

Supplementary Material

Table S1. N fixed per nodule weight means (mg/g; top) and *p*-values from ANOVA (bottom) in chamber experiments 1 and 2. Letters indicate significant differences between genotypes within a treatment ($p < 0.05$).

Genotype	Chamber Experiment 1		Chamber Experiment 2		
	<i>Bradyrhizobia</i> strain		Developmental Stage		
	<i>B. elkanii</i> USDA 31	<i>B. diazoefficiens</i> USDA 110	V5	R5	R6
Benning	284.7	406.3 a	486.51	1368.62	1877.51
Benning hi-pro	267.1	504.6 b	509.39	1374.95	1899.56
Source of variation		Source of variation			
Genotype (G)	0.1647	Genotype (G)	0.7379		
Treatment (T)	<0.0001	Stage (S)	<0.0001		
G × T	0.0512	G × S	0.9887		

Table S2. Leaf area index, aboveground biomass, and aboveground N measured at 84 – 88 DAP in 2017, when Benning and Benning HP were in developmental stage R5; $n = 4$.

Genotype	Leaf area index	Aboveground biomass	Aboveground N		
			(g m ⁻²)		
			Vegetative N	Reproductive N	
Benning	4.484	638.2	19.9	11.2	8.6
Benning HP	4.359	595.7	18.2	9.8	8.4
<i>p</i> -value	0.8097	0.5709	0.4713	0.3587	0.8660

Table S3. Seed N gained from R5 to R8 in the field in 2017. Seed N gained was calculated as the difference in mean seed N between R5 and R8. Values are mean \pm standard error; errors were propagated as described in the Methods; $n = 4$.

Genotype	Seed N at R5	Seed N at R8	Seed N gained R5 – R8	Vegetative N at R5 [†]
	----- g m ⁻² -----			
Benning	5.9 \pm 0.5	12.9 \pm 1.1	7.0 \pm 1.2	11.2
Benning hi-pro	6.2 \pm 1.0	12.7 \pm 0.9	6.5 \pm 1.3	9.8
<i>p</i> -value	0.8240	0.8473	—	0.3587

[†] Vegetative N data from Table S2, shown again here for ease of comparison

Figure S1. Leaf N concentration and leaf C/N across the growing season for Benning and Benning HP grown in the field in 2016 and 2017. Leaf tissue was sampled from the uppermost, fully expanded leaf in the canopy. Significant pairwise differences (FDR-corrected $p < 0.05$) between genotypes on a sampling day are indicated by asterisks. Points and error bars are means \pm standard error.

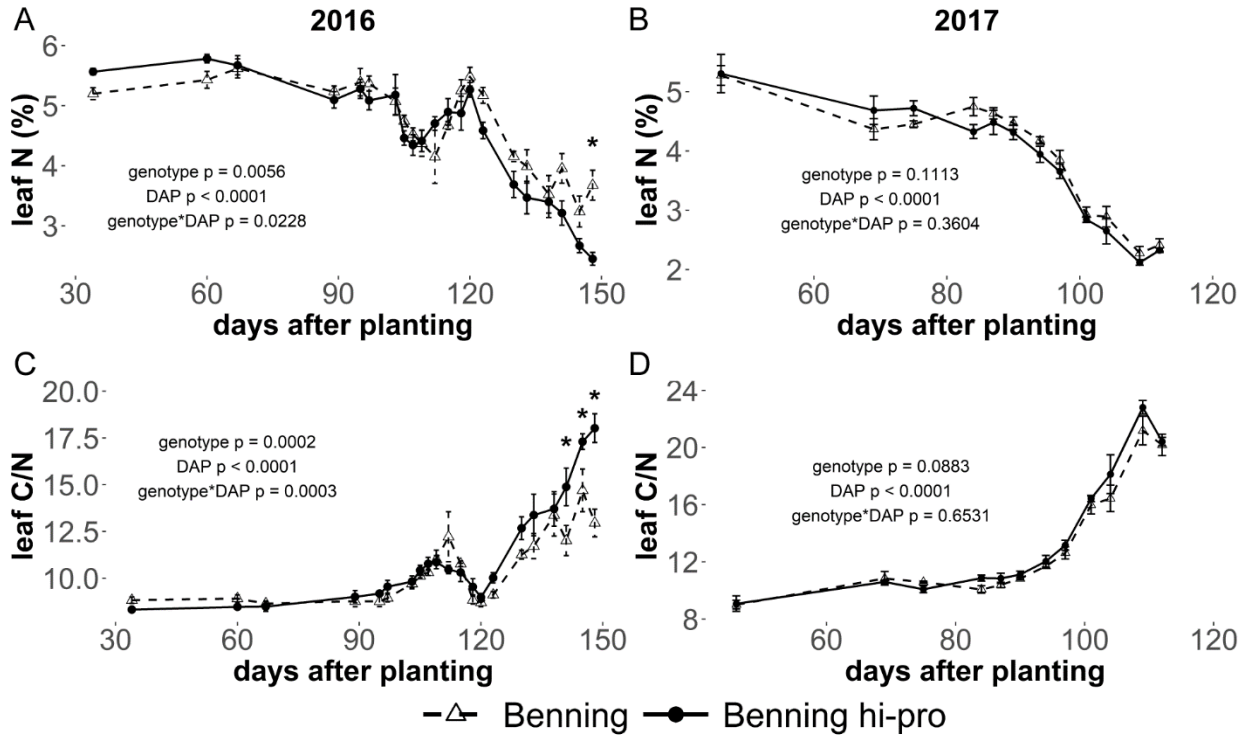


Figure S2. Leaf chlorophyll content during the 2016 seed fill period, R5 and R6. Chlorophyll was isolated from tissue sampled from the uppermost, fully expanded leaf in the canopy. Slopes were not significantly different between the two genotypes.

