CYP701A8: A Rice ent-Kaurene Oxidase Paralog Diverted to More Specialized Diterpenoid Metabolism

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Abstract
All higher plants contain an ent-kaurene oxidase (KO), as such a cytochrome P450 (CYP) 701 family member is required for gibberellin (GA) phytohormone biosynthesis. While gene expansion and functional diversification of GA-biosynthesis-derived diterpene synthases into more specialized metabolism has been demonstrated, no functionally divergent KO/CYP701 homologs have been previously identified. Rice (Oryza sativa) contains five CYP701A subfamily members in its genome, despite the fact that only one (OsKO2/CYP701A6) is required for GA biosynthesis. Here we demonstrate that one of the other rice CYP701A subfamily members, OsKOL4/CYP701A8, does not catalyze the prototypical conversion of the ent-kaurene C4α-methyl to a carboxylic acid, but instead carries out hydroxylation at the nearby C3α position in a number of related diterpenes. In particular, under conditions where OsKO2 catalyzes the expected conversion of ent-kaurene to ent-kaurenoic acid required for GA biosynthesis, OsKOL4 instead efficiently reacts with ent-sandaracopimaradiene and ent-cassadiene to produce the corresponding C3α-hydroxylated diterpenoids. These compounds are expected intermediates in biosynthesis of the oryzalexin and phytocassane families of rice antifungal phytoalexins, respectively, and can be detected in rice plants under the appropriate conditions. Thus, it appears that OsKOL4 plays a role in the more specialized diterpenoid metabolism of rice, and our results provide evidence for divergence of a KO/CYP701 family member from GA biosynthesis. This further expands the range of enzymes recruited from the ancestral GA primary pathway to the more complex and specialized labdane-related diterpenoid metabolic network found in rice.

Disciplines
Biochemistry, Biophysics, and Structural Biology | Genetics and Genomics | Plant Biology

Comments
CYP701A8: A Rice ent-Kaurene Oxidase Paralog Diverted to More Specialized Diterpenoid Metabolism

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All higher plants contain an ent-kaurene oxidase (KO), as such a cytochrome P450 (CYP) 701 family member is required for gibberellin (GA) phytohormone biosynthesis. While gene expansion and functional diversification of GA-biosynthesis-derived diterpene synthases into more specialized metabolism has been demonstrated, no functionally divergent KO/CYP701 homologs have been previously identified. Rice (Oryza sativa) contains five CYP701A subfamily members in its genome, despite the fact that only one (OsKO2/CYP701A6) is required for GA biosynthesis. Here we demonstrate that one of the other rice CYP701A subfamily members, OsKOL4/CYP701A8, does not catalyze the prototypical conversion of the ent-kaurene C4a-methyl to a carboxylic acid, but instead carries out hydroxylation at the nearby C3a position in a number of related diterpenoids. In particular, under conditions where OsKO2 catalyzes the expected conversion of ent-kaurene to ent-kaurenoic acid required for GA biosynthesis, OsKOL4 instead efficiently reacts with ent-sandaracopimaradiene and ent-cassadiene to produce the corresponding C3a-hydroxylated diterpenoids. These compounds are expected intermediates in biosynthesis of the oryzalexin and phytocassane families of rice antifungal phytoalexins, respectively, and can be detected in rice plants under the appropriate conditions. Thus, it appears that OsKOL4 plays a role in the more specialized diterpenoid metabolism of rice, and our results provide evidence for divergence of a KO/CYP701 family member from GA biosynthesis. This further expands the range of enzymes recruited from the ancestral GA primary pathway to the more complex and specialized labdane-related diterpenoid metabolic network found in rice.

The phytohormones required for normal plant growth and development in all higher plants (Yamaguchi, 2008). Accordingly, the genes encoding the relevant biosynthetic enzymes must be present in all plant genomes. These have provided a genetic reservoir from which other, more specialized diterpenoid metabolism has evolved (Peters, 2010). Indeed, such derivation of more specialized metabolism from hormone biosynthesis appears to be an emerging theme in plant metabolism (Chu et al., 2011).

GA biosynthesis is initiated by cyclization of the general diterpenoid precursor (E,E,E)-geranylgeranyl diphosphate to ent-labdadienyl/copalyl diphosphate (ent-CPP), leading to designation of the derived natural products as labdane-related diterpenoids (Peters, 2010). The GAs are more precisely defined by their tetracyclic 6-5-6-5 ring structure (MacMillan and Takahashi, 1968). However, their biosynthesis proceeds through the 6-6-5 tetracycle ent-kauren-16-ene, which is formed from the bicyclic ent-CPP by ent-kaurene synthases (KSs; Yamaguchi, 2008). The ring contraction catalyzed by the cytochrome P450 (CYP) ent-kaurenoic acid oxidase (KAO) is then the committed step in GA-specific biosynthesis (Fig. 1). Hence, the upstream enzymes, ent-CPP synthase (CPS), KS, and kaurene oxidase (KO)/CYP701, can be diverted to alternative labdane-related diterpenoid biosynthesis. Many examples of CPS and KS-like (KSL) diterpene synthases that operate in more specialized metabolism are known (Cho et al., 2004; Nemoto et al., 2004; Otomo et al., 2004a, 2004b; Prisic et al., 2004; Wilderman et al., 2004; Xu et al., 2004, 2007; Harris et al., 2005; Kanno et al., 2006; Morrone et al., 2006; Gao et al., 2009; Toyomasu et al., 2009; Falara et al., 2010). By contrast, no KO/CYP701 family member has been shown to act as anything other than a KO—i.e. catalyze conversion of C19 to a carboxylic acid in ent-kaurene.

Rice (Oryza sativa) produces more than 20 labdane-related diterpenoids that act as antimicrobial phytoalexins (Peters, 2006; Toyomasu, 2008). Sequencing of the rice genome demonstrated the presence of multiple CPS, KS(L), and KO family members (IRGSP, 2005), although only one of each is involved in GA biosynthesis (Sakamoto et al., 2004). Biochemical characterization of the rice CPS and KS(L) families has revealed the expected functional divergence—i.e. as necessary for the known production of alternative labdane-related diterpenoids (Peters, 2006; Toyomasu, 2008). However, these diterpene synthases produce olefins that require further elaboration, particularly the insertion of oxygen by CYP (Kato et al., 1995), to form bioactive phytoalexins (Peters, 2006).

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Intriguingly, the rice genome contains multiple paralogs of KO/CYP701 as a five-gene tandem array on chromosome 6 (Fig. 2A), despite the fact that only one (CYP701A6, termed OsKO2, as enumerated by chromosomal order) is apparently involved in GA biosynthesis (Sakamoto et al., 2004). Notably, almost all of the rice labdane-related diterpenoid phytoalexins contain oxygen at C3, and in many cases this can be traced back to insertion/hydroxylation at the C3α (pro-R) position (Peters, 2006), which is very close to the C4α-methyl (i.e. C19) that KO acts upon (Fig. 2B). In addition, the two more phylogenetically distant rice KO paralogs (thus termed KO like [KOL], hence OsKOL4/CYP701A8 and OsKOL5/CYP701A9) exhibit inducible transcription in response to elicitation with the fungal cell wall component chitin oligosaccharide, and OsKOL4 is not able to complement the GA biosynthetic deficiency of an OsKO2 mutant, although the more closely related OsKO1/CYP701A7 can (Itoh et al., 2004). Together, this suggests that the OsKOL might be involved in more specialized metabolism (Peters, 2006).

Here, we demonstrate that under conditions where OsKO2 exhibits KO activity, OsKOL4 does not, instead catalyzing C3α hydroxylation of ent-sandaracopimaradiene and ent-cassadiene, as well as ent-kaurene. We further report that in planta OsKOL4 transcripts accumulate in response to methyl jasmonate, followed by accumulation of 3α-hydroxy-ent-sandaracopimaradiene and 3α-hydroxy-ent-cassadiene, which are expected intermediates in the similarly inducible production of oryzalexins A to F and phytocassanes A to E, consistent with a role for this CYP in early oxidative steps of the biosynthetic pathways for these phytoalexins.

**RESULTS**

**Recombinant Expression**

Based on previously reported evidence suggesting that OsKOL4 and OsKOL5 might be involved in rice labdane-related diterpenoid phytoalexin biosynthesis (Itoh et al., 2004), we were interested in characterizing their biochemical activity. This was originally attempted using the native genes, obtained from the KOME rice cDNA database (Kikuchi et al., 2003). Due to our previous successful expression of plant CYP in *Escherichia coli* (Swaminathan et al., 2009; Morrone et al., 2010a; Wang et al., 2011; Wu et al., 2011), this was carried out using our bacterial modular metabolic engineering system (Cyr et al., 2007). In particular, by coexpression with the requisite CYP reductase (CPR) and functional pairings of upstream CPS and KS(L) to produce all of the labdane-related diterpenes found in rice (see Supplemental Fig. S1). Unfortunately, this did not lead to any further transformation, even when these native genes were modified at their N termini to optimize functional bacterial expression. Codon optimization has been reported to increase expression efficiency of plant CYP (Chang et al., 2007), and we have found that complete gene recoding to optimize codon usage for expression in *E. coli* can lead to activity when none was observed with the native gene sequence (Wang et al., 2011; Wu et al., 2011). Thus, we had such gene constructs synthesized for OsKOL4 and OsKOL5. For comparative purposes, we also had such a gene construct synthesized for OsKO2 as well. Each of these was further N-terminally modified for bacterial expression, and both full-length and modified constructs were again incorporated into our

![Figure 1](https://www.plantphysiol.org)  
**Figure 1.** GA biosynthesis. Shown are the three pre-GA steps catalyzed by the two relevant diterpene synthases, CPS and KS, and CYP KO/CYP701, as well as formation of the characteristic 6-5-6-5 tetracyclic ring structure by the subsequently acting KAO.

![Figure 2](https://www.plantphysiol.org)  
**Figure 2.** Rice KO and KOL, with potential targeting of neighboring hydrocarbon bonds—i.e. C3α instead of C19 by KOL. A, Tandem array of KO paralogs in the rice genome. Phylogenetically related and coregulated genes, as discussed in the text, share common gene symbols (noninducible KO in white, inducible KOL in black). B, Three-dimensional rendering of ent-kaurene showing position of the hydrocarbon bond targeted by KO (C19) and its proximity to the C3α (pro-R) proton typically targeted for hydroxylation in rice labdane-related diterpenoid phytoalexin biosynthesis.


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metabolic engineering system as described above. The N-terminally modified synthetic OsKO2 construct exhibited the KO activity expected from the previously reported genetic studies (Itoh et al., 2004; Sakamoto et al., 2004), as well as biochemical characterization of the native gene recombinantly expressed in Pichia pastoris (Ko et al., 2008), selectively reacting with ent-kaurene to produce ent-kauren-19-oic acid via sequential oxidation to ent-kauren-19-ol and ent-kauren-19-al intermediates (Supplemental Fig. S2). By contrast, while no activity was observed for either OsKOL5 construct, the N-terminally modified synthetic OsKOL4 construct reacted with three diterpenes (ent-kaurene, ent-sandaracopimaradiene, and ent-cassadiene), with reasonable conversion of these diterpene olefins to apparently hydroxylated diterpenoids (molecular mass = 288 D) in each case (Fig. 3). Furthermore, the ent-kaurene product was not ent-kauren-19-ol, demonstrating a change in regiochemistry relative to KO.

Product Identification

To produce enough of the OsKOL4 products for structural characterization by NMR, we increased the yield of our metabolic engineering system by incorporation of the bottom half of the yeast (Saccharomyces cerevisiae) mevalonate-dependent pathway, enabling production of isoprenoid precursors from fed mevalonate, which significantly increases accumulation of the diterpenoid end product (Morrone et al., 2010b). It was then possible to produce and purify several milligrams of each product by extraction from reasonable quantities of these recombinant cultures (3-L each). From the subsequent NMR analysis (Supplemental Fig. S3; Supplemental Tables S1–S3), it was found that each product contained a C3α-hydroxy group (i.e. (R)-3-OH) group (Fig. 4).

Enzymatic Characterization

The hydroxylase activity of OsKOL4 was further characterized by in vitro enzymatic analysis. This was accomplished via coexpression with a rice CPR (OsCPR1), with determination of the level of functional CYP present by measurement of the carbon monoxide (CO) difference binding spectra from the resulting clarified lysates (Supplemental Fig. S4). However, it should be noted that such spectra are rather inconsistent, with some preparations exhibiting activity in the absence of the characteristic peak at 450 nm. Thus, the resulting catalytic rates must be viewed with some caution. Nevertheless, steady-state kinetic analysis of enzymatic activity was carried out with preparations for which CO difference binding was apparent, which indicated that OsKOL4 exhibits similar catalytic efficiency with ent-sandaracopimaradiene and ent-cassadiene, but an approximately 3-fold reduction in affinity for ent-kaurene (Table I).

Physiological Relevance

C3α-hydroxy-ent-sandaracopimaradiene and C3α-hydroxy-ent-cassadiene already have been suggested as potential intermediates in the production of rice oryzalexin and phytocassane phytoalexins (Peters, 2012).
Transcription of the genes encoding the relevant diterpene synthases, as well as production of the diterpene precursors themselves, is inducible by methyl jasmonate (Prisic et al., 2004; Morrone et al., 2011). Thus, we investigated the effect of such induction on transcription of OsKOL4 and accumulation of its enzymatic products. Similar to the upstream diterpene synthases, OsKOL4 mRNA levels were dramatically increased in rice leaves by induction with methyl jasmonate, accumulating to more than 10-fold-higher levels within 12 h (Fig. 5; Supplemental Fig. S5). By contrast, OsKO2 mRNA levels were relatively unchanged. In addition, it was possible to detect increased accumulation of both C3α-hydroxy-ent-sandaracopimaradiene and C3α-hydroxy-ent-cassadiene following induction, although C3α-hydroxy-ent-kaurene was not detected at any point (Fig. 5; Supplemental Fig. S6). These results are consistent with both the availability of the precursor diterpenes (i.e. ent-kaurene is produced at much lower levels under these conditions; Morrone et al., 2011), and the expression pattern of OsKOL4 (Fig. 5), indicating a causative relationship.

**DISCUSSION**

The mutually exclusive activity reported here for OsKOL4 relative to OsKO2 demonstrates biochemical divergence between these rice KO paralogs. Specifically, while the OsKO2 recombinant construct used here exhibited the expected KO activity (Itoh et al., 2004; Sakamoto et al., 2004; Ko et al., 2008), the analogous OsKOL4 construct was found to only catalyze C3α hydroxylation, even with their common substrate ent-kaurene (Fig. 4). Accordingly, although much more distantly related CYP701 family members retain KO activity—e.g. PpKO/CYP701B1, which falls into a separate subfamily and shares less than 42% amino acid sequence identity with any member of the CYP701A subfamily (Miyazaki et al., 2011)—OsKOL4, which shares 71% amino acid sequence identity with OsKO2, has evolved novel enzymatic function.

While we were unable to identify any activity for OsKOL5, it should be noted that, although its transcription is similarly inducible, OsKOL5 mRNA accumulates at a much lower level than does that of OsKOL4 (Itoh et al., 2004). Thus, it is possible that OsKOL5 may be an inactive pseudogene. However, OsKOL5 is rather divergent, sharing only 79% amino acid sequence identity with OsKOL4, its closest relative. Accordingly, OsKOL5 may function at some later step in rice diterpenoid, or in some other type of natural products biosynthesis.

In any case, our results further indicate that OsKOL4 acts in rice diterpenoid phytoalexin biosynthesis. In particular, the C3α hydroxylation of ent-sandaracopimaradiene and ent-cassadiene catalyzed by OsKOL4 is correlated with the presence of C3(α)-oxy moieties in the respectively derived oryzalexins and phytoassanes (Fig. 6), and induction with the plant defense signaling molecule methyl jasmonate elicits both increased levels OsKOL4 mRNA and subsequent accumulation of its enzymatic products (Fig. 5). Moreover, UV irradiation similarly increases OsKOL4 mRNA levels (Itoh et al., 2004), which further has been shown to lead to accumulation of at least C3α-hydroxy-ent-sandaracopimaradiene (Kato et al., 1995). Perhaps more critically, consistent with suggestions that the oryzalexins and phytoalexins serve as phytoalexins against the blast pathogen *Magnaporthe oryzae* (Peters, 2006).

**Figure 4.** OsKOL4 catalyzed reactions. A, Hydroxylation of ent-kaurene to 3α-hydroxy-ent-kaurene. B, Hydroxylation of ent-sandaracopimaradiene to 3α-hydroxy-ent-sandaracopimaradiene. C, Hydroxylation of ent-cassadiene to 3α-hydroxy-ent-cassadiene.

**Figure 5.** Accumulation of OsKOL4 (+) and OsKO2 (x) mRNA, along with that of 3α-hydroxy-ent-sandaracopimaradiene (white circles) and 3α-hydroxy-ent-cassadiene (white diamonds) in response to methyl jasmonate induction (as indicated). Data points shown are the average values from duplicate samples, each measured twice, with error bars representing the corresponding SD. 3α-Hydroxy-ent-cassadiene was only detected at the 48-h time point, thus fold-induction was calculated assuming a detection limit of 50 pg/g tissue fresh weight.
increased mRNA levels of not only *OsKOL4*, but also the relevant upstream diterpene synthases *OsCPS2*, *OsKSL7*, and *OsKSL10* are observed upon infection with this fungus (Marcel et al., 2010). While the role of *OsKOL4* in oryzalexin biosynthesis seems straightforward, its exact role in phytocassane production is not as clear (Fig. 6). These phytoalexins all contain C3(α)-oxy and C11-keto moieties, and we have previously demonstrated that CYP76M7 catalyzes C11α-hydroxylation of ent-cassadiene, with C11α-hydroxy-ent-cassadiene also being detected in induced rice leaf extracts (Swaminathan et al., 2009). Hence, both C3α- and C11α-hydroxylated ent-cassadienes are present in rice, which would seem to suggest the possibility of a bifurcated biosynthetic network (Fig. 6B). However, at least in vitro, *OsKOL4* does not react with C11α-hydroxy-ent-cassadiene, and nor does CYP76M7 react with C3α-hydroxy-ent-cassadiene, leaving the exact roles of these CYP in phytocassane biosynthesis unclear at this time.

The ability of *OsKOL4* to react with ent-kaurene offers potential competition to the use of this intermediate in GA biosynthesis by *OsKO2*. However, C3α-hydroxy-ent-kaurene is not observed in planta, and *OsKOL4* exhibits a lower affinity for ent-kaurene than its other substrates (Table I). Moreover, while ent-kaurene is constitutively produced in rice plants, it is a minor component of the diterpenes produced following elicitation (Wickham and West, 1992; Mohan et al., 1996; Morrone et al., 2011). Given that *OsKO2* is constitutively expressed throughout rice plants, while *OsKOL4* exhibits a very limited expression pattern, with significant expression levels only observed upon elicitation (Itoh et al., 2004), the ability of *OsKOL4* to react with ent-kaurene does not seem to be physiologically relevant.

Regardless of exact role, the biochemical divergence of *OsKOL4* provides a clear example of a KO/CYP701 family member associated with more specialized, rather than GA metabolism. While stevioside biosynthesis seems likely to proceed via ent-kaurenoic acid presumably produced by one of the two distinct KO family members found in *Stevia rebaudiana*, it remains unclear which, or even if one or the other is dedicated to stevioside versus GA biosynthesis, and these both catalyze the prototypical KO reaction in any case (Humphrey et al., 2006). By contrast, the novel enzymatic activity exhibited by *OsKOL4* precludes any function in GA biosynthesis and, moreover, it is more clearly associated with more specialized (i.e. phytoalexin) metabolism (Fig. 5; Itoh et al., 2004).

The organization of the rice KO/CYP701 family members as a five-gene tandem array with distinct division between phylogenetically related and coregulated KO and KOL has suggested a plausible evolutionary history (Itoh et al., 2004). In particular, this array presumably originated with tandem gene duplication of the ancestral KO required for GA metabolism. This enabled neofunctionalization, including at least divergence in transcriptional regulation of one of these KO genes (i.e. to form an inducible KOL), with subsequent gene duplication/expansion of this ancestral KO and derived KOL pair to yield the currently observed five-gene tandem array. The data presented here indicates divergence of the enzymatic activity of at least one of the KOL (i.e. the targeting of C3α instead of C19 by *OsKOL4*). Notably, although the roles of the

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**Table I.** *OsKOL4* steady-state kinetic constants

<table>
<thead>
<tr>
<th>Substrate</th>
<th>$k_{cat}$</th>
<th>$k_{m}$</th>
<th>$k_{cat}/k_{m}$</th>
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<tr>
<td>ent-cassadiene</td>
<td>0.017 ± 0.001</td>
<td>2.0 ± 0.4</td>
<td>9 × 10^4</td>
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<tr>
<td>ent-sandaracopimaradiene</td>
<td>0.013 ± 0.001</td>
<td>2.3 ± 0.8</td>
<td>6 × 10^3</td>
</tr>
<tr>
<td>ent-kaurene</td>
<td>0.022 ± 0.001</td>
<td>7 ± 2</td>
<td>3 × 10^3</td>
</tr>
</tbody>
</table>
CONCLUSION

In summary, our results demonstrate that rice contains at least one functionally divergent KO/CYP701A family member. The distinct enzymatic activity of OsKOL4 identified here precludes its action in GA metabolism, and it instead appears to play a role in rice diterpenoid phytoalexin biosynthesis. This then further expands the range of enzymes recruited from GA/primary metabolism to play functionally distinct roles in more specialized labdane-related diterpenoid metabolism beyond the diterpene synthases, and supports the emerging paradigm that the requirement for phytohormone production provides a biosynthetic reservoir that often is tapped in the evolution of secondary metabolism.

MATERIALS AND METHODS

General Procedure

Unless otherwise noted, chemicals were purchased from Fisher Scientific, and molecular biology reagents from Invitrogen. Gene mapping was based on the annotated rice (Oryza sativa) genome sequence at GenBank, along with the previously assigned OsKO(L) nomenclature (Itoh et al., 2004; Sakamoto et al., 2004). CYP nomenclature was determined via BLAST searches at the CYP homepage maintained by Dr. David Nelson (http://drnelson.uthsc.edu/CytochromeP450.html). Gas chromatography (GC) was performed with a Varian 3900 GC with Saturn 2100 ion trap mass spectrometer (MS) in electron ionization (70 eV) mode. Samples (1 μL) were injected in splitless mode at 50°C and, after holding for 3 min at 50°C, the oven temperature was raised at a rate of 14°C/min to 300°C, where it was held for an additional 3 min. MS data from 90 to 600 mass-to-charge ratio (m/z) were collected starting 12 min after injection until the end of the run.

Recombinant Constructs

The OsKOL4 and OsKOL5 native cDNA were obtained from the KOME rice cDNA databank (GenBank accessions AY579214 and AY660664). Synthetic constructs for OsKOL2, OsKOL4, and OsKOL5, codon optimized for expression in Escherichia coli, were obtained from Genscript (see Supplemental Information S1 for the corresponding nucleotide sequences). All of these were subcloned into the Gateway vector pENTR/SD/D-TOPO by directional topoisomerization. N-terminal modification of these genes for improved functional bacterial expression was performed in a two-stage PCR process, first removing the N-terminal transmembrane helix (OsKOL2, 39 amino acid; OsKOL4, 42 amino acid; and OsKOL5, 36 amino acid) from the 5’ end of the open reading frame and then adding 10 new codons (encoding the amino acid sequence MKKTSKSGK), based on the modifications used for bacterial expression of the mammalian CYP2B subfamily (Scott et al., 2001). All constructs were verified by complete gene sequencing and then transferred via directional recombination into a modified pCDF-Duet vector (Novagen), which contains a DEST cassette in the first multiple cloning site and a rice CPR (OsCPR2) in the second multiple cloning site, as previously described (Swaminathan et al., 2009).

Recombinant Expression

All CYP were expressed in the C41 overexpress strain of E. coli (Lucigen) using our previously described modular diterpene metabolic engineering system (Cyr et al., 2007). Briefly, these CYP were coexpressed with not only
OsCPR1 (i.e. using the constructs described above), but also with a geranyl-geranyl diphosphate synthase and CPS carried on cocompetible pGCS vectors, as well as OsKSL expressed from the additionally cocompetible pET-based pDEST14 or pDEST15 (i.e. for expression as a fusion to glutathione-S-transferase). The resulting diterpenoids were extracted from liquid cultures (media and cells), typically 50-mL volumes grown for 72 h at 16°C after induction, with an equal volume of hexane, and analyzed by GC-MS, including samples that were methylated to examine potential acid formation. In every case the expected diterpene elute product (i.e. given the coexpressed diterpene synthases) was observed, with hydroxylated diterpenoids detected as described above (Fig. 3), such that the overall yields were consistent.

Diterpenoid Production

The novel enzymatic products were obtained in sufficient amounts for NMR analysis by both increasing flux into isoprenoid metabolism and scaling up the culture volumes. Flux toward isoprenoid biosynthesis was increased by incorporation of the bottom half of the mevalonate-dependent isoprenoid precursor pathway from yeast (Saccharomyces cerevisiae), using the previously described pMBI (Martin et al., 2003). This enables production of the isoprenoid precursors isopentenyl diphosphate and dimethylallyl diphosphate from mevalonate, such that feeding of 20 mM mevalonolactone significantly increased diterpenoid production, as previously described (Morrone et al., 2010b). The resulting diterpenoids were extracted from 3 L of culture (media and cells) with an equal volume of a 1:1 mixture of ethyl acetate and hexanes, and the organic extract then dried by rotary evaporation. The resulting residue was dissolved in 5 mL 45% methanol/45% acetonitrile/10% distilled water, and the hydroxylated diterpenoids purified by HPLC. This was carried out using an Agilent 1100 series instrument equipped with autosampler, fraction collector, and diode array UV detection, over a ZORBAX Eclipse XDB-C8 column (4.6 × 150 mm, 5 μm) at a 0.5 mL/min flow rate. The column was prequillivibrated with 20% acetonitrile/distilled water, sample loaded, then the column washed with 20% acetonitrile/distilled water (0–2 min), and eluted with 20% to 100% acetonitrile (2–7 min), followed by a 100% acetonitrile wash (7–27 min). Following purification, each compound was dried under a gentle stream of N2, and then dissolved in 0.5 mL deuterated methanol (CD3OD; 99.8% D, 95/5 D/H) at a 0.5 mL/min flow rate. The column was reequilibrated with 20% acetonitrile/distilled water, sample loaded, then the column washed with 20% acetonitrile/distilled water (0–2 min), and eluted with 20% to 100% acetonitrile (2–7 min), followed by a 100% acetonitrile wash (7–27 min). Following purification, each compound was dried under a gentle stream of N2, and then dissolved in 0.5 mL deuterated methanol (CD3OD; Sigma-Aldrich), with this evaporation-resuspension process repeated two more times to completely remove the protonated acetonitrile solvent, resulting in a final estimated approximately 5 to 10 mg of each novel diterpene.

Chemical Structure Identification

NMR spectra for the diterpenoids were recorded at 25°C on a Bruker Avance 500 spectrometer equipped with a cryogenic probe for 1H and 13C. Structural analysis was performed using 1D 1H, 1D DQF-COSY, HSQC, HMQC, HMBC, and NOESY experiment spectra acquired at 500 MHz and 13C (125.7 MHz) and DEPT135 spectra using standard experiments from the Bruker TopSpin v1.3 software. All samples were placed in NMR tubes purged with nitrogen gas for analyses, and chemical shifts were referenced using known methanol [13C 49.15 (7), 1H 3.31(5) ppm (m)] signals offset from tetramethylsilane (Supplemental Information S1). Correlations from the HMBC spectra were used to propose a partial structure, while COSY correlations between protonated carbons and HSQC spectra were used to complete the partial structure and assign proton chemical shifts. The configuration of the A and B rings (Cl–C10) is predetermined by the configuration of the CPP intermediate, since chemical bonds in that portion of the molecule are not altered. Thus, nuclear Overhauser effect dipole-dipole signals observed between the C5 proton and the C3 alcohol methyl proton (Supplemental Fig. S4) could be used to assign the α (R) configuration of the C3 hydroxyl group (Supplemental Table S1–S3).

Kinetic Analysis

Kinetic analysis was carried out using the synthetic and N-terminally modified OsKOL4 construct expressed in E. coli using the OsCPR1 coexpression construct described above. Expression cultures in TB medium were supplemented with 1 mM thiamine, 5 mg/L riboflavin, and 75 mg/L 5-aminolevulinic acid, along with induction with 1 mM isopropylthio-β-galactosidase at anOD600 of 0.8 to 1.0. After 72 h at 16°C, the cells were harvested and clarified lyoates prepared for in vitro kinetic assays with quantification of CYP by reduced CO-binding difference spectra using an extinction coefficient of 91 μM−1 cm−1 (Omura and Sato, 1964). Kinetic assays were performed using 220 pM active OsKOL4 in each 1-mL reaction. The three diterpenes were used as substrates with varying concentrations (0.8–196 μM ent-sandaracopimaradiene, 1–200 μM ent-cassadiene, and 1–20 μM ent-kaurenene), but otherwise these assays were carried out as previously described (Swaminathan et al., 2009). After 30 min, 50 μL 1 M HCl was added to stop the reaction, enzymatic products extracted by ethyl acetate, confirmed by GC-MS, and quantified by GC with flame ionization detection, using an external standard curve of ent-kauren-19:0.

Plant Analyses

The rice plants (sepal, Nipponbare) and subsequent mRNA and metabolite analyses were largely carried out as previously described (Wang et al., 2011). Briefly, the plants were cultivated in growth chambers under 12-h light (28°C) and 12-h dark (24°C) cycles to the sixth leaf stage. Induced plants were treated with 1-mL 0.2% (v/v) methyl jasmonate per plant, while control/uninduced plants were only treated with the 0.1% Tween 20 carrier solution, and all plants then incubated (separately) and duplicate samples harvested at 0, 2, 4, 6, 12, 24, 48, and 72 h after induction. OsKOL4 mRNA levels were analyzed by reverse transcription-PCR using the gene-specific primers (forward: TCGTAAAAGTATGTCGCAATC; reverse: ATACATGTCATTCCGTGCGT), with PrimeSTAR HS DNA polymerase (Takara Bio) and the following program: 2 min at 94°C followed by 35 cycles of 30 s at 94°C, 30 s at 55°C, and 90 s at 72°C —with normalization of the resulting yield against that from similar amplification of the rice actin gene. Metabolite analysis was carried out with approximately 2-μg leaf samples, which were frozen and ground to powder in liquid nitrogen, then extracted with 50-mL ethyl acetate. These rice extracts were fractioned by HPLC and analyzed by GC-MS in single ion monitoring mode. To detect the hydroxylated diterpenoids of interest here, the MS was operated in chemical ionization mode with methanol as the reaction solvent, selecting the base peak (m/z = 271, MFH−) for fragmentation (0.6 eV), with quantification of the fragment at m/z = 215. Each of the biological duplicate samples was independently analyzed twice, for both mRNA and metabolites (Fig. 5).

Supplemental Data

The following materials are available in the online version of this article.

Supplemental Figure S1. Functional map of rice diterpene synthases.

Supplemental Figure S2. KO activity of OsKOL2.

Supplemental Figure S3. NMR correlations.

Supplemental Figure S4. OsKOL4 CO difference binding spectra.

Supplemental Figure S5. Reverse transcription-PCR expression data.

Supplemental Figure S6. Rice metabolite analysis (liquid chromatography with mass selective mass spectrometry detection).

Supplemental Table S1. 3α-Hydroxy-ent-kauren-19:0 chemical shifts.

Supplemental Table S2. 3α-Hydroxy-ent-sandaracopimaradiene chemical shifts.

Supplemental Table S3. 3α-Hydroxy-ent-cassadiene chemical shifts.

Supplemental Information S1. Synthetic gene sequences.

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