

**Appendix S1.** Genetic diversity statistics for subsets of CO breeding lines.

Population	<i>N</i>	%P	<i>A<sub>g</sub></i> (± S.E.)	<i>PAL</i>	<i>H<sub>o</sub></i>	<i>H<sub>e</sub></i>
Varieties	11	36.84	1.34 <sup>a</sup> (0.0015)	0.06 <sup>a</sup>	0.003 <sup>a</sup>	0.121 <sup>a</sup>
Elite breeding lines	17	42.11	1.35 <sup>a</sup> (0.0017)	0.07 <sup>a</sup>	0.011 <sup>a</sup>	0.118 <sup>a</sup>
Germplasm conversion	6	35.34	1.35 <sup>a</sup> (0.0014)	0.07 <sup>a</sup>	0.036 <sup>b</sup>	0.131 <sup>a</sup>

*N* number of plants sampled

%P percent polymorphic loci

*A<sub>g</sub>* allelic richness (based on the rarefaction method) averaged across all loci ( $F_{2,130} = 4.68$ )

*PAL* private allelic richness (based on the rarefaction method) averaged across all loci ( $F_{2,130} = 0.74$ )

*H<sub>o</sub>* observed heterozygosity averaged across all loci ( $F_{2,130} = 1.66$ )

*H<sub>e</sub>* expected heterozygosity averaged across all loci ( $F_{2,130} = 5.48$ )

Superscript letters indicate differences in significance levels ( $P < 0.001$ )