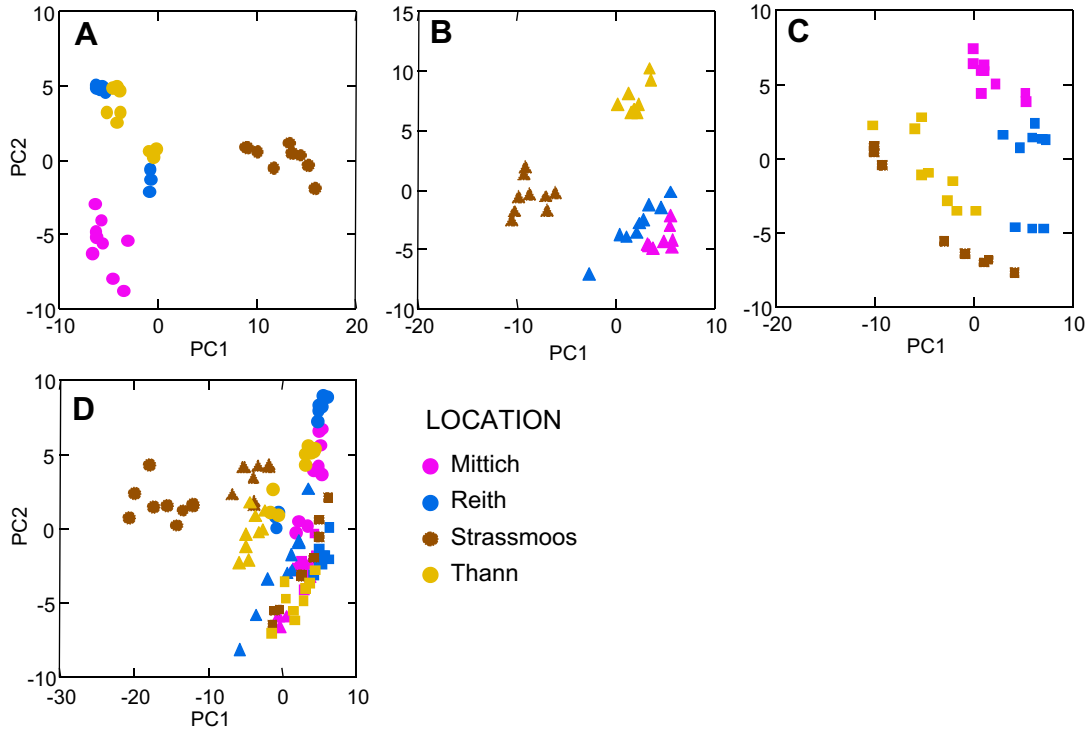

Fig. 2. Principal components analysis of metabolite profiling data from fractions I to IV of cultivar Amadeo in growing seasons 2004 (A), 2005 (B), 2006 (C) and combined 2004–2006 (D) at the four locations Mittich, Reith, Strassmoos and Thann.

(Fig. 2C). Combining data from all three growing seasons resulted in an overlap of clusters with no clear differentiation due to either location or growing season (Fig. 2D).

Peak-by-peak comparisons of GC-MS data and an analysis of variance between the different growing locations performed for one cultivar (Amadeo) showed fewer statistically significant differences ($p < 0.05$) than statistical assessment of the four cultivars grown at one farming location (Fig. 1) which suggests a more pronounced impact of genetic background than of the environment. Similarly, it has been shown that 36% of 58 metabolites differ between maize inbreds crossed against two different testers and that 48% of these statistically significant differences were due to the influence of the location (Harrigan et al., 2007a). Reynolds et al. (2005) also showed that variation caused by environmental factors, e.g. site and year, is dependent on the genotype grown. The interaction between genotype and environmental (G × E) is clearly an important driver of compositional variation.

4.1.3. GM compared with non-GM

Current safety assessment procedures developed for GM crops are primarily based on a targeted compositional analysis of specific safety and nutrition-related compounds (OECD, 1993; FAO/WHO, 2000). To date this has proven to be a valid approach for risk assessment. On a case-by-case basis, non-targeted metabolite profiling approaches can be used as an additional tool if they can really help to reduce any uncertainty (see Davies, 2009 and references therein). In such cases metabolite profiles of the GM should not only be compared with the corresponding parental line, but should also be assessed in the light of natural variability of metabolic profiles of conventional crop material (EFSA, 2006).

To assess the influence of genetic modification under different environmental conditions, a GM maize line (Bt-maize) was grown together with its near isogenic line at three locations in South Africa (Petit, Potchefstroom, Lichtenburg) in 2004. At Petit and Lichtenburg, Roundup ready-maize was also grown together with the Bt-maize and the isogenic line. In addition, the maize lines were grown for two additional years (2005 and 2006) at Petit. Statistical assessment (via PCA) of the metabolite profiling data from the samples grown at the three locations in 2004 revealed clear separations of the GM line(s) from the respective isogenic line at Potchefstroom and Lichtenburg (Fig. 3). For the maize lines grown over three years at Petit, a distinct separation of both GM lines was observed for the location Petit in 2006; the separation of GM lines from the isogenic maize line was less pronounced for this location in 2004 and 2005. However, despite partly obvious differences between GM lines and isogenic maize determined for one

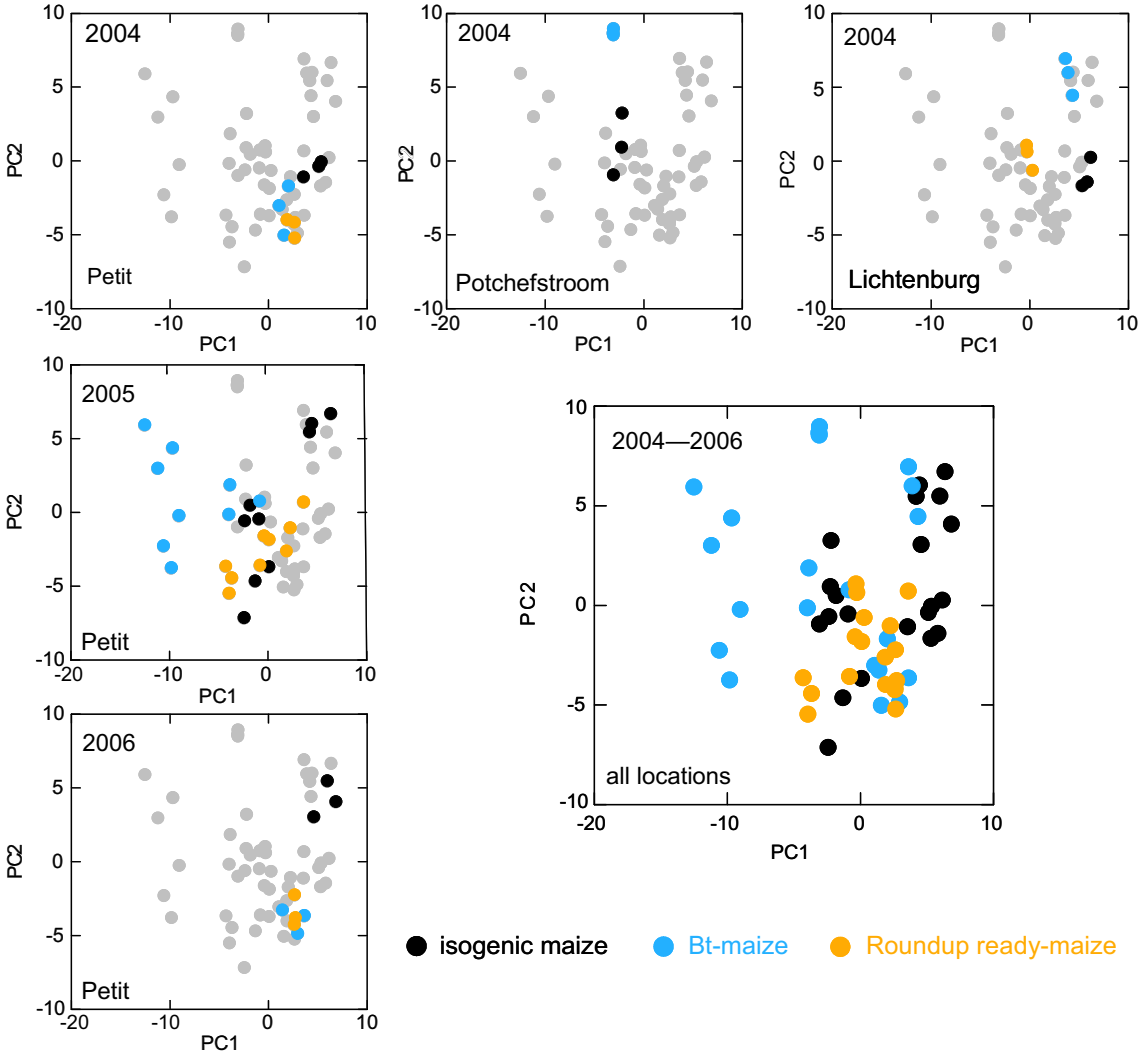

Fig. 3. Principal components analysis of GC/MS metabolite profiling data obtained by triplicate analysis of samples from three maize lines (● GM Bt, ● GM RR, ● non-GM). The material was grown at different environments in South Africa differing in location and growing season (Potchefstroom 2004, Petit 2004–2006, Lichtenburg 2004). Individual environments are highlighted in color in the context of all samples (●). For Petit 2005 three technical replicates were analysed.

location/year, no separations of the different maize lines were detectable when combining the metabolite profiling data obtained from GM lines and isogenic maize for all growing locations/years (Fig. 3). This confirms that, at least in the case of the specific GMOs analysed to date, the effect of environment (location, year) was more pronounced than that of the genetic background (GM, non-GM). With some next generation GMOs this situation may well change.

Similar data have been presented for wheat where Baker et al. (2006) showed that differences observed between GM and the control lines were generally within the same range as the differences observed between the control lines grown on different sites and in different years.

4.2. Rice (mutated, low phytate)

A range of crops (e.g. rice, maize, barley, wheat) have been developed with lowered contents of the anti-nutrient phytic acid (Raboy, 2007). Low phytic acid (*lpa*) crops have been produced by genetic engineering (Shi et al., 2007) and by mutation breeding through chemical mutagenesis (Wilcox, 2000) and γ-irradiation (Yuan et al., 2007). Low phytic acid crop mutants are typically selected on the basis of their altered levels of inorganic phosphorous (P_i). However, in addition to altered levels of phytic acid and P_i, the induced mutations were shown to result in further metabolic changes in these crops (Hitz et al., 2002; Frank et al., 2007, 2009).

Metabolomic analysis has been carried out on two *lpa* rice mutants (*Os-lpa*-XS110-1 and *Os-lpa*-XS110-2), generated by γ-irradiation of the corresponding wild-type rice (Xiushui 110) and grown at five field trials in China in 2005/2006. PCA of the polar fractions III (sugars and sugar alcohols) and IV (acids, amino acids and amines) are shown in Fig. 4. The mutant *Os-lpa*-XS110-1 is separated consistently from the wild-type Xiushui 110 in all field trials indicating a strong influence of the mutation on the polar metabolite profiles in this mutant. Whilst the variance between the mutant *Os-lpa*-XS110-2 and the wild-type is less pronounced, the rice lines were well differentiated by growing location. Samples grown at different locations, e.g. Hainan and Jiaxing (see marked field trials in Fig. 4A and B), were clearly separated from each other which confirms the influence of the environment-related biological/natural variability of the metabolite spectrum in the rice wild-types and the *lpa* mutants.

To identify the compositional differences only caused by the mutations, a univariate analysis was performed. Results obtained by the comparative univariate assessment of the *lpa* mutant and the corresponding wild-type metabolites are shown in Table 1. For the comparison of the wild-type Xiushui 110 and the *lpa* mutants *Os-lpa*-XS110-1 and *Os-lpa*-XS110-2, on average, a total of 126 and 113 peaks were included for comparison of which 40% and 26% were statistically significantly different in each field trial. The percentages of statistically significant differences in metabolites between the two *lpa* mutants and the wild-type for each field trial are within the same order of magnitude as those determined for comparable GC-based metabolite profiling studies on *lpa* mutants of maize and soybean (Hazebroek et al., 2007; Frank et al., 2009).

Results obtained by the comparative univariate assessment of the rice *lpa* mutant and the corresponding wild-type metabolites revealed that the vast majority of differences observed are related to biological variability rather than to the mutation event. Only five metabolites were consistently statistically different between Xiushui 110 and *Os-lpa*-XS110-1 at all five field trials. The compounds were identified as trimethylsilyl (TMS) derivatives of the methyl pentadecanoate, *myo*-inositol, galactose and raffinose and phos-

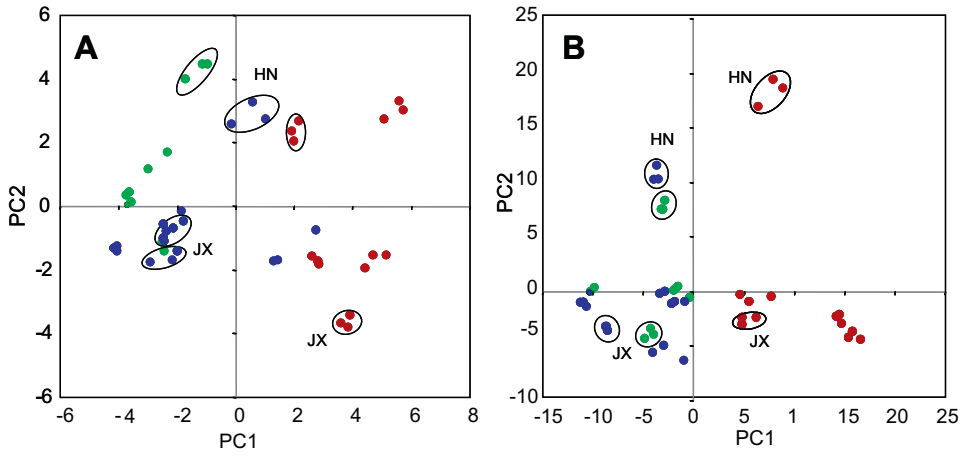

Fig. 4. Principal components analysis of standardised GC-FID metabolite profiling data from the polar fractions III (A) and IV (B) of the *japonica* wild-type rice Xiushui 110 (●) and the low phytic acid mutants *Os-lpa*-XS110-1 (●) and *Os-lpa*-XS110-2 (●) grown at five field trials in 2005/2006; marked field trials: HN, Hainan; JX, Jiaxing.

Table 1
Peak-based comparison of chromatograms obtained by metabolite profiling of wild-type Xiushui 110 and mutant lines *Os-lpa*-XS110-1 and *Os-lpa*-XS110-2 grown in 2005/2006.

Wild-type vs. mutant	Field trial										
	Hainan		Jiaxing		Hangzhou 1		Fuzhou		Guangzhou		Consistent diff.[c]
	Total[a]	Diff.[b]	Total	Diff.	Total	Diff.	Total	Diff.	Total	Diff.	
XS110 vs. *lpa*-XS110-1	144	58	121	47	118	50	135	51	111	48	5
XS110 vs. *lpa*-XS110-2	128	32	107	21	107	28	121	44	101	24	2

[a] Number of peaks included for comparison in fractions I–IV (peak height > 1000 μV).
[b] Number of peaks statistically significant different between wild-type and mutant line in fractions I–IV ($p < 0.05$).
[c] Number of peaks statistically significantly different between wild-type and mutant line at all five analysed field trials where diff. = difference(s).

phate. For *Os-lpa*-XS110-2, only the two TMS derivatives of phosphate and *myo*-inositol were significantly and consistently different at the five field trials. These metabolites are related to the biosynthetic pathways leading to phytic acid (Frank et al., 2007).

4.3. Potato

4.3.1. Genetic and phytochemical diversity in wild populations

The Scottish Crop Research Institute houses the Commonwealth Potato Collection of 83 species and ca. 1600 accessions. This is a valuable germplasm collection used to identify new sources of genes for pest and disease resistance and quality traits. Wild Solanum species (73 accessions representing several taxonomic groups) have been grown from seed and tubers and analysed using metabolomics (Davies, 2006). Metabolomics (GC-MS) with data analysed by PCA was able to separate group series Pinnatisecta from the other taxonomic groups. The compounds driving the difference were both polar and non-polar metabolites. Metabolite fingerprinting using Direct Infusion-Mass Spectrometry (DI-MS; positive ion mode) was particularly effective in discriminating taxonomic groups based on mass ions associated with specific glycoalkaloids demissine, dehydro-demissine, commersonine, α-tomatine, α-solanine and α-chaconine.

In a similar study, Dobson et al. (2008) used metabolomic approaches to analyse 29 genetically diverse potato cultivars and landraces. Material included 27 tetraploid cultivars and landraces – 20 × *Solanum tuberosum* sp. *Tuberosum* (16 with known introgression of a variety of useful traits from a variety of wild species, and 4 with no introgressed disease resistance), 7 Chilean landraces, and 2 × diploid cultivars (*S. phureja)* using GC-MS. Metabolomics was again able to discriminate between some (but not all) of the germplasm.

Beckmann et al. (2007) used flow infusion electrospray ionisation mass spectrometry (FIE-MS) and GC-MS, to assess compositional differences in potato cultivars (5 × *S. tuberosum* cultivars – Agria, Desiree, Granola, Linda and Solara) with no prior genetic, biochemical, or analytical chemistry data available. Data from the FIE-MS suggested large differences existed between tubers of individual cultivars. GC-MS analysis highlighted the fact that many of the identified metabolites that contributed significantly to compositional differences between the cultivars were linked closely to quality traits in potato tubers. For example, levels of the amino acids isoleucine, tyrosine and phenylalanine were higher in certain cultivars.

4.3.2. GM compared with non-GM

Roessner et al. (2001) used GC-MS analysis to phenotype previously characterised GM potato with altered sucrose catabolism. Analysis of these lines allowed detection of 88 metabolites (61 known) including sugars, sugar alcohols, amino acids, organic acids and several miscellaneous compounds. The majority of compounds detected were increased in the transgenic lines compared with the non-GM control, with metabolites associated with several metabolic pathways increasing in tandem. Nine of the 88 compounds in the GM tubers were below detectable limits in the wild-type tubers.

Defernez et al. (2004) applied NMR and Liquid Chromatography (LC)-MS protocols to GM potato lines with modifications in a range of metabolic pathways. Whilst some differences were observed between the GM lines and their controls, the largest differences occurred between the non-GM parental material used to generate the GM lines. This again emphases the importance of generic variability irrespective of the presence or absence of transgenes.

Similarly, Catchpole et al. (2005) used GC-Time of Flight (ToF)-MS and FIE-MS to provide a comprehensive comparison of total metabolites in field-grown potato genetically modified to induce fructan biosynthesis. With the exception of the predicted intended effects of up-regulated fructans and their expected derivatives, the levels of metabolites detected were very similar in the GM and its control. Importantly, metabolite levels in the GM lines fell within the range of the five non-GM commercial cultivars used as reference material. In fact, a major finding from the study was the large variation in the metabolite profile between the five conventional cultivars.

Whilst assessing potato tubers for compositional changes occurring after genetic modifications to different metabolic pathways, Parr et al. (2005) positively identified kukoamine A, and related phenolics compounds, in wild-type tubers. These were subsequently detected in tomato (*S. lycopersicon*) and *Nicotiana sylvestris*, but were not detectable in *Arabidopsis thaliana* or *Beta vulgaris*. This surprising discovery in a range of Solanaceous species, including potato, provides evidence for the potential of non-targeted analysis such as metabolomics in studying plant metabolites, as such metabolites would not have been discovered using a targeted approach. It also illustrates the gaps in our knowledge of the true extent of natural variation.

4.4. Soft fruit

As with many crop species, soft fruit such as blueberry, raspberry, strawberry and blackcurrant are characterised by a wide range of metabolite classes which influence both quality and nutrition value. These include sugars, acids, amino acids, carotenoids and simple to complex polyphenolics to name but a few. Subclass diversity is also evident with the polyphenol group including anthocyanins, flavonols, (iso)flavones, flavanones, catechins, ellgaitannins, cinnamates and hydroxyl benzoic acids and stillbenes (Pietta et al., 2003; D'Archivio et al., 2007; Mullen et al., 2007). These subclasses are further populated by differential levels and patterns of polyphenol polymerisation, glycosylation, methylation and acylation (Clifford, 2000; Reed et al., 2005; Xie and Dixon, 2005; Prior and Wu, 2006).

Metabolite diversity in soft fruit is accompanied by a significantly broad and dynamic content range. For example, total anthocyanin content can be virtually undetectable in fruit such as banana but can reach levels of 2–10 mg g^{-1} fresh weight in blackcurrant, raspberry, blueberry, elderberry, and the lesser researched fruit choke berry (Clifford, 2000). Similarly, other metabolites impacting upon organolepsis (sugars and organic acids), nutrition (vitamins C and A, etc.) and putative bioactive components (flavonoids) also display similar levels of variation (Anon, 2003; Anon, 2009a,b).

The combination of all of the above factors have meant that applications of true metabolomics (i.e. an untargeted study of metabolite changes either by GC-MS, LC-MS, NMR, etc.) to fruit is at a very early stage and have been limited to melon (Biais et al., 2009, 2010), raspberry (McDougall et al., 2008; Stewart et al., 2007) and strawberry (Fait et al., 2008). The approach taken by Biais et al. (2009, 2010) focused on establishing within fruit spatial variation in primary metabolites using a cross-comparative approach mining ^{1}H NMR and GC-ToF-MS data for metabolite trends at a spatial level using independently performed PCA and multiblock hierarchical PCA (HPCA). . In general, the analytical systems yielded similar spatial trends in metabolites. Confirmation of this cross-comparability was revealed by a correlation-based superblock HPCA for direct comparison of both analytical data sets. The HPCA approach allowed different source data sets, with different levels of sensitivity, to be confidently cross-compared thereby extending the validity of the multi-analytical approach to metabolomics. For melon at least this has been extended to determine the underlying factors impacting upon shelf life and associated spoilage via hypoxia related fermentation.

For strawberries, fruit development has been studied using a combined GC-MS and UPLC-QTOF-MS (Fait et al., 2008) covering

not only primary metabolites but also 105 secondary metabolites including phenylpropanoid derivatives. This represents a significant step beyond the state-of-the-art which has generally confined itself to reporting on differences in specific chemical classes such as flavonoids (Wang et al., 2003; Panico et al., 2009) and amino acids (Keutgen and Pawelzik, 2008) due to genetic variation or stress (Capocasa et al., 2008).

The application of metabolomics to study trait inheritance or the influence of the environment on primary and secondary changes is in its infancy with respect to soft fruit. This approach has been hampered, at least with respect to fruit breeding, by the sheer numbers of samples (distinct lines, replication) to be analysed in a standard segregating population. Methods to manage this have been developed by Stewart et al. (2007) and McDougall et al. (2008) who have truncated standard LC-MS to give a short column method that is closer to DI-MS (S-DI-MS). Their study employed the same segregating raspberry population in two distinct growing environments, one a low fertiliser site with minimal standard agronomic management and the other one classified as a high health site with standard and regular inputs of fertiliser and agronomic management. Mature fruit from these sites showed clear differences in global metabolites, but year-on-year variation was likely to be the key driver of metabolite variation observed between the sites. Interestingly, the PCA data for one of the years was clearly differentiated with regard to the high and low input systems the reason for which is most likely the dry weather experienced during fruit development and the differential soil water retention capacities between sites.

When each site and season were analysed independently, segregation of chemical classes within the breeding population was evident. A wide range of polyphenols were characterised but the most evident amongst these were the following: cyanidin 3-glucoside, cyanidin 3-sophoroside, cyanidin 3-glucosylrutinoside cyanidin 3-rutinoside, pelargonidin 3-sophoroside, pelargonidin 3-glucosylrutinoside and quercetin acetylrutinoside. Analysis using PCA indicated segregation within the population for the cyanidin-3-sophoroside and cyanidin-3-rutinoside groups. This is informative and means that the SC-DI-MS approach could facilitate a rapid screen to identify progeny elevated in these compounds. This approach has subsequently been validated as a "near-quantitative" approach, for (poly)phenolic metabolites at least, by McDougall et al. (2008) and is currently being expanded to include strawberry and blackcurrant populations with the aim of correlating metabolomic data with sensory properties.

5. Conclusions

The characterisation of natural diversity in plant metabolites using unbiased metabolite profiling approaches is already providing us with a deeper knowledge of food composition and its variable nature both within and between species. This baseline approach is already being applied in comparisons of GM crops with non-GM comparators with a history of safe use, but metabolomic data are not specifically requested in the risk assessment process (at least not to date). Some argue that these unbiased analytical techniques should indeed be applied to detect unintended effects and reduce uncertainty. However, the potential use of these approaches in food safety and quality assessment need not be confined to GMOs. This should however, be on a case-by-case basis.

6. Conflict of interest statement

None of the authors have any conflicts of interest with regard to this manuscript.

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