

Supplementary information to:

The effects of P on wheat root-associated prokaryotic communities are dependent on soil P content, growth stage and variety

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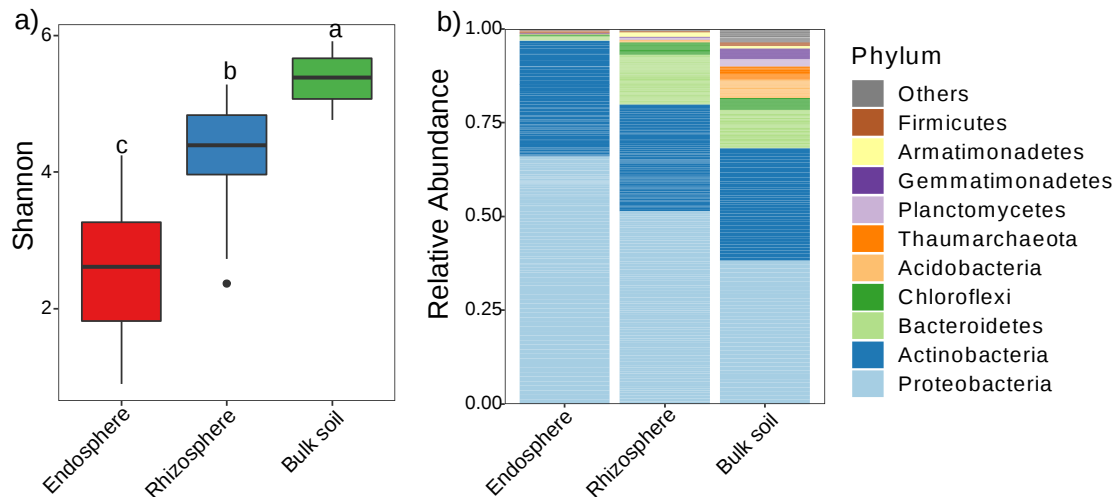


Figure S1. (a) Shannon Indices of prokaryotic communities in root endosphere, rhizosphere and bulk soil samples. Different letters represent significance at $p < 0.05$. (b) Relative abundances of prokaryotes at phylum level based on all samples in each sample type

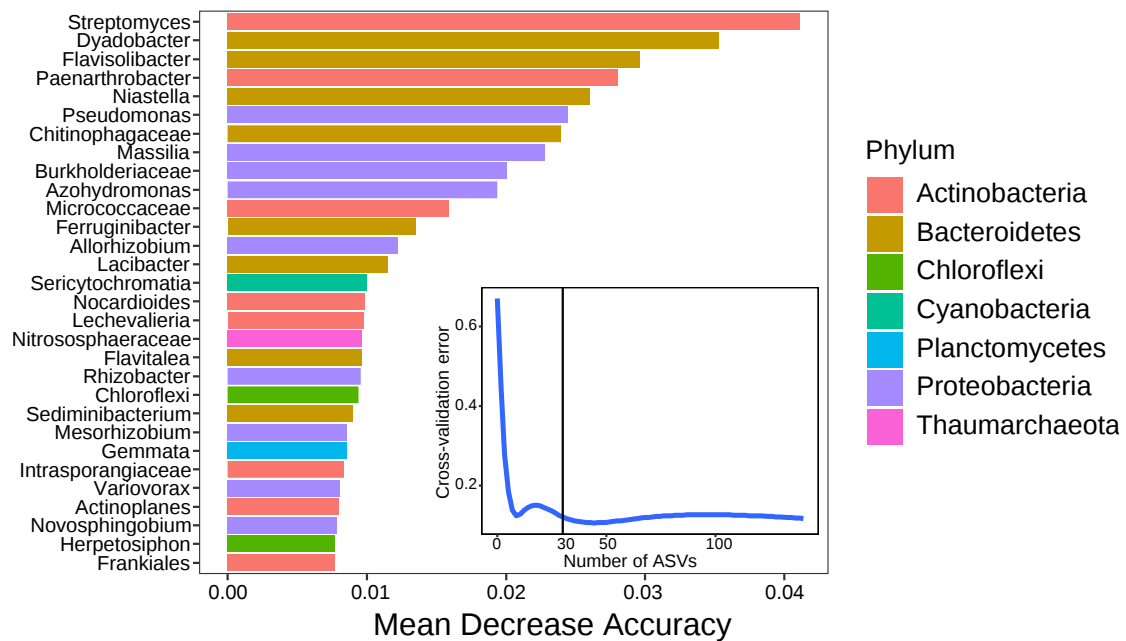


Figure S2. Biomarker taxa that could differentiate endosphere, rhizosphere and bulk soil samples of each growth stage identified by Random-forest model. Ten-fold cross-validation error of the number of input taxa was used to differentiate samples. Top 30 taxa were identified as biomarkers based on all samples. The biomarker genera were ranked in the increasing order of mean of decreased accuracy.

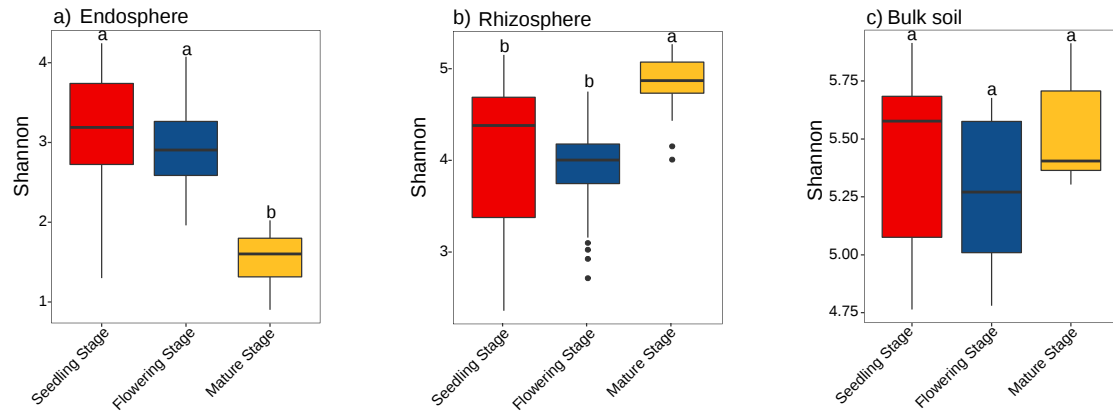


Figure S3. Shannon indices of the prokaryotic communities associated with each growth stage in (a) endosphere, (b) rhizosphere and (c) bulk soil. Different letters represent significance at $p < 0.05$.

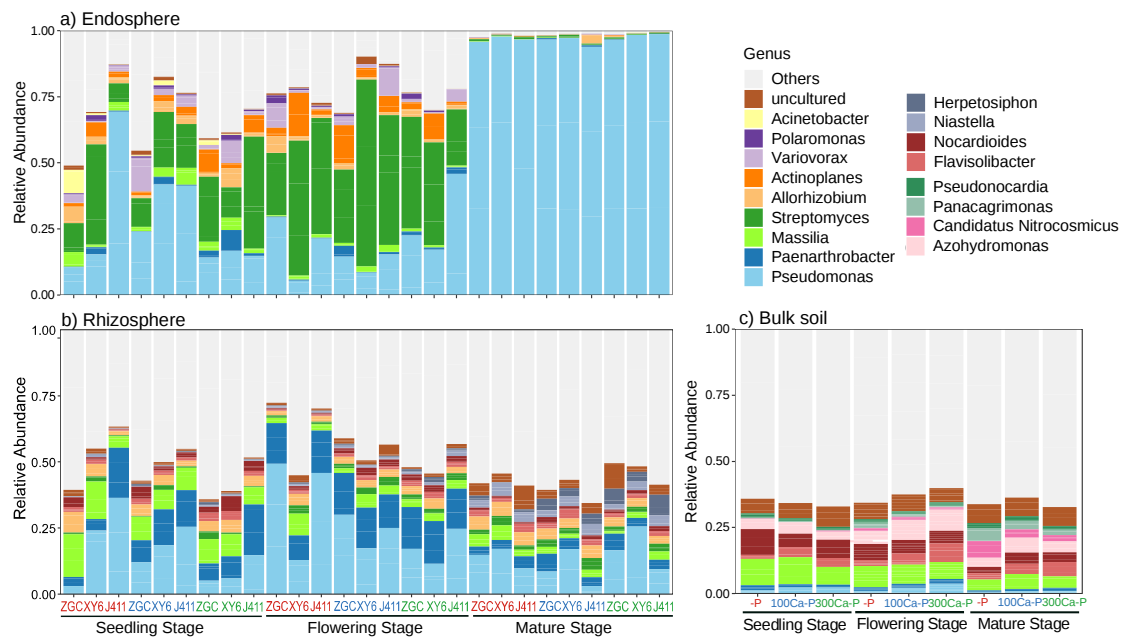


Figure S4. Relative abundances of prokaryotic communities in (a) endosphere, (b) rhizosphere and (c) bulk at genus level. Red labels represent -P treatment, blue labels represent 100Ca-P treatment, and green labels represent 300Ca-P treatment.

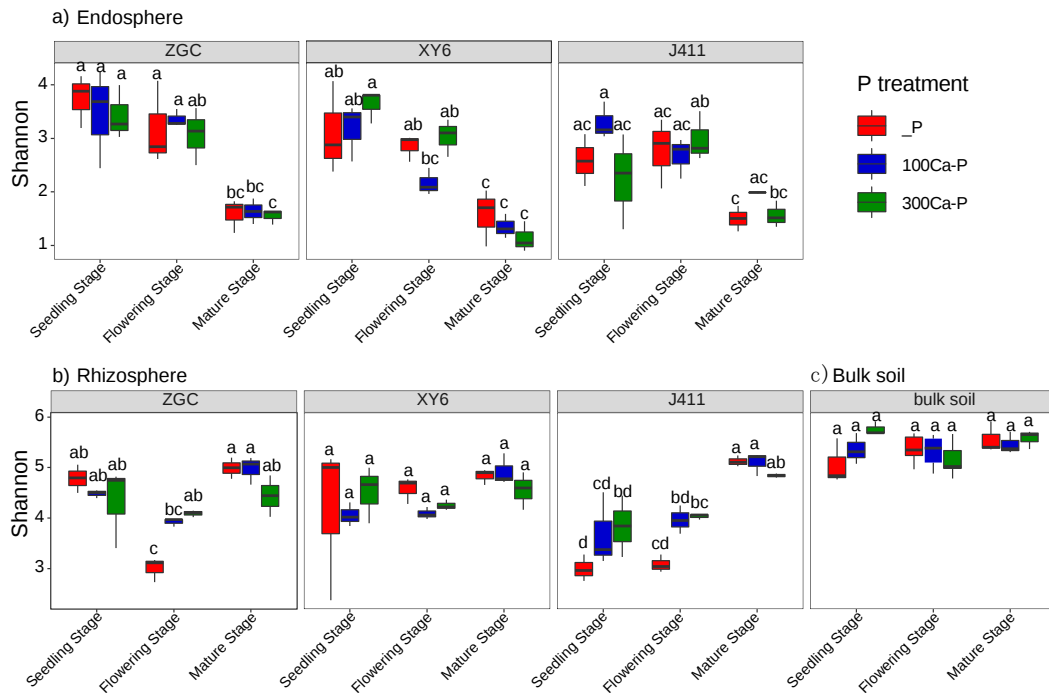


Figure S5. Shannon indices of the prokaryotic communities associated with each P treatments in (a) endosphere and (b) rhizosphere.

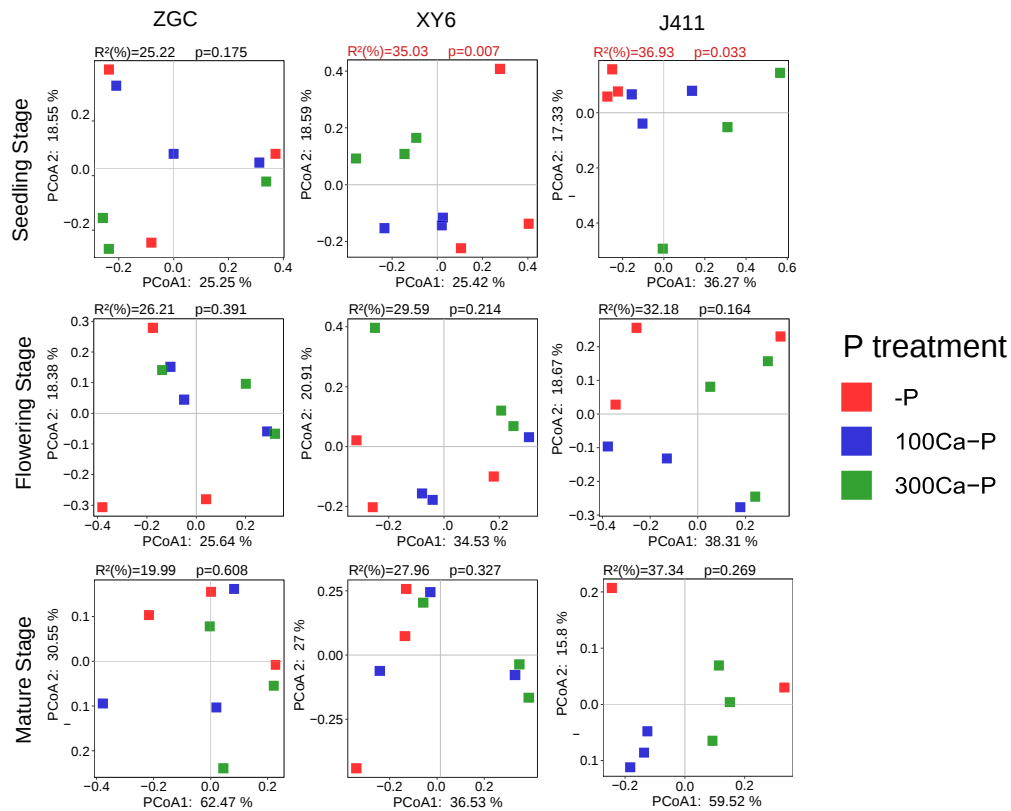


Figure S6. PCoA analysis of endosphere samples at different growth stages for each wheat variety. All variances attributable to the treatments (R^2) and the significance of the factor (p value) were shown in each plot.

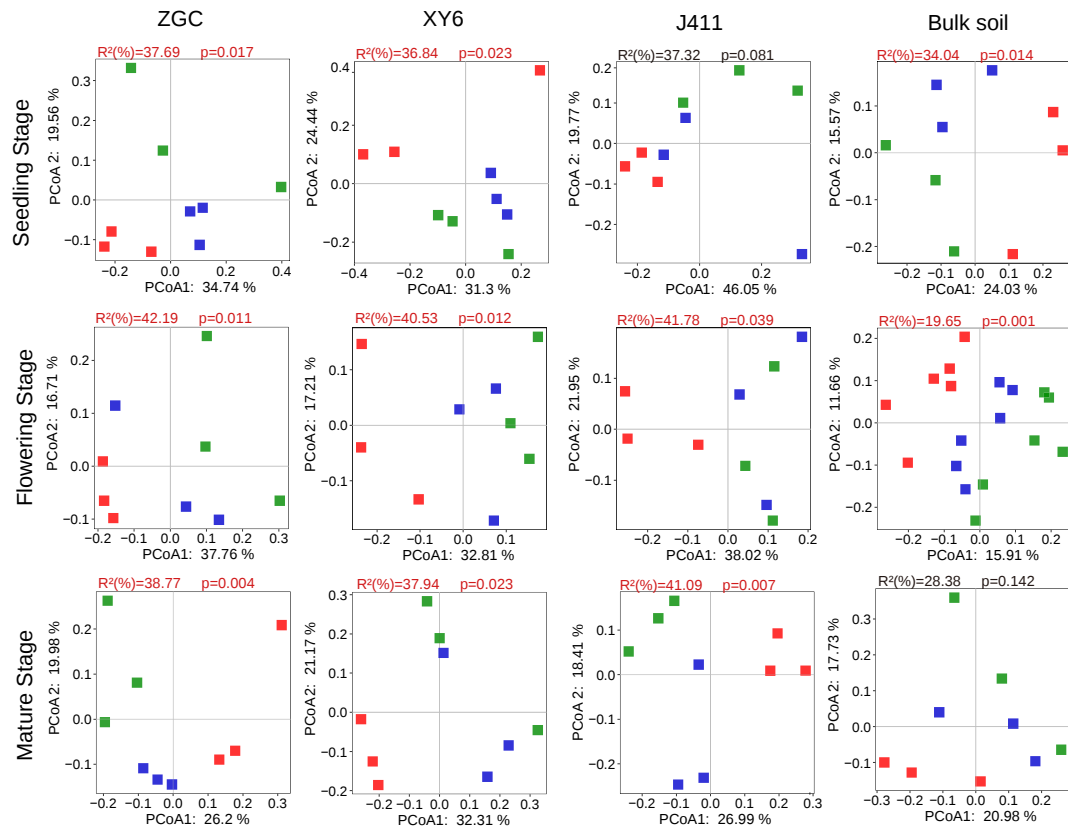


Figure S7. PCoA analysis of rhizosphere and bulk soil samples at different growth stages for each wheat variety. All variances attributable to the treatments (R^2) and the significance of the factor (p value) were shown in each plot.

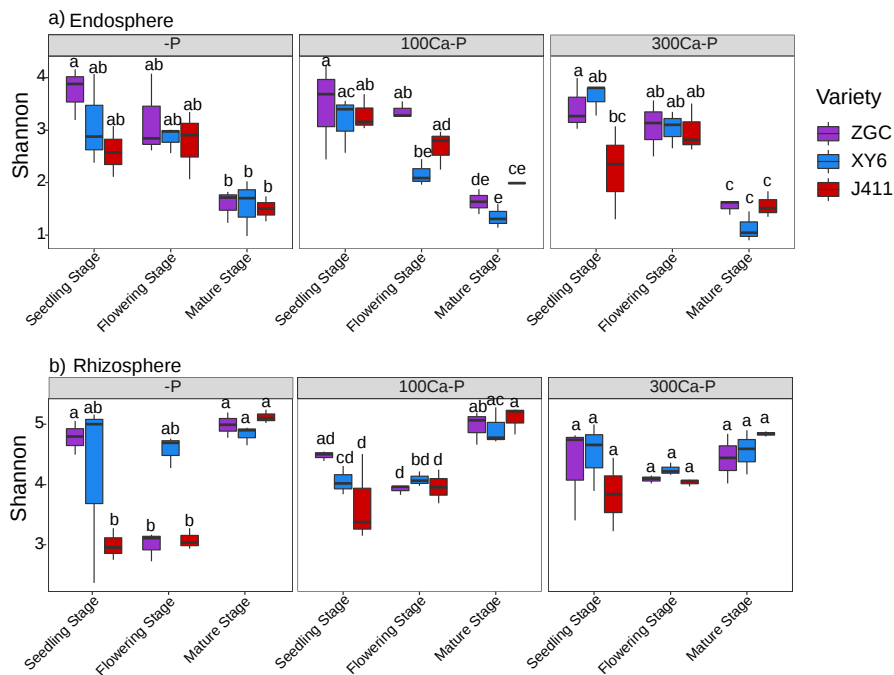


Figure S8. Shannon indices of the prokaryotic communities associated with each variety in (a) endosphere and (b) rhizosphere.

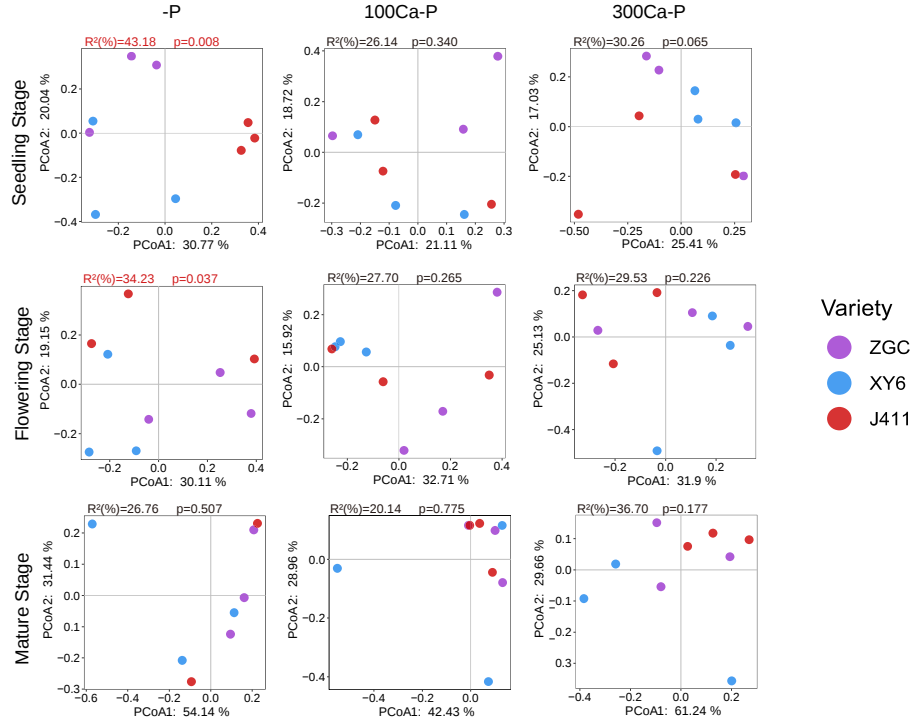


Fig S9. PCoA analysis of endosphere samples at different growth stages for each P-treatments. All variances attributable to the variety (R^2) and the significance of the factor (p value) were shown in each plot.

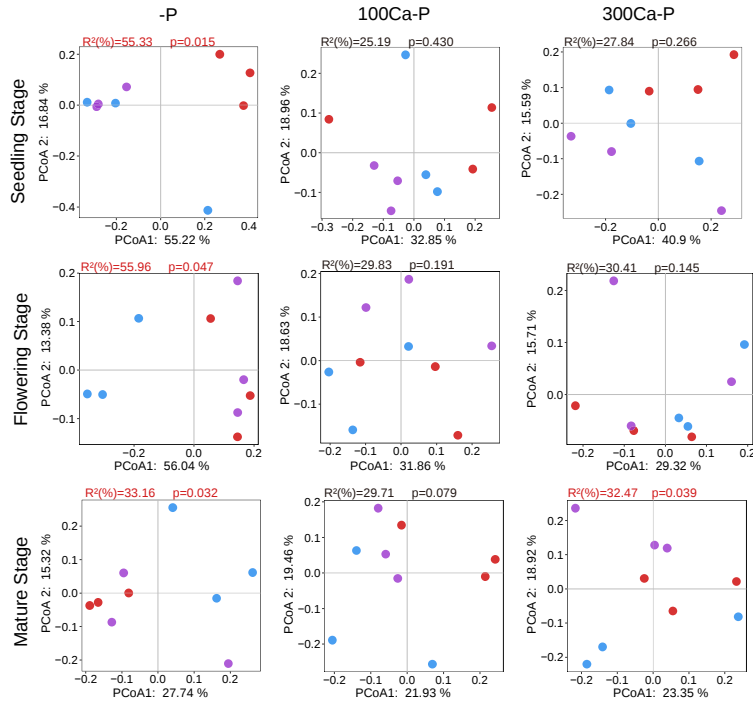


Fig S10. PCoA analysis of rhizosphere samples at different growth stages for each P-treatments. All variances attributable to the variety (R^2) and the significance of the factor (p value) were shown in each plot.

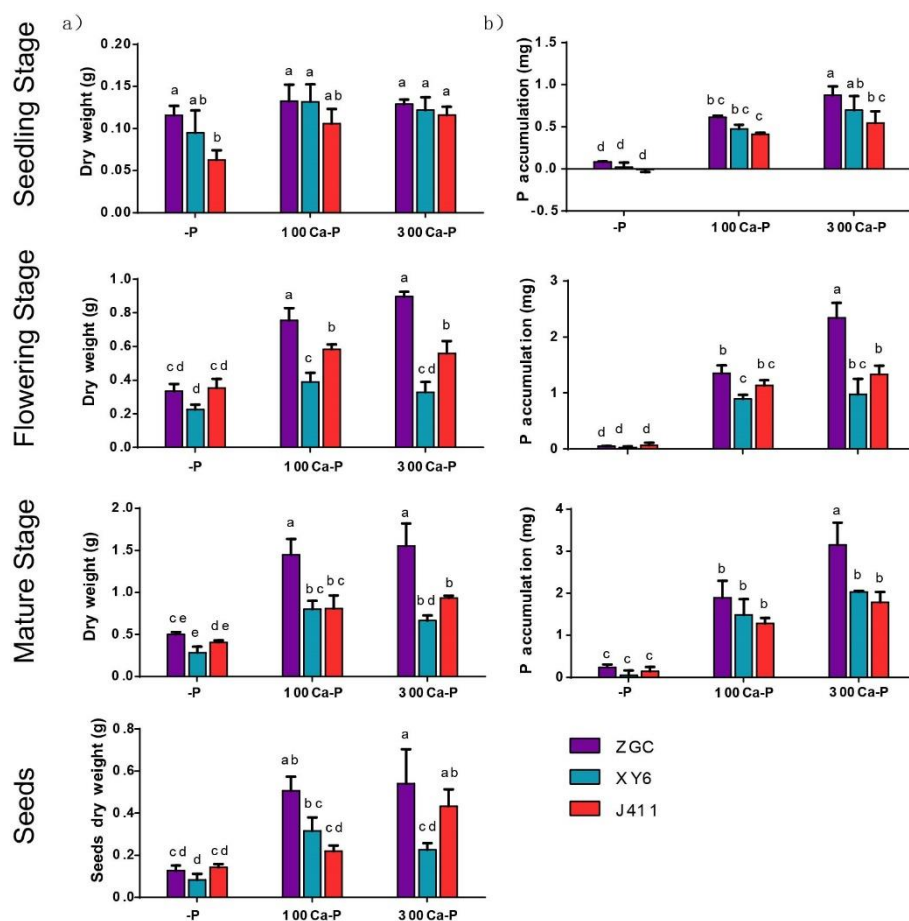


Fig S11. (a) Plant dry weight, seeds dry weight and (b) P accumulation of each wheat variety at different growth stages under different treatments (plant dry weight and P accumulation at transplanting were deducted). Different letters represent significance at $p < 0.05$.

Table S1 PERMANOVA test on the variations of prokaryotic communities for all samples based on Bray-Curtis distance

Variables		R ² (%)	p	
All samples				
Single factor	SampleType	35.53%	0.001	***
	GrowthStage	5.88%	0.001	***
	P-treatment	1.59%	0.001	***
Two factors' interaction	SampleType*GrowthStage	10.42%	0.001	***
	SampleType* P-treatment	1.72%	0.009	**
	GrowthStage* P-treatment	1.37%	0.062	
Three factors' interaction	SampleType*GrowthStage* P-treatment	2.21%	0.184	