

**Table S2** Variance component dissection by using single- and multi-environment yield data

Environment	$\sigma_g^2$	$\sigma_{ge}^2$	$\sigma_\varepsilon^2$	e	r	$H^2$
BJ	203.51	/	264.02	1	2	0.61
XJ	234.17	/	199.73	1	2	0.70
HN	105.19	/	138.13	1	2	0.60
BJ-XJ-HN	125.20	54.40	203.60	3	2	0.71

Note:  $\sigma_g^2$  indicates variance of genotype;  $\sigma_{ge}^2$  indicates variance of genotype-by-environment;  $\sigma_\varepsilon^2$  indicates variance of error; e and r are the number of environments and replicates, respectively;  $H^2$  indicates broad sense heritability; / indicates  $\sigma_{ge}^2$  can't be estimated using single-environment data