Spatial Mapping and Profiling of Metabolite Distributions during Germination\textsuperscript{1}[OPEN]

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Germination is a highly complex process by which seeds begin to develop and establish themselves as viable organisms. In this study, we utilize a combination of gas chromatography-mass spectrometry, liquid chromatography-fluorescence, and mass spectrometry imaging approaches to profile and visualize the metabolic distributions of germinating seeds from two different inbreds of maize (\textit{Zea mays}) seeds, B73 and Mo17. Gas chromatography and liquid chromatography analyses demonstrate that the two inbreds are highly differentiated in their metabolite profiles throughout the course of germination, especially with regard to amino acids, sugar alcohols, and small organic acids. Crude dissection of the seed followed by gas chromatography-mass spectrometry analysis of polar metabolites also revealed that many compounds were highly sequestered among the various seed tissue types. To further localize compounds, matrix-assisted laser desorption/ionization mass spectrometry imaging was utilized to visualize compounds in fine detail in their native environments over the course of germination. Most notably, the fatty acyl chain-dependent differential localization of phospholipids and triacylglycerols was observed within the embryo and radicle, showing correlation with the heterogeneous distribution of fatty acids. Other interesting observations include unusual localization of ceramides on the endosperm/scutellum boundary and subcellular localization of ferulate in the aleurone.

Plants use seeds as the propagule to ensure reproduction to the next generation, and over the past 10,000 years, human civilizations have established agricultural practices to ensure a seed-based food supply (Larson et al., 2014). Therefore, deciphering the processes that enable seeds to perform their biological functions is of importance in understanding how plants are propagated and also is of practical importance to improve agriculture. Seeds are designed to survive long periods of dormancy in a relatively dry state, and the process of germination is initiated by the imbibition of water. During this germination process, many metabolic changes occur, most of which are associated with the catabolism of seed storage products (proteins, polysaccharides, and lipids) into metabolically usable, simpler chemical forms that are either used as precursors to assemble the growing seedling or are oxidized via energy-producing biochemical pathways to thermodynamically support growth (Bewley, 1997, 2001).

The specific metabolic processes that support seed germination are somewhat dependent on the taxonomic clade of the plant, which determines seed tissue/organ organization and the nature of the seed storage compounds. Specifically, the seeds of the Poaceae family of monocots are characterized by a starch- and protein-filled endosperm, and their catabolism by digestive enzymes produced in the outermost layer of the endosperm (i.e. the aleurone) provides the carbon-based and nitrogenous precursors for the growth of the embryo, which is composed of the embryonic axis and the scutellum (Dante et al., 2014). Thus, during seed germination, the glycolytic and oxidative pentose phosphate pathways are induced to metabolize the hydrolyzed starch. Smaller quantities of seed storage proteins also are catabolized to provide the amino acid precursors for new protein synthesis in the embryo, or carbon skeletons for reassimilation into anabolic
processes, or further catabolized for energy generation. Finally, lipid in the form of triacylglycerol (TAG) is stored in a specialized tissue (in maize *Zea mays*, the scutellum), and its catabolism via the β-oxidation of fatty acids can provide the elongating embryo axis an energy source. Alternatively, coupling with the glyoxylate pathway, which is induced during germination, carbon from fatty acids can be used to assemble new metabolic intermediates to support embryo growth (Firenzuoli et al., 1968; He et al., 2015).

Thus, seed germination requires the coordinated induction of a number of processes that are nonuniformly distributed among the tissues and organs of the seed. Many of the metabolic pathways that are induced during the seed germination processes that involve starch, oil, and protein turnover have been studied via molecular, genetic, and biochemical studies (Ingle et al., 1964; Limami et al., 2002; Shu et al., 2008; Zhang et al., 2009). Therefore, techniques that allow for the determination of the spatial localization of metabolites in fine detail, specifically mass spectrometry imaging (MSI), should allow for further insight into the mechanisms and actions of the pathways that are integral to seed germination.

MSI has become an increasingly powerful technique with which to study the spatial distribution of biological molecules within tissues (McDonnell and Heeren, 2007). In a typical MSI experiment, a sampling probe is rastered across a tissue sample, with mass spectra collected at each raster point. Following data acquisition, the spatial distribution of ions of interest can be visualized based on the x-y coordinates of the collected spectra. Various sampling probes have been adopted for MSI along with accompanying ionization methods (McDonnell and Heeren, 2007; Amstalden van Hove et al., 2010). Owing to its ease of use, high sensitivity, and ability to ionize a wide variety of molecules, matrix-assisted laser desorption/ionization (MALDI) has been the most widely used MSI technique. MALDI-MSI can obtain high-spatial-resolution images of ions, allowing for the visualization of fine structures. Spatial resolution of ~20 μm has become routine in MALDI-MSI, and 2- to 5-μm spatial resolution has been demonstrated by several groups, with the latter providing a means to locate metabolites within subcellular compartments (Zavalin et al., 2013; Korte et al., 2015).

Recently, MALDI-MSI has begun to see increased application in the study of plant biology (for review, see Kaspar et al., 2011; Lee et al., 2012). Here, we applied MALDI-MSI in combination with gas chromatography–mass spectrometry (GC-MS) and HPLC-based analyses of extracts to study the distributions and profiles of metabolites in germinating maize seeds at four different time points after imbibition. Two contrasting maize genotypes (inbreds B73 and Mo17) were compared during germination to explore the metabolic differences arising from the genetic differences between these two inbreds. GC-MS and HPLC-based metabolite profiling of extracts prepared from the physically dissected seeds was used to distinguish between the metabolomes of the two inbreds during early germination and to provide a quantitative validation of the MSI localization data. Three different MALDI matrices were used in either positive or negative ion mode to image the spatial distribution of a wide range of metabolites. This integrated approach provides unprecedented insights into the spatially resolved coordination of metabolic processes that are sequestered among the germinating embryo axis, the lipid-rich scutellum, the digestive endosperm, the digestive aleurone, and outer pericarp cell layers during the early stages of seed germination.

**RESULTS**

**Overview of the Experimental Workflow**

A schematic of the experimental workflow is provided in Figure 1. Maize seeds were collected from the B73 and Mo17 inbreds at four time points during the early phases of germination (0.2, 12, 24, and 36 h post-imbibition). At each time point, nine seeds comprising three biological replicates (three seeds each) were immediately flash frozen and extracted for whole-seed metabolite profiling. These extracts were analyzed via a GC-MS nontargeted global metabolite analysis platform and via a liquid chromatography (LC)-fluorescence-based targeted analysis platform for amino acids. In addition, at the 12- and 36-h time points, nine seeds comprising three biological replicates (three seeds each) were collected for GC-MS analysis of seeds dissected into component endosperm, embryo, tip cap, and pericarp. In parallel, three additional seeds from each of the four time points were flash frozen in liquid nitrogen and subjected to MSI analysis. These seeds were sectioned with 10 μm thickness (25 sections per seed), and four sections (5, 11, 17, and 22) were inspected via optical microscopy. The three sections nearest to the most intact section as determined via optical microscopic inspection were used for MSI analysis. Microscopic analysis revealed detailed morphological features of the seed, including the pericarp, which is the outermost layer of the seed, the aleurone layer of the endosperm, the endosperm itself, the embryonic axis, the scutellum, and the tip cap. As germination progressed, the radicle also became visible as it protruded from the embryonic axis of the embryo. It is important to note that it can be difficult to distinguish between the multicellular pericarp and the single-cell aleurone layer at lower magnification. In the cases where these cell layers cannot be distinguished, we will refer to them as the aleurone and/or pericarp.

The analytes that can be characterized through MSI often are significantly limited by the choice of matrix and ion polarity. In this work, MSI analysis was performed on the three tissue sections with one of three different matrices, 1,5-diaminonaphthalene (DAN), 9-aminoacidine (9AA), and 2,5-dihydroxybenzoic acid (DHB), to cover a relatively wide range of analytes. DAN and 9AA were used in negative ion mode (mass-to-charge ratio [m/z] range 50–1,000), while DHB was used in positive ion mode (m/z range 50–800 and m/z...
range 600–1,600). In total, 72 seed sections were analyzed by MSI (2 inbred lines × 3 seeds per time point × 4 time points × 3 sections per seed for each of the three matrices). A spatial resolution of 100 μm was used to minimize the total data acquisition time in this large-scale experiment while still providing sufficient spatial resolution to match the morphological features observed in the optical images.

Over the course of the analyses, hundreds of analytes were observed by both MSI and the gas chromatography (GC)- and LC-based metabolite profiling platforms. However, due to biological and analytical variations, many low-abundance analytes were not reproducibly detected across all data sets. Therefore, we limit our discussion to the more abundant analytes that were consistently observed across three biological replicates. For simplicity of presentation of the MSI data, all the m/z values and mass tolerances used in producing images are summarized in Supplemental Table S1, as are the color scales used to produce false color images.

Analysis of the Metabolomes of Germinating Seeds

The nontargeted GC-MS metabolomics analyses of the whole seeds at four germination time points detected 162 analytes, of which 63 were chemically identified. These metabolites include sugars (monosaccharides and disaccharides), sugar acids, organic acids, phenolics, nitrogenous metabolites, polyols, esters, lipids, fatty acids, and sterols (Supplemental Table S2). There are clear differences in the metabolome between the two inbreds, and the metabolite profile also is affected by the germination process. Using log-ratio plots, we evaluated the degree to which these differential metabolites between the inbreds are differentially affected by the germination process (Fig. 2A). In these comparisons, we used the 12-h time point as the anchor for all comparisons among genotypes and the seed germination time line. At this anchor time point, there are 63 metabolites that accumulate at significantly different levels between the inbreds. By comparing such log-ratio data at each of the four time points, one can gain insights into how the germination process affects the metabolome. One readily recognizable class of metabolites that are clearly distinct between the two inbreds is the amino acids, and this platform detected 10 of the proteinogenic amino acids. Therefore, we confirmed these differences with a second analytical platform, which specifically targeted amine-containing metabolites with LC-fluorescence, and this detected 18 of the proteinogenic amino acids (Supplemental Table S3), the exceptions being Pro and Cys. In both the targeted LC-amino acid platform (log-ratio plot in Supplemental Fig. S1) and the nontargeted GC-MS metabolomics platform (Fig. 2A), most amino acids are at significantly
higher levels in Mo17 seeds than in B73 seeds. These data are consistent with previous studies of these inbreds that identified Mo17 mature seeds having a higher amino acid content than B73 seeds (Römisch-Margl et al., 2010). As the germination process proceeds, these differences in amino acid content between the two inbreds is reduced, so that by 36 h postimbibition, the profiles are almost identical except for Lys, Thr, and Arg, which are still slightly higher in Mo17, and Trp, which is now slightly higher in B73 (Supplemental Fig. S1).

More broadly, 64% of the detected metabolome (i.e. 104 metabolites) accumulates to different levels between the two inbreds at least at one time point during the germination process ($P < 0.05$ in Supplemental Table S2). Among the 104 metabolites that accumulate differentially among any of the time points, 21 are differential at all time points evaluated (Fig. 2B) and 15 are differential among any of three consecutive time points. Seven of the first group are chemically identified and appear to be intermediates of metabolic processes that would be expected to be hyperactive during seed germination. These are specifically associated with carbohydrate metabolism (i.e. sorbitol, cellobiose, rhamnose, and talose), which may be associated with starch mobilization that is occurring during the breakdown of the endosperm tissue or possibly cell wall deposition as the...
new seedling tissues begin to be assembled. Eight of the chemically identified metabolites that are differential among the three consecutive time points are amino acids (i.e. Asp, Glu, and Thr) in the three early time points and lipids (i.e. stigmasterol, sitosterol, and linolenic acid) that are differential among the three latter time points. These profiles are consistent with seed storage protein mobilization, which occurs at the earlier stages of seed germination, and membrane deposition, which occurs later in the process as the seed radicle begins to grow and emerge. Finally, among these chemically identified differentially expressed metabolites are succinic acid and fumaric acid, which are intermediates of the tricarboxylic acid cycle, and these are associated with the high rates of respiration that are needed to support the germination process (Bewley et al., 2013). Collectively, these data indicate that these metabolic processes are differential between the two inbreds, which correlates with the phenotypic observation that these two inbreds germinate at different rates.

Bearing in mind that a germinating maize seed consists of different tissues, each of which expresses diverse metabolic processes, we evaluated the distribution of the metabolome among four distinct seed organs that are readily separable by microdissection (i.e. the pericarp and aleurone layers, the embryo, the endosperm, and the tip cap). The metabolomes of these microdissected organs were evaluated at 12 and 36 h postimbibition. Because of the wider range of metabolites that were detected, the GC-MS analysis of the metabolomes of the microdissected seed organs focused on the polar class of metabolites. These analyses revealed the relative abundances of 218 analytes, of which 75 were chemically defined (Supplemental Table S4). Supplemental Figure S2 shows the log-ratio plot for the relative abundances of all analytes between Mo17 and B73, comparing the metabolomes of each dissected organ and the metabolomes of the whole seed.

An obvious advantage in the microdissected data set is that it reaches lower abundance metabolites, revealing the relative abundances of an extra 56 analytes (Supplemental Table S4) that were not detected when whole seeds were analyzed. More significantly, the metabolites that are the most differential between the metabolomes of the whole seed are different when one considers the metabolomes of the separated organs, which is indicative of the different metabolic processes that are being expressed in these individual organs. At both time points, the endosperm and embryo tissues account for the majority of the differentially expressed metabolites. About half of these are shared among multiple evaluated organs, but about 20% of the metabolome is uniquely differential in either the embryo or endosperm tissues (Fig. 2, C and D). The endosperm-specific differential metabolites are primarily amino acids at 12 h postimbibition, but by 36 h, these are a mixture of amino acids, sugars, and organic acids. This is consistent with the degradation of the starch and seed storage proteins that are concentrated in the endosperm of maize seeds and indicates different rates of their catabolism between the two inbreds.

Therefore, these data indicate that, as the seed germination process proceeds, the expressed metabolome changes between inbred lines, with larger changes occurring in the embryo, followed by the endosperm and tip cap. Fewer differentially expressed metabolites occur in the metabolome of the pericarp and aleurone tissues. More refined analyses of the nonuniform distribution of the metabolites in the different tissues of the germinating maize seed were obtained by MSI.

Heterogeneous Distribution of the Mobilization of Seed Storage Reserves

In the grasses, energy in dormant seeds is stored predominantly as polysaccharide starch granules within the endosperm, which can be mobilized by hydrolytic enzymes (e.g. α- and β-amylases) released by the aleurone and scutellum of germinating seeds (Zeeman et al., 2007). The images in Figure 3A show large hexose polysaccharides (Hex₅–Hex₉), presumably degraded from starch, observed at low abundance levels and localized in the endosperm. Disaccharides, predominantly Suc, also are observed and are present at much higher levels and primarily constrained to the germinating embryo. At the later stages of germination, the disaccharide signal appears to be concentrated more extensively in the emerging radicle of the embryonic axis. Disaccharide also is detected within other tissues, such as the endosperm and pericarp and/or aleurone, but at lower abundance. These nonhomogenous distributions of the polysaccharides are conserved in both B73 and Mo17 inbreds and are consistent with the mobilization of Suc within the scutellum and transport to the embryonic axis, specifically the radicle (Sánchez-Linares et al., 2012).

Seed oil energy reserves in maize are localized to the embryo, which is in contrast to other cereal grains (e.g. wheat [Triticum aestivum] and oat [Avena sativa]) that store oil in the endosperm (Leonova et al., 2010). The embryonic localization of four TAG species differing in fatty acyl chain composition is shown in Figure 3B. At the initial stages of germination (i.e. 0.2 and 12 h), TAGs are distributed homogenously throughout the embryo, including the embryonic axis and the scutellum. As germination progresses and the radicle of the embryonic axis begins to elongate, TAGs begin to display nonuniform localization patterns, similar to fatty acid and phospholipid molecular species, as will be discussed later.

During the germination process, amino acids become available from the breakdown of storage proteins initiated by the hydrolytic activity of protease enzymes synthesized in the protein storage vacuoles. The reduced nitrogen associated with these amino acids can be used for additional de novo synthesis of amino acids (Bewley et al., 2013). Because of their low ionization efficiency and amphiprotic nature, amino acids are difficult to analyze...
by MALDI-MSI (Toue et al., 2014). Despite this known difficulty, three amino acids were reliably detected in the MSI experiments, these being Lys, Arg, and Pro (Fig. 3C). Lys and Arg are barely detectable in B73 seeds but are clearly visible in Mo17 seeds. This striking difference in the abundance of Lys and Arg between the two inbreds is consistent with the parallel profiling data of these amino acids generated by LC-fluorescence analysis of o-phthalaldehyde (OPA) derivatives on extracts of seeds (Supplemental Fig. S1); the concentrations of these amino acids are significantly lower in extracts of B73 seeds than Mo17 seeds throughout the germination process. The LC method could not analyze Pro levels in these extracts because the OPA derivatization requires a primary amine group. Rather, Pro concentrations were compared from parallel GC-MS analyses of the polar extracts of seeds (Fig. 2A; Supplemental Fig. S2). These data are in agreement with the MALDI-MSI data, with Pro levels being similar or slightly higher in B73 seeds than in Mo17 seeds. The MSI data establish that the accumulation of these amino acids (Lys, Arg, and Pro) is concentrated in the embryonic axis and the scutellum of the seed embryo. Moreover, at later time points, Pro is more prominent in the radicle of the seed, but Lys and Arg appear to be less abundant in the radicle. These MSI-based visualizations of the in situ localization of these amino acids are consistent with the direct quantitative measurement of the levels of these amino acids in extracts of microdissected embryo tissues of the maize seeds (Supplemental Fig. S3).

Metabolites Enriched in Pericarp/Aleurone Layers

The pericarp and aleurone layers of the seed are responsible for the protection of the mature seed as well as the initial uptake of water that begins germination. As germination begins in maize, many of the enzymes needed to break down storage molecules in the seed are released from the aleurone layer of the endosperm (Chrispeels and Varner, 1967; Fincher, 1989; Bernier and Ballance, 1993). In this work, three metabolites are found to be uniquely located at the perimeter of the cross section and, therefore, can be surmised to be located either in the pericarp (the outermost layer of the kernel) or the aleurone layer, which is the outermost single cell layer of the endosperm. The three metabolites remained localized to this region of the seed throughout the germination process and were not detected in the embryo or the endosperm (Fig. 4A). This is in contrast to most other metabolites, such as Suc (Fig. 3A) or citrate (Fig. 5), that are found in the aleurone and/or pericarp but also in other tissues. One of these metabolites (m/z 193.051) was identified as ferulate by accurate mass (less than 5 ppm) and tandem mass spectrometry (MS/MS; Supplemental Fig. S4). However, useful MS/MS spectra could not be obtained for the other two ions (m/z 135.046 and 161.025) because of their low abundance. The chemical compositions calculated from the accurate masses, C_8H_8O_2 and C_9H_6O_3, respectively, suggest that they may have at least one aromatic ring.

The spatial resolution used in this experiment, 100 μm, was not sufficient to determine whether these
metabolites are localized specifically to the multiple cell layers of the pericarp or the single cell layer of the aleurone. To further explore the exact location of these compounds, a high-resolution MSI experiment was performed with 10 μm spatial resolution on a small region of the outer perimeter of B73 maize seeds at 24 h postimbibition (Fig. 4, B and C). Because of the limited sensitivity inherent to a much smaller sampling area, only ferulate provided sufficient ion signal to produce a clear image. The ferulate image was compared with that of the phospholipid phosphatidylinositol (PI) 34:2 and malate to better understand the relative localization of these compounds. Comparing these molecular images with the corresponding optical image (Fig. 4B) and overlaying MS images with the optical image (Fig. 4C), ferulate (red) appears to be present exclusively in the aleurone layer, particularly at the boundary between the aleurone and the pericarp, while the phospholipid PI 34:2 (green) is present throughout the aleurone layer and malate (blue) is localized in the endosperm and the pericarp layer of the seeds.

Figure 4. A, MSI of three compounds uniquely localized to the perimeter of the seed. Images were acquired in negative ion mode with DAN as the matrix. No normalization was applied to these images. Bars = 1 mm. B, Optical microscopic (top) and MS (bottom) images of the pericarp and aleurone layers of a B73 maize seed at 24 h postimbibition. Morphological features are labeled on the images. A, Aleurone; E, endosperm; G, gelatin embedding medium; P, pericarp. C, Overlay of the optical and MS images in B. MS images were obtained with DAN as the matrix in negative mode. MS images in B and C are ferulate (red), malate (blue), and PI 34:2 (green). All analytes were detected as deprotonated species, [M−H]^−. Bars = 100 μm.

Localizations of Respiratory Intermediates: Phosphorylated Metabolites and Organic Acids

During the process of seed germination, the respiration of seed reserves enables energy generation in the absence of photosynthesis, supporting the development of the seedling until it protrudes from the soil and is able to harness solar energy via photosynthesis. Respiration initiates within minutes of imbibition by the activation of cytosolic enzymes for glycolysis, the oxidative pentose phosphate pathway, and enzymes for the tricarboxylic acid cycle in mitochondria (Bewley et al., 2013). The distributions of two phosphorylated intermediates of respiration, hexose phosphate and glycerol phosphate, and one or possibly two organic acids of the tricarboxylic acid cycle, citrate and/or isocitrate, are shown in Figure 5. The phosphorylated metabolites are most likely Glc-6-P and glycerol-3-phosphate, respectively, but we cannot distinguish among the possible regioisomers or stereoisomers by MALDI-MSI or MS/MS experiments. Similarly, we are also unable to distinguish between citrate and isocitrate, and the resulting image is likely an integration of the distribution of these two metabolites.

In both inbreds, hexose phosphate and glycerol phosphate are localized in the germinating embryo and the aleurone and/or pericarp of the seeds, and this location is unaltered throughout the germination process. Hexose phosphate appears to be slightly less abundant in the radicle, whereas glycerol phosphate is more homogenously distributed throughout the embryo. The organic acids, citrate/isocitrate, are observed first at 0.2 h postimbibition, and they are concentrated predominantly in the perimeter (i.e. the aleurone and/or pericarp) of the seed. As germination progresses, citrate/isocitrate also occurs within the radicles and scutella of both inbreds, similar to the hexose phosphate and glycerol phosphate compounds; the former is also unable to distinguish between citrate and isocitrate, and the resulting image is likely an integration of the distribution of these two metabolites.

![Figure 4](https://example.com/figure4)

**Figure 4.** MSI of three compounds uniquely localized to the perimeter of the seed. Images were acquired in negative ion mode with DAN as the matrix. No normalization was applied to these images. Bars = 1 mm. B, Optical microscopic (top) and MS (bottom) images of the pericarp and aleurone layers of a B73 maize seed at 24 h postimbibition. Morphological features are labeled on the images. A, Aleurone; E, endosperm; G, gelatin embedding medium; P, pericarp. C, Overlay of the optical and MS images in B. MS images were obtained with DAN as the matrix in negative mode. MS images in B and C are ferulate (red), malate (blue), and PI 34:2 (green). All analytes were detected as deprotonated species, [M−H]^−. Bars = 100 μm.

![Figure 5](https://example.com/figure5)

**Figure 5.** Distribution of hexose phosphate (Hex6P), glycerol phosphate (GlycP), and citrate/isocitrate. Phosphorylated metabolites were detected as deprotonated water-loss species, [M−H_2O]^−, in negative ion mode with DAN as the matrix. Citrate/isocitrate was detected as a deprotonated species, [M−H]^−, in negative ion mode with 9AA as the matrix. Bars = 1 mm.
probably associated with the induction of the glyoxylic acid cycle, which is induced during germination to convert lipid-derived carbon to sugars via an acetyl-CoA intermediate, while the latter two are an intermediate and side product of glycolysis, respectively (Bewley et al., 2013).

Malate is another molecule involved in the tricarboxylic acid cycle and is detected in all replicates at all time points. Unlike citrate, its localization is found only in the endosperm of the seed and radicle of some more fully developed seeds (Supplemental Fig. S5A). This is not compatible with GC-MS analysis of the micro-dissected seed samples, which indicated that most of the malic acid is present in the embryo of the seed rather than the endosperm (Supplemental Fig. S5C). In contrast, citrate is much more abundant in embryos (Fig. 5), matching well with the dissected GC-MS data (Supplemental Fig. S5D). According to our previous experience on MSI of leaf tissues, it is often difficult to obtain reproducible results with malate unless the tissues are prepared fresh and analyzed as soon as possible. Hence, we suspect that this observation may be an artifact coming from the degradation of malate during tissue storage. To confirm this hypothesis, a separate MSI experiment was conducted on a seed that was analyzed on the same day it was collected. In this experiment, we found the majority of the malic acid in the embryo as expected (Supplemental Fig. S5B).

**Differential Distributions of Lipid Classes Accentuated in the Emerging Radicle**

In monocots such as maize, the embryonic axis develops into two main parts: the radicle, which is the primary root and is protected by the coleorhiza, and the plumule, or collection of leaf primordia, which is protected by the coleoptile. The germination process transitions into seedling growth with the protrusion of the radicle from the embryo. These anatomical structures develop with significant cell extension with or without cell division. Radicle growth through cell extension is a turgor-driven process that will involve the assembly of new membranes, requiring lipid biosynthesis (Bewley, 1997, 2001). Therefore, we applied MALDI-MSI to localize lipids during the germination process. MALDI-MSI efficiencies are dramatically different for each lipid class, depending on their chemical functionalities. Three matrices were used in positive and negative ion modes to visualize different classes of lipids. DHB was used in positive ion mode for phosphatidylcholine (PC) and ceramides; 9AA was used in negative ion mode for fatty acids; and DAN was used in negative ion mode for phosphatidylethanolamine (PE), phosphatidic acid (PA), and PI.

Figure 6 compares the spatial distribution of four fatty acids, palmitate (16:0), stearate (18:0), oleate (18:1), and linoleate (18:2), between the two inbreds at four germination stages. Over the course of the germination process, palmitate and linoleate occur homogenously throughout the embryo in both inbreds. In contrast, stearate is partially absent and oleate is almost completely absent from the radicles of both inbreds. This unprecedented finding is similar to the localization of TAGs (Fig. 3) and phospholipid classes (Fig. 7). However, it is in contrast to the GC-MS metabolomics data, which do not provide any spatial localization information for these fatty acids between the genotypes or changes associated with germination time points (Supplemental Fig. S6) and do not offer any indication of this unique, nonuniform localization of oleate.

The spatial localization of four different classes of phospholipids (PE, PA, PI, and PC) was compared in germinating seeds at 36 h postimbibition (Fig. 7A). These analyses also evaluated the distribution of different phospholipid molecular species arising from different combinations of fatty acyl chains. As may be expected from the fact that new cells are being generated as the embryo is undergoing expansion (in contrast to the endosperm, which is being consumed), all four phospholipids are most highly abundant in the embryo. There are contrasting localization patterns depending on the phospholipid class and on the molecular species of the phospholipids. With all four phospholipids and in both inbreds, the phospholipids with the most unsaturated acyl chains (36:4) show an even distribution between the radicle and the other embryonic tissues. For PI, PC, and PA, the more saturated phospholipids (i.e., in the order 36:3, 36:2, and 36:1) are less concentrated in the radicle compared with other embryonic tissues. In contrast, PE shows a unique localization pattern, with molecules of an even number of double bonds (36:4 and 36:2) being distributed homogeneously over the entire embryo, including the radicle, but molecules with an odd number of double bonds (36:3 and 36:1) being less abundant in the developing radicle. These differential localization patterns also were
observed at all time points during the germination process (Supplemental Fig. S7).

To further investigate the nonuniform distribution of phospholipids, quantitative comparison was made from two mass spectra averaged over selected pixels from the radicle and scutellum of seeds developed with a radicle. Figure 7B shows the ratio of each lipid molecular species, comparing signal strength for pixels in the radicle with the signal strength for pixels in the scutellum. This analysis confirms the visual patterns observed from the MS images; namely, the signal strength for the more saturated PA, PI, and PC is lower in the radicle region, whereas the signal strength of PE is lower only for those species with an odd number of double bonds. The unique localization of PE compared with the other phospholipid molecular species may be related to the unusually high abundance of PE 36:2. Figure 7C illustrates these abundance differences among the phospholipids in the radicle region. Whereas the most abundant molecular species are 36:4 for PC, PA, and PI and the more saturated forms of these phospholipids occur at lower levels, 36:2 is the most abundant PE, followed by PE 36:4. With the exception of PE 36:2, which is slightly but statistically higher in Mo17 than in B73 (P = 0.01), and, accordingly, the lower abundance of PE 36:4 (P = 0.03), there are no other significant differences between the genotypes.

The differential localization of phospholipids between the radicle and scutellum of the embryo is consistent with the relatively lower abundance of oleate (18:1) in the radicle (Fig. 6). To investigate this possible correlation, we took advantage of the MS/MS capabilities of the MALDI-MSI instrument used in this study and performed MS/MS imaging experiments. In MS/MS, a specific precursor ion can be selected and fragmented, and the mass spectra of fragment ions can be interpreted to extract structural information of the precursor ions. In the current MS/MS imaging experiment, a four-step data acquisition pattern (Supplemental Fig. S8) was used to selectively acquire the MS/MS data for four PA and PE molecular species (PE 36:3, PE 36:2, PA 36:3, and PA 36:2). Figure 8A shows MS/MS spectra obtained from the MS/MS imaging experiment for PA 36:2 and PE 36:2 in the radicle region of a 24-h Mo17 seed (similar results were seen for B73). For these 36:2 lipid species, there are two fatty acyl chain combinations possible: 18:2/18:0 and 18:1/18:1. The MS/MS spectrum of PA 36:2 has each of the three fatty acyl fragments (18:2, 18:1, and 18:0), indicating the presence of both the 18:2/18:0 and 18:1/18:1 combinations. In contrast, MS/MS of PE 36:2 shows only the 18:2 acyl fragment in the radicle of Mo17, indicating that it is composed primarily of the 18:2/18:0 combination. Because MS/MS preferentially induces fragmentation at the sn-2 position for PE and PA species (Hou et al., 2011), the inability to observe the 18:0 acyl fragment could indicate that PE 36:2 has the 18:2 fatty acyl chain located predominantly at the sn-2 position. Parallel MS/MS experiments of PA 36:3 and PE 36:3
reveal the occurrence of both 18:2 and 18:1 acyl fragments, confirming the occurrence of these two fatty acyl chains in these lipids (Supplemental Fig. S9).

Relative quantification between 18:2/18:0 and 18:1/18:1 was performed from this data set for PA and PE species in the radicle and scutellum, as shown in Figure 8B. Similar to Figure 7, B and C, in this calculation, MS/MS spectra were averaged from pixels in the radicle and the scutellum and fatty acyl fragments were summed to calculate the proportion of each molecular species. It should be noted, however, that because of the difference in the fragmentation efficiency between the sn-2 and sn-1 positions, this is not an exact quantification of the four lipids. Regardless, these calculations indicate that PE 36:2 (18:2/18:0) is the predominant PE species both in the radicle and scutellum, matching the homogenous images of the distribution of PE 36:2 (Fig. 7A) and of linoleate (Fig. 6) throughout the embryo. In contrast, PA 36:2 (18:1/18:1) occurs at significantly higher levels in the scutellum than in the radicle, consistent with the heterogeneous distribution of oleate among these two tissue types (Fig. 6).

The nonsymmetric distribution of 18:2-containing phospholipids between scutellar and radicle tissues suggests that the supply of 18:2 fatty acid may be different between these two tissues. We directly tested this hypothesis by assaying the expression of the fatty acid desaturase that converts 18:1 to 18:2. Specifically, we evaluated FAD2 mRNA levels by qRT-PCR using RNA isolated from dissected scutellar and radicle tissues. Bioinformatic analysis of maize genome data (Sen et al., 2010; Petryszak et al., 2016) identified six putative FAD2 genes based upon sequence homology to the Arabidopsis FAD2 gene (Atg12120); these were annotated as GRMZM2G169240, GRMZM2G169261, GRMZM2G174766, GRMZM2G056252, GRMZM2G16792, and GRMZM2G064701. Initial assays (Supplemental Table S5) identified that only GRMZM2G056252 and GRMZM2G064701 are expressed at measurable levels in germinating embryonic tissue during the initial 36 h after imbibition; the expression of the other four FAD2-like genes was detectable by RT-PCR, but their levels were too low to obtain robust quantitative expression data. However, later in the germination process (at 48 h post-imbibition), two of these FAD2-like genes were induced (i.e. GRMZM2G169240 and GRMZM2G169261; Supplemental Table S5), but this induction was not relevant to testing of the MSI-generated hypothesis.

Figure 9 shows the expression profile of the GRMZM2G056252 and GRMZM2G064701 mRNAs over the seed germination time period evaluated by MSI and metabolomics analyses. These data indicate that these two FAD2 genes are initially expressed at similar levels between the radicle and scutellum, but expression increases subsequently in the radicle by between 3- and 7-fold. This increased expression in the radicle occurs in both inbreds (B73 and Mo17), reaching peak expression at 36 h postimbibition. These data are consistent with the elevated levels of 18:2-containing PE in the radicle.

Several ceramide (Cer) molecular species also were observed in both inbreds, and their accumulation is persistent throughout the course of germination. Figure 10A shows the distribution of Cer d42:1 and Cer t42:0, and the distributions of other Cer species (Cer d42:2, Cer d40:1, and Cer t40:0) are shown in Supplemental Figure S10. We previously performed MS/MS of Cer d42:1 in a germinated B73 maize seed, confirming its structure (Feenstra et al., 2015), and we also are confident of the assignment of other ceramides based on the accurate mass determinations of the ions, all within 5 ppm mass error; however, MS/MS was not successful for other ceramides due to their low abundances. All ceramides have unique localization patterns that are different from the other lipid classes that were imaged. In both inbreds, and throughout the course of germination, all the detected ceramides are located on the endosperm side of the endosperm-scutellum boundary. Figure 10B shows this contrasting localization, comparing the distribution of Cer d42:1 with the embryo-specific PC 34:2 relative to the endosperm-scutellum boundary.
DISCUSSION

The process of seed germination is a particularly interesting biological process driven by cellular and metabolic coordination among several spatially distinct compartments to successfully establish the seedling. Because of the agricultural importance of cereal grains, previous metabolomics-based work has focused on these processes during the germination of rice (Oryza sativa; Shu et al., 2008) and the malting process for barley (Hordeum vulgare; Frank et al., 2011). However, traditional metabolomics analyses often prove laborious and challenging, with limited spatial information. Conversely, MSI presents a straightforward analytical capability that provides high-resolution spatial distribution data for small metabolites (less than 1.5 kD) but at the cost of limited quantitative information and total number of metabolites detected. In this work, a combination of GC- and LC-based metabolomics analyses was combined with a MALDI-MSI approach to study the quantitative metabolite profile data and spatial distribution of metabolites during the germination of seeds of two maize inbreds, Mo17 and B73. These complementary strategies provided a path to investigate both genotypic and developmental differences that occur during germination as well as provide quantitative and finely detailed spatial localization of metabolites.

The genetic diversity within maize is vast, as evidenced recently by rampant structural variation in genomic content and copy number variation across maize inbreds (Springer et al., 2009; Lai et al., 2010; Swanson-Wagner et al., 2010; Hirsch et al., 2014). Inbreds B73 and Mo17 were selected in state-sponsored public breeding programs led by the Land Grant institutions Iowa State University and University of Missouri, respectively, in the early 1900s and continuing to today. B73 is derived from the Stiff Stalk Synthetic population generated and maintained at Iowa State University, and Mo17 was selected from Lancaster Sure Crop material first developed in Lancaster, Pennsylvania (Troyer, 2004). The B73 and Mo17 inbreds share a rich history in the public sector as key founders of U.S. germplasm (Lu and Bernardo, 2001) and the development of agronomically important hybrids, both in the public and private sectors (Troyer, 2009). These important inbreds differ significantly in their genomic structures, both in terms of presence-absence variation in gene content and in the prevalence of single-nucleotide polymorphisms, occurring on average every ~80 bp (Fu et al., 2006; Vroh

Figure 9. Relative FAD2 expression in radicle and scutellar tissues of germinating maize seeds. FAD2 transcript levels encoded by GRMZM2G056252 (squares) and GRMZM2G064701 (triangles) were determined in RNA isolated from the radicle and scutellar tissues of germinating seeds from the inbreds B73 (gray lines) and Mo17 (red lines) 12 to 48 h postimbibition. The expression of FAD2 transcripts was calculated by 2^(-ΔΔCT), using the ubiquitin mRNA (GenBank accession no. BT018032) as the internal control. The expression of each FAD2 transcript was normalized relative to the level found in the scutellar tissue.

Figure 10. Distribution of ceramide species. A, Distributions of two ceramide molecular species (Cer d42:1 and Cer t42:0). Both are detected as protonated species, [M+H]^+ in positive ion mode with DHB as the matrix. Bars = 1 mm. B, Combined images of PC 34:2 (green) and ceramide d42:1 (red) in a B73 inbred seed at 12 h postimbibition. Bar = 1 mm.
Bi et al., 2006) based on comparison of published genome sequences (Schnable et al., 2009). The genetic diversity between B73 and Mo17 translates into metabolic, physiological, and phenotypic differences, including differences in germination rates and germination efficiency for inbreds B73 and Mo17 that have been observed under different environmental conditions (Munamava et al., 2004). This genetic diversity between the two inbreds also has led to differences in the metabolome, as was observed in our metabolic assessment of the early germination of maize seedlings. The most significant metabolic difference between germinating B73 and Mo17 seeds was in the enhanced accumulation of free amino acids in Mo17.

The fact that four of the amino acids (i.e. Arg, Asn, Gln, and Lys) showing higher abundance in Mo17 versus B73 are the carriers of reduced nitrogen may indicate that these metabolic processes are of significance in the interaction between carbon and nitrogen metabolism, as the germinating seeds adjust the physiological needs of the emerging seedling from different starting points in the amino acid profiles available in each inbred. Consistent with this hypothesis is the fact that these amino acid profiles are differentially affected by the germination processes, with Thr, Lys, Arg, and Asn occurring at higher levels in Mo17 than in B73 at the earlier stages of germination (12 and 24 h post-imbibition) and Gln levels also increasing in abundance in Mo17 at early stages and in B73 by 36 h post-imbibition. Germination efficiency has been shown to be correlated to the differential expression of enzymes involved in Asp-derived metabolism and, in turn, the differential metabolism of specific amino acids (Anzala et al., 2006) as well as to nitrogen-derived amino acid metabolism, specifically related to an amino acid anabolism enzyme, Gln synthetase (Limami et al., 2002).

Moreover, quantitative genetic approaches utilizing B73 × Mo17-derived germplasm to dissect the genetic basis for germination phenotypes have identified candidate genes involved in amino acid metabolism (Kollipara et al., 2002).

A second clear metabolome difference between the two inbreds is in the preferential accumulation of small organic acids in B73 (i.e. malate, pyruvate, and fumarate) compared with Mo17. Interestingly, quantitative genetic analyses of recombinant inbred populations derived from B73 and Mo17 parental inbreds have identified quantitative trait loci associated with germination under both optimal and low-temperature conditions. Although numerous candidate genes were identified (more than 3,000), one encodes a malate dehydrogenase (Hu et al., 2016). Collectively, the observed differences in metabolite accumulation between Mo17 and B73 across early germination provide testable hypotheses regarding their impacts on differential germination efficiency and other germination-related traits that have been shown to differ across maize inbreds.

Chromatography-based metabolite profiling generated quantitative data of small molecules, such as sugar monomers, organic acids, amines and amino acids, fatty acids, and sterols, which establish that germinating seeds of the two maize inbreds are readily distinguishable at the level of the expressed metabolome (Fig. 2). While these analyses provided global profiles of the seed metabolomes from which one can generate statistical quantitative correlations among individual metabolite abundances as affected by development and genotype, detailed information on the localization of the metabolites at the cellular level was lost. Further such analyses of seeds microdissected to separate different seed organs provided compartmentalization information of the metabolites and demonstrated that the metabolome of these different organs vary with respect to the developmental program of germination and is further differentially affected by different genotypes (Fig. 2, C and D). In general, however, even with the microdissected organs, the localization of the metabolites is limited to large, physically separable structures, each of which is made up of a combination of different tissue types with differing metabolic capabilities. Cell type-specific analysis can be done by sorting cells or using laser-capture microdissection, but such analysis is not typically applicable for metabolomic profiling because of the potential metabolite turnover during the laborious sample preparation process. Furthermore, the unknown degree to which these physically separated organs may be cross-contaminated complicates the interpretation of these data. MSI, therefore, offers a convenient means of overcoming the limitations of the chromatography-based metabolite profiling techniques in generating spatially resolved data, with fine-scale localization information in maize seeds at the cellular level.

Combining MALDI-MSI data with chromatography-based analyses allows for more comprehensive coverage of the metabolome beyond that obtainable by either one individually. For example, GC-MS revealed the relative abundance of small sugar molecules (tetroses, pentoses, hexoses, and disaccharide), and analysis of microdissected seed organs indicated that these small sugars are localized primarily to the embryo compared with the endosperm, and they also occur in the pericarp and/or aleurone tissues. MSI was only able to visualize the disaccharide species, and those data are in agreement with the distribution determined from the chromatographic analysis of microdissected organs. However, MSI provided additional information by successfully visualizing the location of large polysaccharides (Hex5–Hex9), all of which are localized to the starchy endosperm of the seed (Fig. 3A). These results are consistent with the expectation that starch breakdown during germination occurs initially by the action of α- and β-amylase secreted from the scutellum and aleurone. These oligosaccharides are broken down to their constituent Glc units and are transported to and taken up by the scutellum, where they are reassembled into Suc, the disaccharide likely visualized by MSI (Bewley, 2001; Nonogaki, 2008). The localization of the presumable Suc disaccharide in the emerging radicle is consistent with the previously reported mobilization of Suc within the scutellum and the subsequent transport.
to the embryonic axis, specifically to fuel cell elongation in the radicle (Sánchez-Linares et al., 2012).

A similar benefit of combining metabolomic and MSI data is observed when one considers the patterns observed for the different fatty acids and lipid molecular species. GC-MS analysis was limited to being able to detect fatty acids primarily of 16- and 18-carbon chain lengths after derivatization to volatile methyl esters. In contrast, MALDI-MSI not only cannot detect these fatty acids without derivatization but also cannot detect larger nonvolatile lipid molecules such as phospholipids, ceramides, and TAGs. Both MSI and GC-MS showed similar fatty acid profiles, with minor differences in their relative abundances between the two inbreds. However, MSI revealed differential localization of the fatty acids dependent on the degrees of unsaturation. Homogenous distributions were observed within the embryo for palmitate and linoleate, but absences were seen in radicles for oleate and partially for stearate (Fig. 6).

Similar differential patterns of spatial distribution were observed for phospholipids and TAGs depending on their fatty acyl species, in that oleate contributes to the absence in radicles and linoleate contributes to the homogenous embryonic distributions. For example, fully unsaturated TAG 54:6 (18:2/18:2/18:2) is highly homogenous throughout the embryo but becomes absent in the radicle as the degree of saturation increases (Fig. 3B). Phospholipids of PI, PA, and PC show the same trend as TAGs, with their absence in the radicle being correlated with the degree of saturation (Fig. 7). PE shows apparently different localization from other phospholipids by having PE molecular species with even numbers of unsaturation (36:4 and 36:2) evenly distributed throughout the radicle and embryo. However, MS/MS experiments revealed that this is due to the high radicle content of 18:1/18:1 in other 36:2 phospholipids, while PE 36:2 is mostly composed of 18:2/18:0 (Fig. 8B). These results suggest that the heterogeneous distribution of fatty acids dictates the fatty acyl chain-dependent differential localization of lipids. Such nonuniform distribution has been observed previously in cotton (Gossypium hirsutum; Horn et al., 2012) and Camelina spp. seeds (Horn et al., 2013); thus, this is not unique to maize but, apparently, is a more general phenomenon. However, the specifics of the distribution are unique for each species, likely owing to the different anatomy and biological properties of these seeds.

Because plant systems use PC as the substrate for fatty acid desaturation, specifically the FAD2 enzyme that generates 18:2 (Bates et al., 2013; Li-Beisson et al., 2013), we evaluated whether this nonuniform distribution of the unsaturated phospholipids may reflect the distribution of this biosynthetic enzyme. We found that only two of the six FAD2-encoding genes of maize are expressed at this stage of seed germination (namely, GRMZM2G056252 and GRMZM2G064701). Moreover, consistent with the hypothesis generated from the MSI data, we found that these two FAD2 genes are preferentially expressed in the radicle tissue relative to the scutellar tissue, providing a potential explanation for the enrichment of the 18:2-containing lipids in the former.

Ceramide molecular species detected by MSI showed incredibly unique localizations that were significantly different from any other lipid species detected in this work. By directly comparing with PC molecular species, we found that the ceramides are localized to the endosperm side of the endosperm/scutellum boundary. Previous work has reported the presence of ceramides in maize (Dietrich et al., 2005) as well as in the bran and endosperm of rice grains (Fujino et al., 1985), supporting our observed localization of ceramides in the endosperm of the maize seeds. Although detailed biochemical understanding of the biological functions that ceramides play in plants is relatively poor in comparison with mammalian and fungal organisms (Kolesnick, 2002; Levy and Futerman, 2010), they are thought to be important for plant growth and defense. Inhibition of their biosynthesis by a mycotoxin (Williams et al., 2007) or mutations in the biosynthesis pathway lead to programmed cell death and disease states in plants (Lynch and Dunn, 2004; Markham et al., 2013), whereas induction of their biosynthesis via the overexpression of ceramide synthases leads to impacts in biomass accumulation, growth, and mycotoxin resistance (Lützgreharm et al., 2015).

In conclusion, this study successfully demonstrated the combined use of chromatography-based metabolite profiling and MALDI-MSI-based chemical imaging to elucidate the metabolite profile and spatial distribution of metabolites in the complex processes of seed germination in maize. The traditional metabolomics approaches offered comprehensive metabolite coverage of small molecules, which demonstrated that there are significant differences in the metabolite profiles between inbreds during germination as well as between different seed organ/tissue types of the same inbred. Conversely, MALDI-MSI offers more detailed spatial information on the distribution of the metabolites, especially in terms of unusual localizations of lipids. This study demonstrates the synergy that can be gained by combining these strategies to reveal new insights into complex biological processes that integrate the capabilities of different cellular compartments.

MATERIALS AND METHODS

Seed Germination and Harvest

Seeds of maize (Zea mays) inbreds B73 and Mo17 were imbibed and germinated as described previously (Liu et al., 2013). Briefly, seeds were placed in deionized water and imbibed while shaking at 300 rpm for 10 min. These seeds were then placed embryo side down on moist filter paper in petri dishes. Plates were incubated in a greenhouse under a diurnal cycle of 15 h of light and 9 h of dark at 27°C and 24°C, respectively.

Germinating seeds were collected at four time points, 0.2, 12, 24, and 36 h, with the 0.2-h time point corresponding to those taken immediately after 10 min of imbibition. At each time point, seeds were collected that appeared similar in terms of their developmental stage. Three seeds chosen for MSI were sectioned longitudinally, immediately flash frozen in liquid nitrogen, and stored at −80°C. From another batch of seeds grown in identical conditions, nine seeds were chosen at each time point for total metabolite and amino acid analyses.

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Whole seeds were frozen in liquid nitrogen and dried using a vacuum lyophila-
izer (Labconco); then, three seeds were combined as one biological replicate 
and pulverized using a Mixer Mill 301 (Retsch) in 2-mL Eppendorf tubes for 
total metabolite analysis. Companion sets of germinating seeds of similar 
shapes were collected at the 12- and 36-h time points, microdissected to separate 
the pericarp and/or aleurone (these two layers could not be separated), tip cap, 
embryo, and endosperm, and then the same lyophilization/pulverization 
process described above was followed for each dissected tissue.

Cryosectioning
Each seed was removed from ~80°C storage and quickly placed cut side 
down into a plastic cryo-mold (Electron Microscopy Sciences). A warm, 10% 
(w/v) gelatin solution was poured into the cryo-mold such that the solution 
completely covered the seed. The mold was then held over liquid nitrogen until 
the gelatin became mostly opaque (approximately one-half of the gelatin) and 
than transferred to a ~20°C freezer to complete the freezing process.

The frozen gelatin block was removed from the cryo-mold and mounted on a 
cryostat chuck. The seed was then cut down to the tissue region of interest (e.g. 
the embryo axis containing the radicle, if the radicle was present in the seed) 
using a Leica CM1520 cryostat (Leica Biosystems) until the embryonic tissue was 
visible, following which consecutive 10-μm tissue sections were collected on 
adhesive tape windows (Leica Biosystems) to preserve the structural integrity 
(developmental stage and section 

Microscopy and MALDI Imaging Preparation
Microscope images of four sections (nos. 5, 11, 17, and 22 of the 25 collected) 
were obtained using an Olympus SAH-10 stereomicroscope (Olympus Scientific 
Solutions) with an AxioCam HRC and Axio Vision software (Carl Zeiss) to 
provide finely detailed images. From these images, the highest quality section 
was selected based on the clear visualization of developmental stage and section 
integrity. The sections nearest to this section were chosen for MSI. The sections 

Mali-MSi
MSI data were acquired using a MALDI-linear ion trap-Orbitrap mass 
spectrometer (MALDI-LTQ-Orbitrap Discovery; Thermo Finningan) modified to 
use an external diode-laser pumped frequency-tripled Nd:YAG laser (335 nm, 
UVIF series; Elfloright). For DAN and 9AA in negative ion mode, Orbitrap MS 
data were acquired using a 100-μm raster size for the m/z range of 50 to 1,000. 
For DHB in positive ion mode, each raster step (100 μm) was broken down into 
two spiral steps (50 μm each), and Orbitrap MS scans were performed for m/z 
50 to 800 and m/z 600 to 1,600, respectively. For all imaging runs, the laser 
spot size was kept at 2 μm estimated from the burn mark on this DHB film, except 
the high-spatial-resolution experiment in Figure 5, where the laser spot size was 
~10 μm adjusted using a beam expander in the optical beam path. Laser pulse 
energy and number of shots were optimized for each matrix.

Data analysis and image generation were performed using ImageQuest and 
Xcalibur software (Thermo). Image normalization was performed for some 
images and is noted in the figure legends. Mass values and tolerances used 
to generate images are summarized in Supplemental Table S1. For some metabolites, 
MS images were generated after normalization to the total ion count at each pixel (defined by the raster step) to minimize spot-to-spot variation, and the same color scale is used regardless of genotype or germination time point. For most of the metabolites, however, MS images are produced in absolute ion 
scales without normalization, due to the fact that normalization can distort the images for low-abundance ions, and the color scheme was adjusted arbitrarily for each image to obtain an image with the highest contrast to display where the metabolite is localized without accentuating background noise. Separate MS/MS experiments were performed using collision-induced dissociation of the linear ion trap. For m/z 193,051, a collision energy of 100 (arbitrary unit) was used with an activation time of 30 ms and an isolation mass window of 0.8 Da. For phospholipid MS/MS, a collision energy of 45 was used with an activation time of 30 ms and an isolation mass window of 1.0 Da.

Total Metabolite Analysis
Total metabolite extractions were carried out as described previously 
(Schmidt et al., 2011). Extracts were prepared from ~20 mg of lyophilized 
and pulverized whole seeds and dissected seed fractions. Each sample was spiked 
with two internal standards (25 μg of ribitol and 25 μg of nonadecanoic acid for 
the polar and nonpolar fractions, respectively), and 0.35 mL of hot methanol (60°C) 
was added and incubated at the same temperature for 10 min, followed by 
sonication for 10 min at full power. To this slurry, 0.35 mL of chloroform and 
0.3 mL of water were added, and the mixture was vortexed for 1 to 3 min. After 
centrifugation for 5 min at 13,000g, 200 μL of the upper phase (polar fraction) 
and 200 μL of the lower phase (nonpolar fraction) were removed separately into 
2-mL GC-MS vials and dried in a Speed-Vac concentrator (model SVC 100H; 
Savant). Both polar and nonpolar extracts were analyzed for whole-seed sam-
ples, and only the polar fractions were analyzed for microdissected samples.

Double derivatization via methoximation and silylation was performed to 
protect ketone functional groups and to increase the volatility of the compounds, 
respectively. For methoximation, 50 μL of 20 mg mL−1 methoxamine hydro-
dchloride dissolved in dry pyridine was added, and the reaction was conducted 
for 30 min at 37°C. Silylation was performed by the addition of 70 μL of N,N-di-(trimethylsilyl)trifluoroacetamide with 1% trimethylchlorosiliane and incubated at 65°C for 30 min. One microliter of the derivatized samples was injected for GC-MS in splitless mode. GC-MS analysis was performed using an Agilent 6890 gas chromatograph interfaced to an 
Agilent 5973 quadrupole mass spectrometer with an HP-5ms column (30 μm x 
0.25 mm x 0.25 μm; Agilent). The temperature gradient was programmed from 
70°C to 320°C at 5°C min−1 with helium flow rate at 1 mL min−1 and inlet 
temperature at 280°C. EI-MS ionization energy was set to 70 eV, and the 
interface temperature was 280°C.

Amino Acid Analysis
Amino acid analysis was carried out following a method similar to that 
described previously by Guan et al. (2015). About 10 mg of lyophilized maize 
seed powder was extracted with 1 mL of hot water at 85°C for 30 min and 
spiked with 10 μg butylamine internal standard. The samples were centrifuged 
brieﬂy for 5 min, passed through a syringe ﬁlter with a 0.2-μm pore size, and 
subjected to LC-ﬂuorescence amino acid analysis with precolumn derivatiza-
tion of primary amino acids with OPA.

LC-ﬂuorescence analysis was performed using an Agilent 1110 HPLC de-
vice with a fluorescence detector with a Hypersil ODS C18 reverse-phase col-
umn (250 mm x 4 mm, 5 μm; Thermo). Excitation and emission wavelengths 
for ﬂuorescence detection were set at 337 and 454 nm, respectively. The solvent 
systems used were buffer A (10% methanol in 10 mM NaH2PO4, pH 7.3), buffer B (80% methanol in 10 mM NaH2PO4, pH 7.3), and OPA solution (12.25 mg of 
OPA in 312.5 μL of methanol, 6 mL of 0.4 M borate buffer, and 19.22 μL of 
mercaptoethanol). The precolumn OPA derivatization reaction was achieved 
using an in-loop-reaction program. The solvent program was a linear gradient from 
100% buffer A to 100% buffer B in 46 min at a flow rate of 1 mL min−1. The amino 
acid standard mixture included butylamine and 18 of the 20 proteogenic 
amino acids at the concentration of 10 μM each. Cys and Pro cannot be analyzed 
by this method and were not included as standards. The amino acid standard 
mixture was used to calculate the response factors for the detector, and butyl-
amine was used to generate a standard curve.

Data Analysis
Three biological replicates were used for GC or LC analysis of the extracts. 
Those compounds that were observed in two or three data sets were subjected 
to statistical analysis and reported here. For those compounds observed only in 
two data sets, the missing values were replaced by one-third of the estimated 
minimum value. Log−ratio plots were calculated for each metabolite as
described previously (Quanbeck et al., 2012). The raw data and averages and se calculations were determined from three biological replicates and are available in the PMR database and Supplemental Tables S2 to S4, respectively. Student’s t test was used to calculate P values.

The GC-MS data files were deconvoluted and searched against an in-house MS library and the NIST 14 Mass Spectral Library using NIST AMDIS software (Stein, 1999). Total metabolite analysis results obtained with GC-MS and amino acid analysis from LC fluorescence are publicly available in the PMR database (http://metnetdb.org/PMR/). They are available from the site in the name Seed Germination under the species Zea mays.

RNA Extraction and Quantitative PCR

Embryos were microdissected from germinating seeds at different times after imbibition, and the scutellar tissue was separated from the radicle. The flash-frozen tissues were pulverized, and RNA was extracted (Wang et al., 2012). The isolated RNA preparations were treated with DNase (Ambion), and 8 µg of RNA was reverse transcribed using Double Primed RNA to cDNA EcoDry isolated RNA.

The GC-MS data files were deconvoluted and searched against an in-house MS library and the NIST 14 Mass Spectral Library using NIST AMDIS software (Stein, 1999). Total metabolite analysis results obtained with GC-MS and amino acid analysis from LC fluorescence are publicly available in the PMR database (http://metnetdb.org/PMR/). They are available from the site in the name Seed Germination under the species Zea mays.

Supplemental Table S4. Metabolite abundance data detected from microdissected seed organs analyzed by GC-MS.

Supplemental Table S5. Normalized expression levels of six individual FAD2-encoding mRNAs in radicle tissues relative to scutellar tissues of germinating seeds from inbred B73 and Mo17.

Supplemental Table S6. List of primer sequences used for qRT-PCR analysis.

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