

Isolation and characterization of linalool UDP-Glc glycosyltransferases from Coffea arabica

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<RATIONALE> The aroma is principal to decide the value of coffee beans. Linalool, which is one of the volatile terpene compounds, is constitutive in the coffee aroma. Since terpenoids are generally accumulated as glycosides in plants, the glycosylation is catalyzed by the UDP-glucose glycosyltransferases (UGTs). To reveal the mechanism of accumulation of those volatile compounds in coffee, the functional analysis of the UGT genes that work terpenoids such as linalool was performed. We expect to develop coffees with a rich aroma using this information. In this study, we identified those UGT genes from Coffea arabica and analyzed them with recombinant enzymes. Here, we report the isolation and characterization of UGT genes that have activity towards linalool.



▶ Fig1. Glycosylation of linalool

In coffee, linalool accumulates as a nonvolatile glycoside catalyzed by UGT and GGT. UGT85K11, which catalyzes the alvcosylation of geraniol and linalool, was isolated from Camellia sinensis in a previous study (Shoji et ai., (2015)). In this study, we chose six genes based on the sequence of UGT85K11 to identify and functional analysis.

▶ Fig2. Methods of this study

(A) We performed in silico screening of the genes from C. arabica based on the nucleotide sequence of UGT85K11. Then, six genes were candidates to identify and analyze(termed Ca4, Ca5, Ca10, Ca14, Ca15 and Ca20). To prepare the cDNAs, total RNAs were extracted from young leaves and flower buds. Those six genes were amplified by RT-PCR using specific primers and those cDNAs as a template. After sequence analysis, those recombinant enzymes were produced using a pETsystem. Those enzyme activities were measured by radioisotope mediated TLC assay. (B) UGTs catalyze the transfer of ¹⁴Cglucose to the aglycone. The radioactivity is detected by TLC. (C) These terpenoids were used as substrates with reference to Caupti et al.,(2008).

Chose candidate genes

Gene cloning

Subcloning

Vector : pET23d

Enzymatic reaction

Solvent Composition ethyl acetate : acetone :

= 20:15:6:5:4

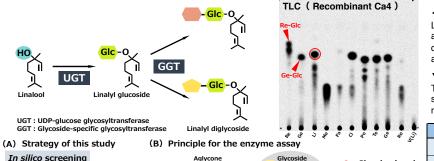
30℃、2h reaction

TLC assav

Detection

Escherichia coli : Rosetta2

(DE3) pLysS



▼Fig3. Activity of recombinant enzymes

Lanes on the left side were positive controls which revealed that has the activities towards retinoic acid and geraniol. Transition of ¹⁴C glucose was detected as a radioactivity. Then, black signals were detected as the activity.

▼Table1. Results of the functional analysis

Three recombinant enzymes showed activity linalool and the other substrates. Ca10 had same activities as Ca4. Furthermore. Ca4 showed most clearly signal towards linalool.

| | name | Li | Me | Fa | Ci | Pe | Te | Ge | Re |
|---|------|----|------------|----|----|-------------|-------------|-------------|----|
| | Ca4 | 0 | _ | _ | 0 | 0 | 0 | 0 | _ |
| | Ca5 | _ | - | _ | _ | \triangle | \triangle | \triangle | - |
| I | Ca10 | 0 | ı | _ | 0 | 0 | 0 | 0 | - |
| | Ca15 | Δ | \bigcirc | _ | 0 | 0 | 0 | 0 | _ |

◆Fig4. A phylogenetic tree of candidate genes from C. arabica

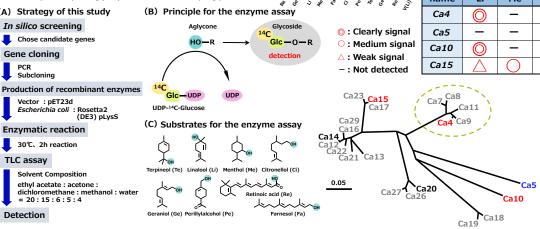
These UGT genes of C. arabica were selected by in silico screening with BLAST. In this study. Ca4, Ca5, Ca10 and Ca15 showed activity towards terpenoids. After this, we will analyze the genes which are classified as the same clade of Ca4.

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Red: Accept linalool

Blue: Accept to except linalool Gray: Not yet be analyzed

Black: No activity



<CONCLUSION> We identified six genes, Ca4, Ca5, Ca10, Ca14, Ca15 and Ca20, encode polypeptide of 483, 479, 489, 483, 494 and 503 amino acid residues respectively. The amino acid sequence identities among these enzymes with UGT85K11 were 60.8, 60.1, 59.3, 59.0, 58.5 and 58.1%, respectively. Although Ca4, Ca10 and Ca15 can catalyze glycosylation of linalool, the activity was not the dominant activity (Table1). Now, we proceed to produce recombinant enzymes of Ca14 and Ca20. These recombinant enzymes will be used for enzyme assay too. The structurefunction relationship of these isolated UGT genes would be clarified. Hereafter, to develop high-quality coffee with a rich aroma, we will utilize that information.