

Table 2 Genetic diversity parameters and neutrality tests for the two studied genes

	<i>TIP</i> (accession N ^o : DQ202710.1)	<i>PIP2</i> (accession N ^o : DQ202708.1)
Primer	F : CTT AAG TTT GCC ACT GGT GGA CTC G R : GGT AGG GAG CTG TTG ATG GCT CTG	F : GCT GGC ATA GCA GAG TTC ATA GCC R : CTA CGT TTG GCA TCA GTA GCA GAG
Annealing temperature (°C)	60	60
Total length sequenced (bp)	519	1064
Coding region (bp)	350	42
Non-coding region (bp)	169	1022
Coding region SNP number	45	8
Non-coding region SNP number	9	57
Average frequency of SNP (bp/SNP)	9.80	16.8
Total Nucleotide diversity ($\pi \times 10^{-3}$)	0.0024	0.0017
Θ_w ($\pi \times 10^{-3}$)	0.0020	0.0013
Non-coding sites ($\pi \times 10^{-3}$)	0.0024	0.0016
Coding sites ($\pi \times 10^{-3}$)	0.0024	0.0019
Syn. Sites ($\pi \times 10^{-3}$)	0.0021	0.0030
Non-syn. Sites ($\pi \times 10^{-3}$)	0.0024	0.0031
% Observed Homozygosity	65.0	55.0
% Expected Heterozygosity	24.3	18.7
Tajima's D_T	0.560	0.33
Fu and Li's F	0.598	0.498
Fu's F_s	1,068	-0,129