

**Table S1.** Cross-species transferability of developed gSSRs markers in different *Dalbergia* species

Dhup141	✓	✓	✓	✓	✓	✓	✓	✓	✓	100.00%
Dhup142	✗	✗	✗	✗	✗	✗	✗	✗	✗	0.00%
Dhup144	✓	✗	✗	✓	✗	✓	✓	✗	✗	44.44%
Dhup153	✗	✗	✗	✓	✗	✗	✗	✗	✓	22.22%
Dhup159	✓	✗	✗	✗	✓	✗	✓	✗	✗	33.33%
Dhup163	✓	✓	✓	✗	✓	✓	✗	✓	✗	66.67%
Dhup164	✓	✓	✓	✓	✓	✓	✓	✓	✓	100.00%
Dhup167	✗	✗	✗	✗	✓	✓	✓	✗	✗	33.33%
Dhup171	✗	✗	✗	✗	✗	✗	✓	✗	✗	11.11%
Dhup181	✓	✗	✓	✗	✓	✓	✓	✓	✗	66.67%
Dhup183	✗	✗	✗	✗	✗	✓	✓	✗	✗	22.22%
Dhup185	✗	✓	✓	✗	✗	✓	✓	✓	✓	66.67%
Dhup191	✗	✗	✗	✗	✗	✗	✓	✗	✗	11.11%
Dhup194	✗	✗	✓	✗	✗	✓	✗	✓	✗	33.33%
Total	20	18	18	16	23	22	26	16	15	-

‘✓’ indicated expected amplicon is present; ‘✗’ indicated expected amplicon is absent.

**Table S2. Parameters of genetic diversity for *D. hupeana* populations at loci level**

Locus	DJY (n=30)							JY (n=30)							XX (n=30)						
	<i>N<sub>a</sub></i>	<i>N<sub>e</sub></i>	<i>I</i>	<i>H<sub>o</sub></i>	<i>H<sub>e</sub></i>	<i>uH<sub>e</sub></i>	PIC	<i>N<sub>a</sub></i>	<i>N<sub>e</sub></i>	<i>I</i>	<i>H<sub>o</sub></i>	<i>H<sub>e</sub></i>	<i>uH<sub>e</sub></i>	PIC	<i>N<sub>a</sub></i>	<i>N<sub>e</sub></i>	<i>I</i>	<i>H<sub>o</sub></i>	<i>H<sub>e</sub></i>	<i>uH<sub>e</sub></i>	PIC
Dhup14	4	2.236	0.952	0.333	0.553	0.562	0.471	4	3.947	1.379	0.333	0.747	0.759	0.699	5	4.615	1.566	0.333	0.783	0.797	0.748
Dhup61	6	3.896	1.490	0.700	0.743	0.756	0.703	5	2.616	1.171	0.633	0.618	0.628	0.567	7	5.556	1.826	0.767	0.820	0.834	0.797
Dhup64	8	5.056	1.838	0.200	0.802	0.816	0.780	7	4.286	1.620	0.400	0.767	0.780	0.733	10	5.143	1.910	0.367	0.806	0.819	0.784
Dhup70	4	1.522	0.684	0.067	0.343	0.349	0.321	5	1.915	0.959	0.167	0.478	0.486	0.446	6	1.895	0.960	0.167	0.472	0.480	0.435
Dhup78	6	4.091	1.525	0.667	0.756	0.768	0.716	8	5.128	1.812	0.967	0.805	0.819	0.779	9	6.250	1.950	0.933	0.840	0.854	0.820
Dhup89	9	4.905	1.801	0.133	0.796	0.810	0.768	6	4.545	1.624	0.533	0.780	0.793	0.747	10	7.895	2.154	0.133	0.873	0.888	0.860
Dhup90	7	4.390	1.647	0.633	0.772	0.785	0.740	5	3.220	1.312	0.533	0.689	0.701	0.634	10	4.206	1.758	0.567	0.762	0.775	0.737
Dhup104	6	2.773	1.253	0.100	0.639	0.650	0.582	9	2.752	1.426	0.167	0.637	0.647	0.608	9	3.061	1.436	0.100	0.673	0.685	0.618
Dhup106	12	6.377	2.101	0.538	0.843	0.860	0.826	13	6.897	2.189	0.333	0.855	0.869	0.840	18	6.122	2.380	0.300	0.837	0.851	0.828
Dhup108	6	4.317	1.603	0.467	0.768	0.781	0.736	12	7.759	2.233	0.200	0.871	0.886	0.858	7	4.986	1.746	0.533	0.799	0.813	0.772
Dhup114	5	2.123	1.023	0.367	0.529	0.538	0.487	4	1.734	0.722	0.300	0.423	0.431	0.358	7	3.279	1.447	0.267	0.695	0.707	0.658
Dhup115	6	2.799	1.294	0.500	0.643	0.654	0.599	5	3.000	1.240	0.467	0.667	0.678	0.607	10	6.691	2.099	0.600	0.851	0.865	0.836
Dhup116	6	3.125	1.323	0.733	0.680	0.692	0.625	6	2.490	1.266	0.667	0.598	0.608	0.567	5	3.025	1.306	0.600	0.669	0.681	0.625
Dhup118	4	1.636	0.766	0.333	0.389	0.395	0.361	4	1.575	0.723	0.333	0.365	0.371	0.339	5	2.086	1.045	0.167	0.521	0.529	0.489
Dhup120	6	3.543	1.434	0.400	0.718	0.730	0.673	8	4.045	1.671	0.367	0.753	0.766	0.721	8	5.325	1.810	0.500	0.812	0.826	0.786
Dhup122	4	1.647	0.791	0.367	0.393	0.399	0.370	3	2.299	0.937	0.467	0.565	0.575	0.489	7	2.736	1.283	0.400	0.634	0.645	0.580
Dhup123	6	3.982	1.496	0.533	0.749	0.762	0.705	4	2.866	1.198	0.267	0.651	0.662	0.597	11	6.081	2.008	0.667	0.836	0.850	0.816
Dhup125	7	4.091	1.555	0.533	0.756	0.768	0.715	6	3.346	1.399	0.200	0.701	0.713	0.657	7	3.905	1.608	0.267	0.744	0.756	0.715
Dhup129	2	1.342	0.423	0.233	0.255	0.259	0.222	3	1.462	0.603	0.267	0.316	0.321	0.293	6	1.603	0.862	0.300	0.376	0.382	0.363
Dhup130	8	5.422	1.846	0.367	0.816	0.829	0.792	5	4.119	1.518	0.100	0.757	0.770	0.722	15	8.911	2.391	0.433	0.888	0.903	0.878
Dhup132	9	6.102	1.972	0.500	0.836	0.850	0.817	7	3.482	1.572	0.433	0.713	0.725	0.686	13	7.087	2.199	0.533	0.859	0.873	0.845
Dhup133	16	6.923	2.300	0.467	0.856	0.870	0.842	17	10.651	2.573	0.767	0.906	0.921	0.899	13	6.122	2.146	0.433	0.837	0.851	0.821
Dhup139	4	2.667	1.166	0.433	0.625	0.636	0.578	5	2.659	1.153	0.500	0.624	0.634	0.562	6	3.607	1.452	0.433	0.723	0.735	0.679

Dhup141	5	2.476	1.102	0.633	0.596	0.606	0.533	4	2.786	1.106	0.467	0.641	0.652	0.569	5	2.013	1.035	0.267	0.503	0.512	0.475	
Dhup142	5	1.472	0.691	0.033	0.321	0.326	0.304	3	1.985	0.779	0.100	0.496	0.505	0.402	6	2.105	1.005	0.100	0.525	0.534	0.465	
Dhup144	7	3.888	1.578	0.267	0.743	0.755	0.709	8	4.286	1.702	0.267	0.767	0.780	0.736	10	7.258	2.119	0.433	0.862	0.877	0.848	
Dhup153	13	7.087	2.215	0.833	0.859	0.873	0.845	12	5.471	2.060	0.800	0.817	0.831	0.800	15	10.465	2.502	0.800	0.904	0.920	0.897	
Dhup159	8	4.176	1.641	0.500	0.761	0.773	0.724	6	1.833	0.937	0.233	0.454	0.462	0.421	9	3.147	1.479	0.167	0.682	0.694	0.637	
Dhup163	6	3.564	1.442	0.400	0.719	0.732	0.674	7	3.600	1.568	0.633	0.722	0.734	0.694	9	5.357	1.896	0.800	0.813	0.827	0.792	
Dhup164	5	2.975	1.243	0.600	0.664	0.675	0.605	4	2.980	1.170	0.267	0.664	0.676	0.597	4	3.030	1.202	0.400	0.670	0.681	0.610	
Dhup167	7	2.956	1.312	0.633	0.662	0.673	0.603	5	2.616	1.189	0.767	0.618	0.628	0.567	4	3.010	1.233	0.400	0.668	0.679	0.617	
Dhup171	5	3.035	1.288	0.100	0.671	0.682	0.618	4	2.667	1.127	0.200	0.625	0.636	0.559	6	4.455	1.600	0.233	0.776	0.789	0.741	
Dhup181	6	3.220	1.394	0.500	0.689	0.701	0.646	6	4.511	1.602	0.400	0.778	0.792	0.745	7	4.511	1.665	0.367	0.778	0.792	0.746	
Dhup183	7	2.871	1.422	0.600	0.652	0.663	0.623	5	1.471	0.682	0.167	0.320	0.325	0.303	14	3.814	1.809	0.433	0.738	0.750	0.712	
Dhup185	13	6.522	2.246	0.367	0.847	0.861	0.836	10	5.960	1.976	0.600	0.832	0.846	0.812	15	5.941	2.182	0.367	0.832	0.846	0.817	
Dhup191	6	4.176	1.608	0.233	0.761	0.773	0.731	6	3.321	1.448	0.367	0.699	0.711	0.664	6	3.482	1.437	0.133	0.713	0.725	0.674	
Dhup194	6	3.629	1.452	0.533	0.724	0.737	0.679	5	2.880	1.265	0.433	0.653	0.664	0.606	7	4.972	1.745	0.200	0.799	0.812	0.771	
Mean		6.757	3.703	1.430	0.428	0.674	0.685	0.637	6.378	3.599	1.376	0.408	0.659	0.670	0.618	8.676	4.696	1.682	0.403	0.740	0.752	0.711

Note:  $N_a$ = number of alleles,  $N_e$ = effective number of alleles,  $I$ =Shannon's information index,  $H_o$ =observed heterozygosity,  $H_e$ =expected heterozygosity,  $uH_e$ = unbiased expected heterozygosity  
PIC=polymorphic information content.

**Table S3. Parameters of genetic diversity for *D. balansae* and *D. polyadelpha* populations at loci level**

Locus	<i>D. balansae</i> (n=27)						Locus	<i>D. polyadelpha</i> (n=27)							
	<i>N<sub>a</sub></i>	<i>N<sub>e</sub></i>	<i>I</i>	<i>H<sub>o</sub></i>	<i>H<sub>e</sub></i>	<i>uH<sub>e</sub></i>		<i>N<sub>a</sub></i>	<i>N<sub>e</sub></i>	<i>I</i>	<i>H<sub>o</sub></i>	<i>H<sub>e</sub></i>	<i>uH<sub>e</sub></i>	PIC	
Dhup14	4	1.417	0.616	0.185	0.294	0.300	0.278	Dhup14	3	1.303	0.463	0.259	0.233	0.237	0.217
Dhup61	6	4.109	1.546	0.885	0.757	0.771	0.720	Dhup61	4	2.348	1.032	0.704	0.574	0.585	0.509
Dhup64	9	4.812	1.810	0.407	0.792	0.807	0.765	Dhup64	5	3.233	1.317	0.444	0.691	0.704	0.641
Dhup70	4	1.655	0.759	0.111	0.396	0.403	0.363	Dhup70	3	1.078	0.184	0.074	0.072	0.073	0.071
Dhup78	-	-	-	-	-	-	-	Dhup78	2	1.117	0.215	0.037	0.105	0.107	0.099
Dhup90	8	3.953	1.610	0.769	0.747	0.762	0.709	Dhup90	3	2.219	0.868	0.852	0.549	0.560	0.448
Dhup104	15	6.910	2.320	0.556	0.855	0.871	0.845	Dhup104	10	7.839	2.138	0.519	0.872	0.889	0.859
Dhup108	15	11.267	2.543	0.846	0.911	0.929	0.904	Dhup108	5	2.585	1.106	0.519	0.613	0.625	0.542
Dhup114	9	2.730	1.453	0.185	0.634	0.646	0.609	Dhup114	11	5.855	1.988	0.630	0.829	0.845	0.808
Dhup116	10	4.220	1.828	0.542	0.763	0.779	0.744	Dhup116	11	4.571	1.827	0.333	0.781	0.796	0.752
Dhup118	4	3.336	1.279	0.630	0.700	0.713	0.646	Dhup118	-	-	-	-	-	-	-
Dhup120	8	5.896	1.897	0.640	0.830	0.847	0.809	Dhup120	1	1.000	0.000	0.000	0.000	0.000	0.000
Dhup122	6	3.025	1.321	0.704	0.669	0.682	0.616	Dhup122	14	9.000	2.375	0.222	0.889	0.906	0.879
Dhup123	5	3.347	1.386	0.654	0.701	0.715	0.660	Dhup123	-	-	-	-	-	-	-
Dhup129	5	1.474	0.681	0.259	0.322	0.328	0.302	Dhup129	4	1.520	0.660	0.259	0.342	0.349	0.312
Dhup139	5	2.735	1.218	0.444	0.634	0.646	0.587	Dhup139	4	2.976	1.149	0.556	0.664	0.676	0.596
Dhup141	7	3.941	1.572	0.704	0.746	0.760	0.709	Dhup141	7	4.796	1.704	0.704	0.791	0.806	0.762
Dhup144	8	5.729	1.878	0.577	0.825	0.842	0.803	Dhup144	2	1.202	0.308	0.037	0.168	0.171	0.154
Dhup159	4	1.457	0.598	0.370	0.313	0.319	0.283	Dhup159	-	-	-	-	-	-	-
Dhup163	-	-	-	-	-	-	-	Dhup163	8	4.942	1.754	0.778	0.798	0.813	0.769
Dhup164	3	1.818	0.774	0.074	0.450	0.458	0.395	Dhup164	3	1.818	0.774	0.370	0.450	0.458	0.395
Dhup167	4	1.634	0.724	0.120	0.388	0.396	0.348	Dhup167	5	3.149	1.331	0.889	0.682	0.695	0.638
Dhup171	6	2.599	1.205	0.519	0.615	0.627	0.558	Dhup171	-	-	-	-	-	-	-

Dhup181	10	5.341	1.932	0.481	0.813	0.828	0.790	<i>Dhup181</i>	2	1.202	0.308	0.111	0.168	0.171	0.154
Dhup183	6	1.846	0.978	0.360	0.458	0.468	0.434	<i>Dhup183</i>	2	1.957	0.682	0.407	0.489	0.498	0.369
Dhup185	9	5.297	1.889	0.640	0.811	0.828	0.789	<i>Dhup185</i>	3	2.039	0.764	0.074	0.510	0.519	0.397
Dhup191	7	3.407	1.516	0.407	0.706	0.720	0.675	<i>Dhup191</i>	-	-	-	-	-	-	-
Dhup194	6	1.633	0.825	0.077	0.388	0.395	0.363	<i>Dhup194</i>	-	-	-	-	-	-	-
Mean	7.038	3.676	1.391	0.467	0.635	0.648	0.604	Mean	5.091	3.079	1.043	0.399	0.512	0.522	0.471

Note:  $N_a$ = number of alleles,  $N_e$ = effective number of alleles,  $I$ =Shannon's information index,  $H_o$ =observed heterozygosity,  $H_e$ =expected heterozygosity,  $uH_e$ = unbiased expected heterozygosity  
 PIC=polymorphic information content.