

Table 2 Rice genetic resources used for the SSR analysis and genetic diversity (mean±standard deviation)

Variety	<i>A</i>	<i>A_e</i>	<i>N_a</i>	<i>K</i>	<i>P</i> (%)	<i>H_o</i>	<i>H_e</i>	<i>I</i>
BJLJ-1	2.0417±0.9991	1.2424±0.2840	49	16	66.67	0.0000±0.0000	0.1615±0.1652	0.2899±0.0899
BJLJ-2	1.4167±0.6539	1.0285±0.0539	34	8	33.33	0.0000±0.0000	0.0256±0.0469	0.0570±0.0999
BJLJ-3	1.7083±0.8065	1.0661±0.0941	41	13	54.17	0.0000±0.0000	0.0563±0.0748	0.1186±0.1508
BJLJ-4	2.0417±0.9991	1.1480±0.1662	49	16	66.67	0.0000±0.0000	0.1144±0.1151	0.2254±0.2205
BJLJ-5	1.8333±1.0072	1.1440±0.2308	44	13	54.17	0.0000±0.0000	0.1022±0.1332	0.1974±0.2533
BJ_POP	3.0417±1.4590	1.5275±0.5772	73	22	91.67	0.0000±0.0000	0.2716±0.2171	0.4875±0.3768
YLG-1	2.0417±1.2676	1.1763±0.3110	49	14	58.33	0.0008±0.0041	0.1132±0.1558	0.2173±0.2769
YLG-2	2.4583±1.1788	1.2188±0.3013	59	18	75.00	0.0008±0.0041	0.1451±0.1581	0.2831±0.2853
YLG-3	2.2917±0.9991	1.2150±0.3576	55	18	75.00	0.0008±0.0041	0.1371±0.1565	0.2691±0.2741
YLG-4	1.7083±0.6241	1.1697±0.2792	41	15	62.50	0.0008±0.0041	0.1136±0.1480	0.1956±0.2252
YLG-5	1.9583±0.9546	1.2734±0.4371	47	15	62.50	0.0000±0.0000	0.1534±0.1979	0.2671±0.3216
YL_POP	3.4583±1.3181	1.2319±0.3531	83	23	95.83	0.0007±0.0019	0.1465±0.1587	0.3070±0.2833
HJLJ-1	2.0833±0.9286	1.4695±0.4535	50	17	70.83	0.0008±0.0041	0.2581±0.2220	0.4019±0.3332
HJLJ-2	2.2083±0.9771	1.5361±0.4766	53	19	79.17	0.0008±0.0041	0.2863±0.2260	0.4450±0.3386
HJLJ-3	2.4583±1.2847	1.4851±0.5448	59	20	83.33	0.0050±0.0122	0.2529±0.2269	0.4301±0.3733
HJLJ-4	2.3333±1.6330	1.5812±1.1871	56	19	79.17	0.0000±0.0000	0.2356±0.2241	0.4232±0.4497
HJLJ-5	2.1250±1.0759	1.3883±0.4826	51	17	70.83	0.0000±0.0000	0.2084±0.2249	0.3389±0.3402
HJ_POP	3.1667±2.0572	1.7616±0.6103	76	21	87.50	0.0013±0.0025	0.3610±0.2315	0.5911±0.4037
CJ26-1	1.0833±0.2823	1.0034±0.0115	26	2	8.33	0.0000±0.0000	0.0033±0.0112	0.0082±0.0277
CJ26-2	1.1250±0.3378	1.0146±0.0551	27	3	12.50	0.0000±0.0000	0.0122±0.0443	0.0235±0.0782
CJ26-3	1.1250±0.4484	1.0129±0.0486	27	2	8.33	0.0000±0.0000	0.0110±0.0406	0.0233±0.0857
CJ26-4	1.0417±0.2041	1.0072±0.0352	25	1	4.17	0.0000±0.0000	0.0062±0.0304	0.0116±0.0569
CJ26-5	1.0000±0.0000	1.0000±0.0000	24	0	0.00	0.0000±0.0000	0.0000±0.0000	0.0000±0.0000
C26_POP	1.2083±0.5090	1.0261±0.0963	29	4	16.67	0.0000±0.0000	0.0196±0.0663	0.0363±0.1073
CJ27-1	1.2083±0.5090	1.0060±0.0141	29	4	16.67	0.0017±0.0056	0.0058±0.0137	0.0152±0.0357
CJ27-2	1.0417±0.2041	1.0035±0.0170	25	1	4.17	0.0000±0.0000	0.0032±0.0158	0.0070±0.0343
CJ27-3	1.0833±0.2823	1.0106±0.0359	26	2	8.33	0.0000±0.0000	0.0095±0.0322	0.0189±0.0641
CJ27-4	1.0833±0.2823	1.0144±0.0487	26	2	8.33	0.0000±0.0000	0.0124±0.0420	0.0232±0.0787
CJ27-5	1.1250±0.3378	1.0104±0.0281	27	3	12.50	0.0000±0.0000	0.0097±0.0262	0.0210±0.0567
C27_POP	1.3333±0.5647	1.0087±0.0212	32	7	29.17	0.0003±0.0011	0.0083±0.0198	0.0205±0.0448
HX22-1	1.0417±0.2041	1.0017±0.0083	25	1	4.17	0.0000±0.0000	0.0016±0.0081	0.0041±0.0200
HX22-2	1.0000±0.0000	1.0000±0.0000	24	0	0.00	0.0000±0.0000	0.0000±0.0000	0.0000±0.0000
HX22-3	1.0833±0.2823	1.0034±0.0115	26	2	8.33	0.0000±0.0000	0.0033±0.0112	0.0082±0.0277
HX22-4	1.5000±0.7802	1.2737±0.4424	36	8	33.33	0.0025±0.0068	0.1440±0.2220	0.2158±0.3314
HX22-5	1.1250±0.4484	1.0043±0.0149	27	2	8.33	0.0008±0.0041	0.0041±0.0142	0.0105±0.0365
HX_POP	1.5417±0.8836	1.0780±0.1284	37	8	33.33	0.0007±0.0019	0.0612±0.0989	0.1110±0.1758
30POP	4.2917±1.8528	2.0510±0.7539	103	24	100.00	0.0005±0.0007	0.4561±0.1779	0.7728±0.3479

Note: *A*: Average number of alleles; *A_e*: Effective number of alleles; *N_a*: Total number of alleles; *K*: Number of polymorphic loci; *P*: The percentage of polymorphic loci; *H_o*: Observed heterozygosity; *H_e*: expected heterozygosity; *I*: Shannon's information index