

In this approach, we create subsets of our plot data. Each subset contains the information of only two sites. Since we have 10 sites, there are 45 different site pairs and thus 45 subsets we need to analyze. For each subset, we fit a model that allows for a genetic correlation between sites as:

	vc.1	vc.2	estimate
G	L.corr		0.599
G	LBarisal		0.121
G	LBhanga		0.181
L	NA		1.020
Residual	NA		0.352
Y	NA		0.026
Y:G	NA		0.161
Y:L	NA		0.274
Y:L:Rep	NA		0.008

[illegible]