Bioinformatics analysis of the predicted polyprenol reductase genes in higher plants

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Abstract. The present study evaluates the bioinformatics methods to analyze twenty-four predicted polyprenol reductase genes from higher plants on GenBank as well as predicted the structure, composition, similarity, subcellular localization, and phylogenetic. The physicochemical properties of plant polyprenol showed diversity among the observed genes. The percentage of the secondary structure of plant polyprenol genes followed the ratio order of α-helix > random coil > extended chain structure. The values of chloroplast but not signal peptide were too low, indicated that few chloroplast transit peptide in plant polyprenol reductase genes. The possibility of the potential transit peptide showed variation among the plant polyprenol reductase, suggested the importance of understanding the variety of peptide components of plant polyprenol genes. To clarify this finding, a phylogenetic tree was drawn. The phylogenetic tree shows several branches in the tree, suggested that plant polyprenol reductase genes grouped into divergent clusters in the tree.

1. Introduction
Higher plants are known to produce long-chain polyisoprenoids, which is classified into polyprenol and dolichol concerning the α-isoprene unit [1]. The occurrence of polyisoprenoids has been reported in various plant tissues: leaves [2-3], roots [2-5], flowers [5], fruits [6], shoots [7], seeds [5-7], and needles [8]. These studies revealed the omnipresent distribution of polyisoprenoids in the plant kingdom. Polyprenols are predominant polyisoprenoids in plant photosynthetic tissues, and few dolichols occurred [1]. On the other hand, dolichols were found abundantly in plant roots, yeast, and animal (livers) tissues [2-5,9-10].

However, recently dolichols have been shown as the primary polyisoprenoid alcohols in mangrove and coastal plants [2-4]. The presence of abundant dolichols even in the mangroves leaves implies that the enzyme of polyprenol reductase might be energetic in the mangrove. This enzyme corresponding to the SRD5A3 protein in animals has been shown to catalyze the final step of polyprenol converted to dolichols in the biosynthesis of dolichol [11].

In this circumstance, it is crucial to further understand the polyprenol reductase genes in higher plants. Two polyprenol reductase genes from Arabidopsis thaliana have been reported [11]. Nonetheless, bioinformatics information on the plant polyprenol reductase is scarce. The present study aimed to analyze the predicted polyprenol reductase from higher plants using the bioinformatics method.
2. Materials and method

2.1. Materials

A total of twenty-one predicted polyprenol reductase genes, were collected, along with predicted polyprenol reductase gene from *Kandelia obovata: KoPPRDI* (1192 bp, encoding for 382 amino acids). The Genebank accession numbers of the DNA and amino acid sequence used in this analysis are as follows: XM_016081788 (*Arachis duranensis* polyprenol reductase 2), XM_021109944 (*A. ipaensis* polyprenol reductase 2), XM_020359734 (*Cajanus cajan* polyprenol reductase 2), XM_019849699 (*Elaeis guineensis* polyprenol reductase 1), XM_018861897 (*Eucalyptus grandis* polyprenol reductase 2), XM_003537780 (*Glycine max* polyprenol reductase 2), XM_017765134 (*Gossypium arboreum* polyprenol reductase 2-like), XM_016848239 (*G. hirsutum* polyprenol reductase 2-like), XM_012601789 (*G. raimondii* polyprenol reductase 2-like), XM_019302562 (*Ipomoea nil* polyprenol reductase 2-like), XM_012210100 (*Jatropha curcas* polyprenol reductase 2), XM_018985852 (*Juglans regia* polyprenol reductase 2-like), XM_017330714 (*Malus x domestica* polyprenol reductase 2-like), XM_017840866 (*Phoenix dactylifera* polyprenol reductase 1), XM_011038928 (*Populus euphratica* polyprenol reductase 2-like), XM_007200320 (*Prunus persica* polyprenol reductase 2), XM_018642260 (*Pyrus x bretschneideri* polyprenol reductase 2-like), XM_015715302 (*Ricinus communis* polyprenol reductase 2), XM_018128982 (*Theobroma cacao* polyprenol reductase 2), XM_014668834 (*Vigna radiata* var. *radiata* polyprenol reductase 2), and XM_016036804 (*Ziziphus jujuba* polyprenol reductase 2).

2.2. Physicochemical properties of the polyprenol reductase

The physical and chemical properties of DNA and amino acid sequences of polyprenol reductase were analyzed using ProtParam online analysis (web.expasy.org/protparam/). The computed parameters consist of the molecular weight, theoretical isoelectric point values, composition of amino acid, atomic composition, extinction coefficient, estimated half-life, instability index, fat coefficient, and overall average hydropopicity as previously described [12].

2.3. Potential transit of peptide and subcellular localization of predicted polyprenol reductase

The targetP 1.1 server online (www.cbs.dtu.dk/services/targetp) was used to determine the prediction of transit peptide. The location assignment is according to the predicted presence of any of the N-terminal pre-sequences chloroplast transit peptide (cTP), mitochondrial targeting peptide (mTP) and secretory pathway signal peptide (SP). The subcellular localization of plant polyprenol reductase was predicted using PSORT Prediction online (psort.hgc.jp/form.html) as previously reported [13].

2.4. Phylogenetic analysis of predicted polyprenol reductase

The amino acid sequences were aligned, and similarity scores were obtained using the FASTA ver. 3.4t26 [14] of the DNA Data Bank of Japan (Mishima, Shizuoka, Japan). Phylogenetic analysis of deduced amino acid alignment from polyprenol reductase genes was conducted with CLUSTAL W ver. 1.83 [15] of the DNA Data Bank of Japan followed by drawing with TREEView ver. 1.6.6 [16] based on a neighbour-joining method. Bootstrap analysis with 1000 replications was used to increase the strength of the nodes in the tree [17]. The GenBank accession numbers of the DNA and amino acid sequence of using this analysis is described in the Materials subsection.

3. Results and Discussions

3.1. Physical and chemical properties and secondary structure of the polyprenol reductase gene

Table 1 shows the initiation codon of plant polyprenol reductase genes was ATG, where the stop codons consisted of TGA and TAG. The open reading frame length was varied among the genes observed. A number of encoded amino acids were 101 to 357. It is noteworthy to note the diversity of relative molecular mass, theoretical isoelectric point value, positively or negatively charged residues,
extinction coefficient, Fat coefficient, and overall average hydrophilicity among the evaluated genes. *M. x domestica* was distinguishable from other plant polyprenol reductase genes in the total number of atoms, as there is at least one ambiguous position (B, Z or X) in the sequence considered, the atomic composition, therefore, cannot be computed.

The estimated half-life period was accurately same among the genes and was much longer that triterpenoid and cycloartenol synthase genes, the members of oxidoqualene cyclase (OSC) genes [13] and mangrove actin genes [19]. Based on stability coefficients, only three plant polyprenol reductase genes namely *G. max*, *G. arboretum*, and *G. raimondii* were stable proteins, the mostly remaining genes were non-stable proteins. These results suggested the importance of understanding the diversity and function of physicochemical properties of the different amino acids in plant polyprenol reductase genes [19].

### Table 1. Physical and chemical properties of the plant polyprenol reductase in the database

| Plant species   | A. duranensis | A. ipaensis | C. cajan | E. grandis | E. guineensis |
|-----------------|---------------|-------------|----------|------------|--------------|
| Length of genes/bp | 2031          | 1556        | 1411     | 1320       | 1229         |
| Open reading frame length/bp | 1915         | 1415        | 1165     | 1057       | 909          |
| Start site and codon | 902ATG       | 402ATG      | 122ATG   | 41ATG      | 239ATG       |
| Stop site and codon | 1915TGA      | 1415TGA     | 1165TGA  | 1057TGA    | 909TGA       |
| Number of encoded amino acids | 337         | 337         | 347      | 338        | 223          |
| Relative molecular mass | 38916.89    | 38998.16    | 40210.04 | 39149.63   | 24760.07     |
| Theoretical isoelectric point values | 9.11      | 9.34        | 9.35     | 8.58       | 8.23         |
| Positively charged residues | 24         | 26          | 26       | 26         | 16           |
| Negatively charged residues | 18        | 17          | 18       | 23         | 14           |
| Total number of atoms | 5527       | 5550        | 5692     | 5509       | 3512         |
| Extinction coefficient | 2.456     | 2.310       | 2.448    | 2.480      | 2.334        |
| Half-life period | 30h          | 30h         | 30h      | 30h        | 30h          |
| Instability coefficient | 48.48     | 48.13       | 51.95    | 57.23      | 112.06       |
| Fat coefficient | 109.35       | 110.21      | 105.07   | 99.79      | 112.06       |
| Overall average hydrophilicity | 0.487      | 0.478       | 0.349    | 0.326      | 0.537        |

Table continued

| Plant species   | G. arboreum | G. hirsutum | G. max | G. raimondii | I. nil |
|-----------------|-------------|-------------|--------|--------------|-------|
| Length of genes/bp | 1348       | 1310        | 1682   | 1438         | 2755  |
| Open reading frame length/bp | 1151     | 1036        | 1441   | 1229         | 2143  |
| Start site and codon | 81ATG      | 128ATG      | 413ATG | 180ATG       | 1244ATG |
| Stop site and codon | 1151TGA    | 1036TGA     | 1441TGA| 1229TGA      | 2143TGA |
| Number of encoded amino acids | 357       | 302         | 342    | 349          | 299   |
| Relative molecular mass | 40749.35  | 34808.15    | 39109.94| 39842.36     | 34118.14 |
| Theoretical isoelectric point values | 7.25    | 9.45        | 9.23   | 8.17         | 9.30  |
| Positively charged residues | 24        | 27          | 24     | 24          | 28    |
| Negatively charged residues | 24     | 17          | 17     | 22          | 17    |
| Total number of atoms | 5737     | 4953        | 5550   | 5611        | 4830  |
| Extinction coefficient | 2.520    | 2.819       | 2.227  | 2.578       | 2.063 |
| Half-life period | 30h         | 30h         | 30h    | 30h         | 30h   |
| Instability coefficient | 37.89   | 55.65       | 36.13  | 38.36       | 46.07 |
| Fat coefficient | 100.59       | 107.55      | 106.81 | 98.97       | 102.11 |
| Overall average hydrophilicity | 0.432   | 0.428       | 0.488  | 0.437       | 0.381 |
|                  | J. curcas | J. regia | Ko PPRD1 | M. domestica | P. dactylifera |
|------------------|----------|----------|----------|--------------|---------------|
| Length of genes/bp | 1333     | 1727     | 1193     | 1464         | 928           |
| Open reading frame length/bp | 1175     | 1369     | nd       | 1306         | 633           |
| Start site and codon | 261ATG   | 353ATG   | nd       | 290ATG       | 145ATG        |
| Stop site and codon  | 1175TGA  | 1369TGA  | nd       | 1306TGA      | 633TGA        |
| Number of encoded amino acids | 304      | 338      | 357      | 338          | 162           |
| Relative molecular mass | 35067.13 | 38978.60 | 41140.93 | 38483.31     | 18250.43      |
| Theoretical isoelectric point values | 8.61     | 8.88     | 8.44     | 9.31         | 9.30          |
| Positively charged residues | 22       | 26       | 30       | 27           | 13            |
| Negatively charged residues | 19       | 21       | 25       | 18           | 9             |
| Total number of atoms | 4969     | 5507     | 5739     | -            | 2600          |
| Extinction coefficient | 2.569    | 2.952    | 2.350    | 2.523        | 2.688         |
| Half-life period | 30h      | 30h      | 1.3h     | 30h          | 30h           |
| Instability coefficient | 40.65    | 57.59    | 49.02    | 47.79        | 53.92         |
| Fat coefficient | 111.64   | 105.30   | 1306TGA  | 107.57       | 116.91        |
| Overall average hydrophilicity | 0.481     | 0.400    | 0.185    | 0.441        | 0.530         |

|                  | P. euphratica | P. persica | Pyrus x | R. communis | T. cacao |
|------------------|---------------|------------|---------|-------------|---------|
| Length of genes/bp | 1335          | 1569       | 472     | 1288        | 1317    |
| Open reading frame length/bp | 1117       | 1340       | 321     | 1133        | 1083    |
| Start site and codon | 197ATG       | 339ATG     | 16ATG   | 258ATG      | 58ATG   |
| Stop site and codon  | 1117TGA      | 1340TGA    | 321TGA  | 1133TGA     | 1083TGA |
| Number of encoded amino acids | 306        | 333        | 101     | 291         | 341     |
| Relative molecular mass | 35383.78    | 38143.66   | 11555.41 | 33656.41    | 38280.72 |
| Theoretical isoelectric point values | 9.33        | 9.41       | 5.88    | 9.33        | 8.09    |
| Positively charged residues | 26          | 27         | 7       | 26          | 23      |
| Negatively charged residues | 16          | 17         | 10      | 18          | 21      |
| Total number of atoms | 5009        | 5409       | 1639    | 4768        | 5395    |
| Extinction coefficient | 2.498        | 2.401      | 2.202   | 2.381       | 2.465   |
| Half-life period | 30h          | 30h        | 30h     | 30h         | 30h     |
| Instability coefficient | 49.75        | 42.98      | 47.89   | 47.90       | 41.75   |
| Fat coefficient | 105.13       | 103.00     | 110.99  | 102.51      | 102.90  |
| Overall average hydrophilicity | 0.549      | 0.401      | 0.319   | 0.390       | 0.481   |

|                  | V. radiata | Z. jujuba |
|------------------|-----------|----------|
| Length of genes/bp | 1548      | 1724     |
| Open reading frame length/bp | 1309      | 1510     |
| Start site and codon | 287ATG     | 494ATG   |
| Stop site and codon  | 1309TGA    | 1510TGA  |
| Number of encoded amino acids | 340       | 338      |
| Relative molecular mass | 39015.67   | 39208.84 |
| Theoretical isoelectric point values | 9.03        | 9.31     |
| Positively charged residues | 25          | 28       |
| Negatively charged residues | 20          | 18       |
| Total number of atoms | 5544        | 5539     |
| Extinction coefficient | 2.268       | 2.730    |
| Half-life period | 30h          | 30h       |
| Instability coefficient | 43.61        | 49.24    |
| Fat coefficient | 108.97       | 99.79    |
| Overall average hydrophilicity | 0.465      | 0.330    |
Table 2 depicts the percentage of the secondary structure of plant polyprenol genes followed the proportion order of $\alpha$ helix > random coil > extended chain structure. This similar pattern has been previously reported in the oxidosqualene cyclase genes [13] and mangrove actin genes [18]. The variation was notable among the genes observed, implied that the important function of secondary structure analysis of plant polyprenol reductase in the plant kingdom. Polyprenol may play a key role in early steps of protein N-linked glycosylation, the enzyme was required for the alteration of polyprenol into dolichol [10].

Table 2. Secondary structure analysis of plant polyprenol reductase

| Protein accession number | $\alpha$ helix number | $\alpha$ helix ratio (%) | Extended chain structure number | Extended chain structure ratio (%) | Random coil number | Random coil ratio (%) |
|--------------------------|-----------------------|--------------------------|---------------------------------|----------------------------------|--------------------|-----------------------|
| XP_003537828             | 159                   | 46.49                    | 63                              | 18.42                            | 120                | 35.09                 |
| XP_007200382             | 159                   | 47.75                    | 63                              | 18.92                            | 111                | 33.33                 |
| XP_011037230             | 167                   | 54.58                    | 52                              | 16.99                            | 87                 | 28.43                 |
| XP_012065490             | 181                   | 59.54                    | 31                              | 10.20                            | 92                 | 30.26                 |
| XP_012457243             | 190                   | 54.44                    | 45                              | 12.89                            | 114                | 32.66                 |
| XP_014524320             | 173                   | 50.88                    | 59                              | 17.35                            | 108                | 31.76                 |
| XP_015570788             | 154                   | 52.92                    | 43                              | 14.78                            | 94                 | 32.30                 |
| XP_015892290             | 186                   | 55.03                    | 49                              | 14.50                            | 103                | 30.47                 |
| XP_015937274             | 177                   | 52.52                    | 59                              | 17.51                            | 101                | 29.97                 |
| XP_016703728             | 173                   | 57.28                    | 31                              | 10.26                            | 98                 | 32.45                 |
| XP_017186203             | 175                   | 51.78                    | 50                              | 14.79                            | 113                | 33.43                 |
| XP_017620623             | 190                   | 53.37                    | 49                              | 13.76                            | 117                | 32.87                 |
| XP_017696355             | 99                    | 61.11                    | 12                              | 7.41                             | 51                 | 31.48                 |
| XP_017984471             | 147                   | 43.11                    | 67                              | 19.65                            | 127                | 37.24                 |
| XP_018497776             | 30                    | 29.70                    | 32                              | 31.68                            | 39                 | 38.61                 |
| XP_018717442             | 175                   | 51.78                    | 48                              | 14.20                            | 115                | 34.02                 |
| XP_018841397             | 175                   | 51.78                    | 52                              | 15.38                            | 111                | 32.84                 |
| XP_019158107             | 163                   | 54.52                    | 42                              | 14.05                            | 94                 | 31.44                 |
| XP_019705258             | 122                   | 54.71                    | 21                              | 9.42                             | 80                 | 35.87                 |
| XP_020215323             | 181                   | 52.16                    | 58                              | 16.71                            | 108                | 31.12                 |
| XP_020965603             | 180                   | 53.41                    | 53                              | 15.73                            | 104                | 30.86                 |
| KoPPRD1                  | 157                   | 43.98                    | 51                              | 14.29                            | 149                | 41.74                 |

3.2. Potential transit of peptide and subcellular localization of OSC gene

Table 3 shows the possibility of the possible transit peptide in plant polyprenol reductase genes. There are four reliabilities analyzed: chloroplast transit peptide, mitochondrial target peptide, the signal peptide of the secretory pathway, and the prediction probability. The values of chloroplast but not signal peptide were too low, indicated that few chloroplast transit peptide or relatively high signal peptide of secretion pathway in twenty-four plant polyprenol reductase genes. It is interesting to note that target peptide value of mitochondria diversified from 0.042 to 0.540, indicating that it likely existed. The highest mitochondrial target peptide was KoPPRD 1, a candidate of K. obovata polyprenol reductase gene. This result supported the previous report on the highest mitochondrial target peptide among the OSC genes from mangrove plants, was found in KcCAS, K. candel cycloartenol synthase gene with the product of 100% cycloartenol [13, 20].
Table 3. Possibility of the potential transit peptide in polyprenol reductase genes

| Protein accession number | Chloroplast transit peptide | Mitochondrial target peptide | Signal peptide of secretory pathway | Reliability prediction |
|--------------------------|-----------------------------|-------------------------------|------------------------------------|------------------------|
| XP_003537828             | 0.011                       | 0.056                         | 0.399                              | 4                     |
| XP_007200382             | 0.005                       | 0.376                         | 0.364                              | 5                     |
| XP_011037230             | 0.025                       | 0.094                         | 0.242                              | 5                     |
| XP_012065490             | 0.037                       | 0.308                         | 0.024                              | 5                     |
| XP_012457243             | 0.027                       | 0.075                         | 0.197                              | 5                     |
| XP_014524320             | 0.036                       | 0.042                         | 0.286                              | 5                     |
| XP_015570788             | 0.004                       | 0.181                         | 0.371                              | 5                     |
| XP_015892290             | 0.006                       | 0.264                         | 0.296                              | 5                     |
| XP_015937274             | 0.021                       | 0.059                         | 0.098                              | 4                     |
| XP_016703728             | 0.002                       | 0.217                         | 0.313                              | 5                     |
| XP_017186203             | 0.004                       | 0.225                         | 0.380                              | 5                     |
| XP_017602623             | 0.015                       | 0.025                         | 0.184                              | 3                     |
| XP_017696355             | 0.024                       | 0.276                         | 0.806                              | 3                     |
| XP_017984471             | 0.072                       | 0.069                         | 0.287                              | 5                     |
| XP_018497776             | 0.014                       | 0.100                         | 0.129                              | 1                     |
| XP_018717442             | 0.006                       | 0.477                         | 0.118                              | 4                     |
| XP_018841397             | 0.023                       | 0.422                         | 0.084                              | 4                     |
| XP_019158107             | 0.002                       | 0.105                         | 0.687                              | 3                     |
| XP_019705258             | 0.026                       | 0.393                         | 0.308                              | 5                     |
| XP_020215323             | 0.037                       | 0.435                         | 0.025                              | 4                     |
| XP_020965603             | 0.013                       | 0.084                         | 0.128                              | 4                     |
| KoPPRD1                  | 0.000                       | 0.540                         | 0.922                              | 4                     |

Table 4 shows subcellular localization of plant polyprenol reductase genes in higher plants. The subcellular localization of these genes mostly resided in Golgi bodies, plasma membrane, and endoplasmic reticulum. A few genes were chloroplast thylakoid membrane and microbody. Recently, it has been reported that the expression of two triterpenoid synthases, BgbAS and RsM1 under a GAL1 promoter in GIL77 enhanced the triterpenoid content of plasma membrane portions [13]. In the present data (Table 4), both gene BgbAS and RsM1 were located at the plasma membrane, supported previous results on their subcellular localization situated in the plasma membrane [13].

3.3. Phylogenetic analysis of polyprenol reductase gene

To confirm the similarity among the plant polyprenol reductase gene, a phylogenetic tree was drawn on the source of their amino acid sequences (Figure 1). The phylogenetic tree shows that there are five clusters in the tree. The first branch was Z. juja; the second cluster consisted G. hirsutum. The third branch comprised five members of polyprenol reductase genes. The fourth cluster was the largest members consisting of 13 genes. This cluster was the center of the phylogenetic tree in term of evolution.

A new member of KoPPRD1 K. obovata polyprenol reductase joined in the center branch. This gene joined with other plant polyprenol reductase in higher plants: R. communis, I. nil, P. euphratica, and E. grandis. Our present result, therefore, suggested that KoPPRD1 gene is a new member of plant polyprenol reductase.

The close relationship between KoPPRD1 gene with plant as mentioned earlier polyprenol reductase can be explained by their habitat in the tropical forests [2,3]. The apparent similarity and joining these five genes in the tree may due to the result of tropical or subtropical climatic conditions [2,21]. Mangrove forests are distributed in the tropical and sub-tropical area as well as R. communis, I. nil, P. euphratica, and E. grandis.species [21].
Figure 1. Phylogenetic tree of plant polyprenol reductase. Phylogenetic tree of deduced amino acid sequences was constructed with the neighbour-joining method of the CLUSTAL W [15]. The indicated scale represents 0.1 amino acid substitutions per site. Numbers point out bootstrap value from 1000 replicates. The GenBank accession numbers of the amino acid sequence of using this analysis are mentioned in the Materials subsection.
Table 4. Subcellular localization of plant polyprenol reductase

| Protein accession number | Chloroplast thylakoid membrane | Golgi bodies | Plasma membrane | Endoplasmic reticulum | Microbody | Mitochondrial inner membrane |
|--------------------------|--------------------------------|--------------|-----------------|-----------------------|-----------|-----------------------------|
| XP_003537828             | 0.426                          | 0.400        | 0.600           | 0.300                 | nd        | nd                          |
| XP_007200382             | nd                             | 0.460        | 0.640           | 0.685                 | nd        | nd                          |
| XP_011037230             | nd                             | 0.460        | 0.640           | 0.685                 | nd        | 0.822                       |
| XP_012065490             | nd                             | 0.460        | 0.640           | 0.685                 | nd        | nd                          |
| XP_012457243             | nd                             | 0.400        | 0.600           | nd                    | nd        | 0.340                       |
| XP_014524320             | 0.375                          | 0.400        | 0.600           | nd                    | nd        | nd                          |
| XP_015570788             | nd                             | 0.460        | 0.640           | 0.685                 | nd        | nd                          |
| XP_015892290             | nd                             | nd           | 0.730           | 0.640                 | 0.388     | nd                          |
| XP_015937274             | 0.438                          | 0.400        | 0.600           | 0.300                 | nd        | nd                          |
| XP_016703728             | nd                             | 0.460        | 0.640           | 0.685                 | nd        | nd                          |
| XP_017186203             | nd                             | 0.460        | 0.640           | 0.685                 | nd        | nd                          |
| XP_017620623             | nd                             | 0.400        | 0.600           | 0.300                 | 0.300     | nd                          |
| XP_017696355             | nd                             | 0.460        | 0.640           | 0.685                 | nd        | nd                          |
| XP_017984471             | 0.354                          | 0.400        | 0.600           | 0.300                 | nd        | nd                          |
| XP_018497776             | 0.249                          | nd           | 0.700           | 0.200                 | 0.640     | nd                          |
| XP_018717442             | nd                             | 0.460        | 0.640           | 0.685                 | nd        | nd                          |
| XP_018841397             | nd                             | nd           | 0.460           | 0.100                 | 0.388     | nd                          |
| XP_019158107             | nd                             | 0.460        | 0.640           | 0.685                 | nd        | nd                          |
| XP_019705258             | nd                             | 0.460        | 0.640           | 0.685                 | nd        | nd                          |
| XP_020215323             | 0.426                          | 0.400        | 0.600           | 0.300                 | nd        | nd                          |
| XP_020965603             | 0.438                          | 0.400        | 0.600           | 0.300                 | nd        | nd                          |
| KoPPRD1                  | nd                             | 0.460        | 0.640           | 0.685                 | nd        | nd                          |

nd= not detected

4. Conclusions
The present study confirmed the diversity and function of physicochemical properties of the plant polyprenol reductase genes. Furthermore, our data supported previous results on the subcellular localization of triterpenoid synthase genes located in the plasma membrane.

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