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## Author Correction: Comparison of eight complete chloroplast genomes of the endangered *Aquilaria* tree species (Thymelaeaceae) and their phylogenetic relationships

Muhammad Syahmi Hishamuddin, Shiou Yih Lee, Wei Lun Ng, Shairul Izan Ramlee, Dhilia Udie Lamasudin & Rozi Mohamed

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This Article contains errors in the gene names.

This has resulted in errors in Figure 5, and in Table 6. The correct Figure 5 appears below as Figure 1, and the correct Table 6 appears below as Table 1.

Additionally, in the Results and discussion section under subheading ‘Identification of highly variable regions within the *Aquilaria* cp genomes’,

“They are in the range from 0 to 0.01370 (Fig. 5). There are nine highly divergent regions ( $P_i > 0.005$ ), divided between the intergenic spacer (IGS) region (*trnD-trnY*, *trnT-trnL*, *trnL-trnF*, *trnFndh*), *trnV-trnM*) and the coding sequence (CDS) regions (*matK-rps16*, *rpoC1-rpoC2*, *petA-cemA* and *rpl32*) (Fig. 5). In total, there are 144 variable sites, 72 parsimony informative sites and  $P_i$  values from 0.00630 to 0.01370, in the nine regions (Table 6). Among these, *rpl32* has the most nucleotide variation (0.01370). Meanwhile, we found that the IR region is extremely conserved ( $P_i < 0.005$ ) because highly variable region/divergent sequences were not found.”

should read:

“They are in the range from 0 to 0.01244 (Fig. 5). There are nine highly divergent regions ( $P_i > 0.006$ ), divided between the intergenic spacer (IGS) region (*matK-rps16*, *ndhC-trnV*, *ndhF-rpl32*, *psbJ-petA* and *trnT-trnL*) and the coding sequence (CDS) regions (*accD*, *trnD*, *trnF* and *ycf3*) (Fig. 5). In total, there are 207 variable sites, 75 parsimony informative sites and  $P_i$  values from 0.00706 to 0.01244, in the nine regions (Table 6). Among these, *ndhF-rpl32* has the most nucleotide variation (0.01244). Meanwhile, we found that the IR region is extremely conserved ( $P_i < 0.006$ ) because highly variable region/divergent sequences were not found.”

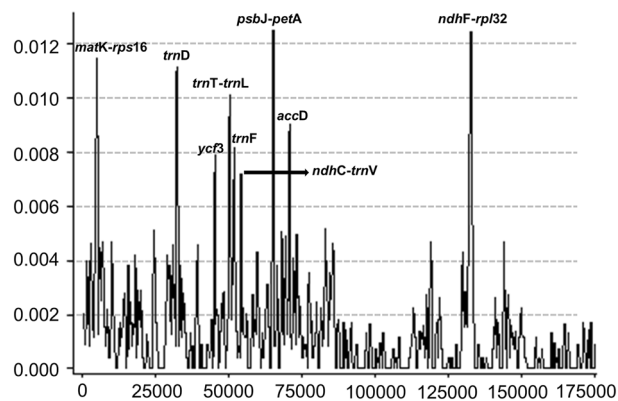
Finally, in the Conclusion section,

“Comparison of the eight *Aquilaria* cp genomes revealed 832 LSR and nine divergent regions (*trnD-trnY*, *trnT-trnL*, *trnL-trnF*, *trnF-ndh*), *trnV-trnM*, *matK-rps16*, *rpoC1-rpoC2*, *petA-cemA* and *rpl32*.”

should read:

“Comparison of the eight *Aquilaria* cp genomes revealed 832 LSR and nine divergent regions (*matK-rps16*, *trnD*, *ycf3*, *trnT-trnL*, *trnF*, *ndhC-trnV*, *psbJ-petA*, *accD*, and *ndhF-rpl32*.”

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**Figure 1.** A correct version of the original Figure 5.

No	High variable marker	Length (bp)	Variable sites	Parsimony informative sites	Nucleotide diversity (Pi)
1	<i>matK-rps16</i>	605	17	10	0.01093
2	<i>trnD</i>	1,017	27	11	0.01077
3	<i>ycf3</i>	1,022	15	2	0.00792
4	<i>trnT-trnL</i>	801	28	9	0.01012
5	<i>trnF</i>	619	14	6	0.00815
6	<i>ndhC-trnV</i>	1,033	16	1	0.00706
7	<i>psbJ-petA</i>	804	34	14	0.01208
8	<i>accD</i>	865	20	10	0.00905
9	<i>ndhF-rpl32</i>	1,328	36	12	0.01244
<b>Total</b>		<b>8,094</b>	<b>207</b>	<b>75</b>	<b>0.08852</b>

**Table 1.** A correct version of the original Table 6.



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