

Table 1 Broad-sense heritability calculated on a plot-mean basis and SNP heritability estimates, variance components and coefficients of variation of 14 traits in cassava GWAS panel (Rabbi et al., 2020)

Trait	SNP-h <sup>2</sup>	H <sup>2</sup>	$\sigma_g$	$\sigma_{g \times e}$	$\sigma_e$	CV
CMD severity	0.434	0.766	0.783	0.086	0.140	63
CGM severity	0.165	0.149	0.074	0.177	0.244	19
Apical pubescence	0.502	0.531	0.175	0.083	0.071	113
Leaf shape	0.499	0.510	0.679	0.475	0.178	22
Apical leaf colour	0.496	0.567	1.160	0.629	0.601	23
Mature leaf greenness	0.586	0.531	0.427	0.186	0.191	18
Petiole colour	0.716	0.754	3.322	0.602	0.485	33
Harvest index	0.308	0.538	0.010	0.002	0.007	28
Plant type	0.384	0.369	0.376	0.180	0.465	38
Quater stem colour	0.516	0.388	0.907	0.191	1.241	22
Total carotenoids content (colour chart)	0.675	0.726	0.401	0.066	0.085	49
Dry matter content	0.565	0.521	14.776	3.385	10.184	15
Root periderm colour	0.548	0.610	0.190	0.035	0.086	19
Root cortex colour	0.518	0.415	0.070	0.036	0.062	20

Note:  $H^2$  is the broad-sense heritability,  $\sigma_g$  is the clonal genotypic variance,  $\sigma_{g \times e}$  is the variance due to genotype by environment (G×E), and  $\sigma_e$  is the being the residual variance