

Van Cauwenberghe, J., Visch, W., Michiels, J.
and Honnay, O. 2016. Selection mosaics
differentiate *Rhizobium*-host plant interactions
across different nitrogen environments. – Oikos
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Appendix 1

Table A1. Distances between sampled populations in kilometres.				
Population	W	B	SV	NV
W	0			
B	96.09	0		
SV	425.34	357.40	0	
NV	373.58	293.08	93.45	0

Table A2. Regional averages (\pm SE) of macronutrients measured previously (Van Cauwenberghe et al., 2015) and regional atmospheric N deposition levels obtained from the UNECE/EMEP air quality data base (webdab.emep.int).

Population	Exchangeable potassium (cmolc K ⁺ /kg)	Labile phosphorus fraction (mg P/kg soil)	Mean Ellenberg value for nitrogen	Total atmospheric N deposition (mg N/m ²)
W	0.20 \pm 0.06	28.14 \pm 14.12	6.29 \pm 0.23	1687.89
B	0.10 \pm 0.02	22.13 \pm 5.53	5.94 \pm 0.22	1315.43
SV	0.11 \pm 0.04	1.67 \pm 0.70	5.34 \pm 0.35	1299.79

Table A3. F-values from mixed general linear models for normal distributed data and χ^2 values from mixed generalised linear models with log link function for data which follow a negative binomial distribution, are shown for plant and mutualistic traits for five *R. leguminosarum* biovar *viciae* genotypes and three *V. cracca* genotypes grown under two contrasting N conditions lineages in all possible factorial combinations. DF = degrees of freedom. * $0.05 \geq p > 0.01$; ** $0.01 \geq p > 0.001$; *** $0.001 \geq p$.

	DF	Shoot length	Shoot dry weight	Root dry weight	Plant N	Plant C	Plant P	Tendrils no.	Shoot no.	Nodule no.
N	1	0.57	8.75**	22.89***	3.53	4.20*	0.06	1.53	2.15	49.36***
<i>Rhizobium</i> genotype	4	1.34	2.52*	2.52*	4.06**	2.45*	0.24	2.55*	5.71***	4.74**
Plant genotype	2	14.94***	12.31***	10.87***	0.70	0.26	0.62	0.24	2.92	4.09*
<i>Rhizobium</i> genotype \times N	4	0.70	2.04	2.31	0.74	1.68	0.42	3.57**	2.14	4.98***
Plant genotype \times N	2	0.91	2.75	3.43*	3.40*	2.16	0.60	0.24	2.16	14.24***
<i>Rhizobium</i> genotype \times <i>Plant</i> genotype	8	0.51	2.28*	2.35*	0.71	0.90	0.46	1.28	2.0*	2.78**
<i>Rhizobium</i> genotype \times Plant genotype \times N	8	0.45	1.57	1.35	1.59	0.79	0.68	1.97*	2.27*	4.21***
Error DF		187	187	187	182	182	177	187	187	187

Figure A1. NeighborNet network build using SplitsTree v. 4.12.8 (Huson and Bryant, 2006), showing the genetic distance among the chromosomal (*recA-glnII*) sequence types (STs) of the *Rhizobium leguminosarum* biovar *viciae* isolates obtained from West-Flanders, Brabant and the Vosges regions, in Van Cauwenberghe et al. (2015) with regional abundances higher than 5%. STs used in this study are underlined.

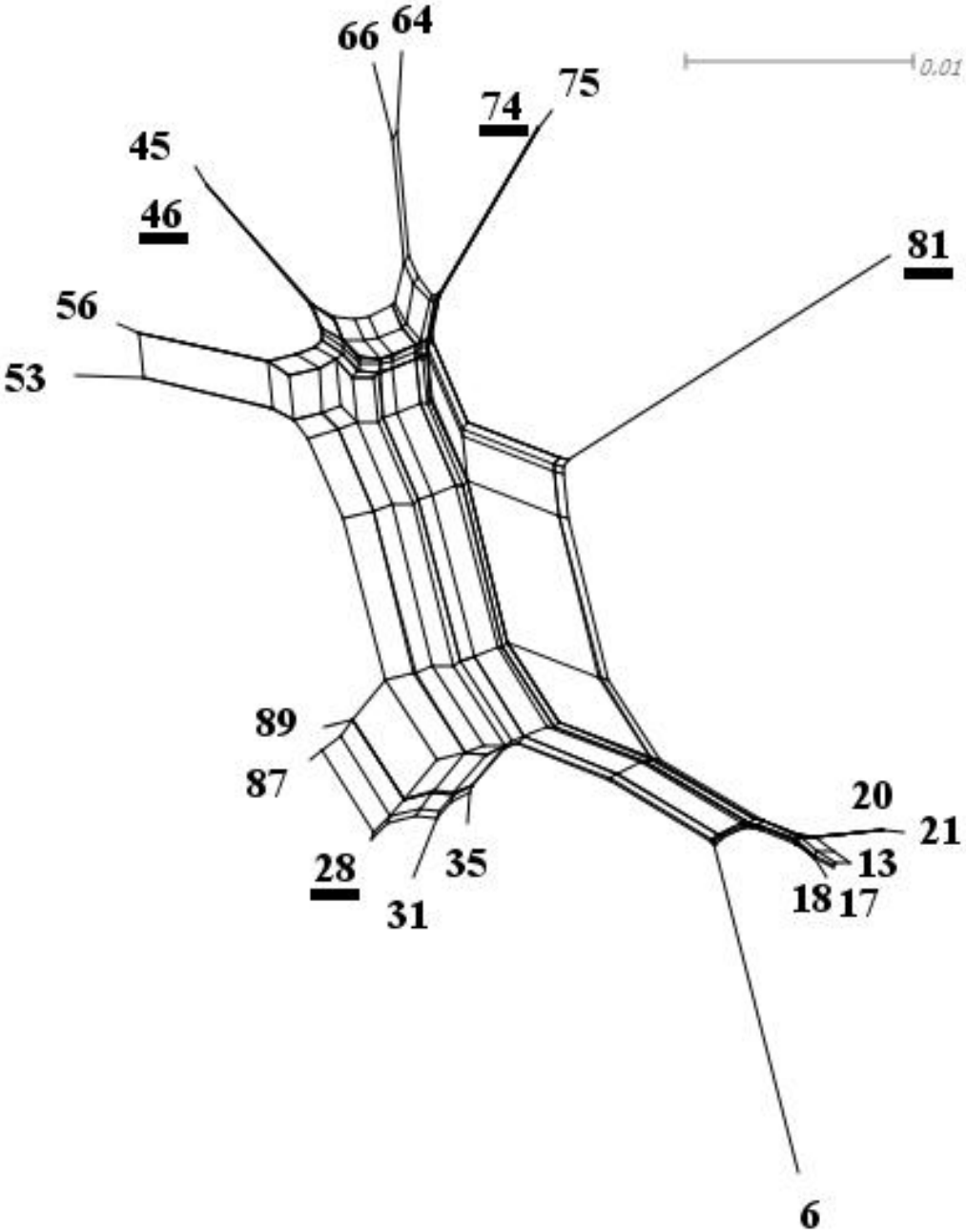


Figure A2. NeighborNet network build using SplitsTree v. 4.12.8 (Huson and Bryant, 2006), showing the genetic distance among the *nodC* sequence types (STs) of the *Rhizobium leguminosarum* biovar *viciae* isolates obtained from West-Flanders, Brabant and the Vosges regions, in Van Cauwenberghe et al. (2015) with regional abundances higher than 5%. STs used in this study are underlined.

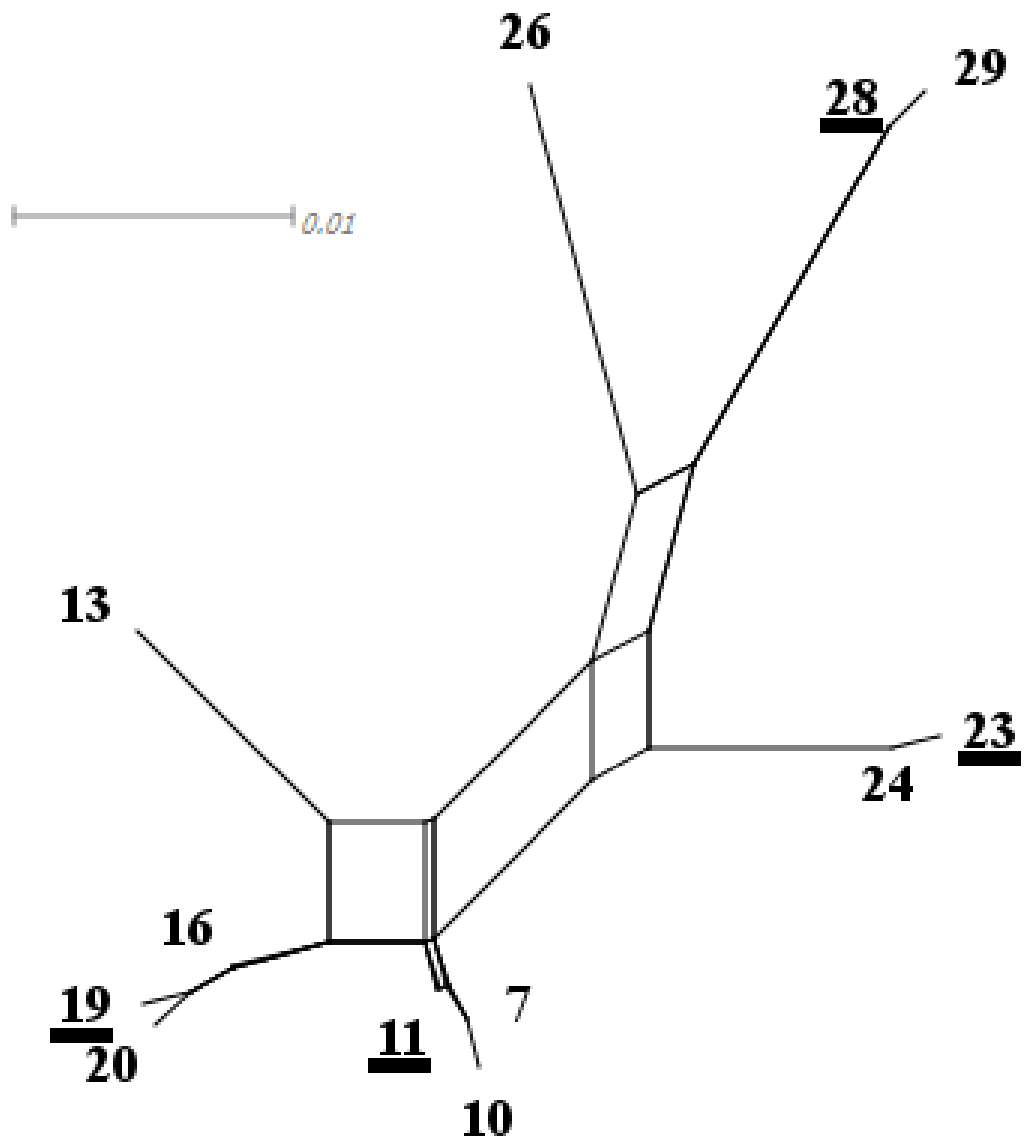


Figure A3. Mean (\pm SE) number of nodules (up), mean (\pm SE) number of tendrils (middle) and mean (\pm SE) shoot dry weight per plant (g) (down) formed by either allopatric (blue) or sympatric (gray) combinations of *V. cracca* genotypes and *Rhizobium* genotypes.

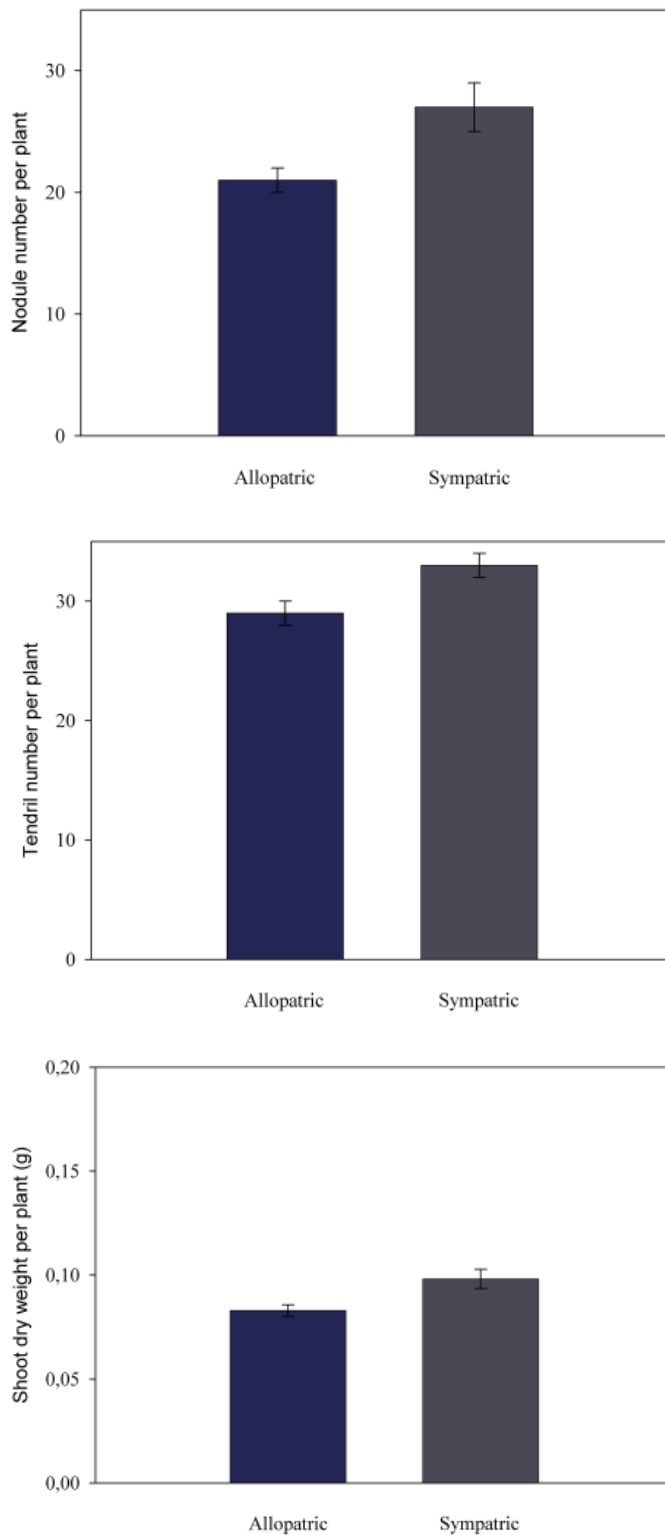


Figure A4. Mean (\pm SE) number of shoots formed by *V. cracca* genotypes from populations W, B and SV, either uninoculated (control) or in association with *R. leguminosarum* biovar *viciae* genotypes W_ST81-C23, B_ST46-C28, SV_ST74-C19, NV_ST28-C11 or W_ST28-C11 in soils with low (upper plot) and high (lower plot) N conditions.

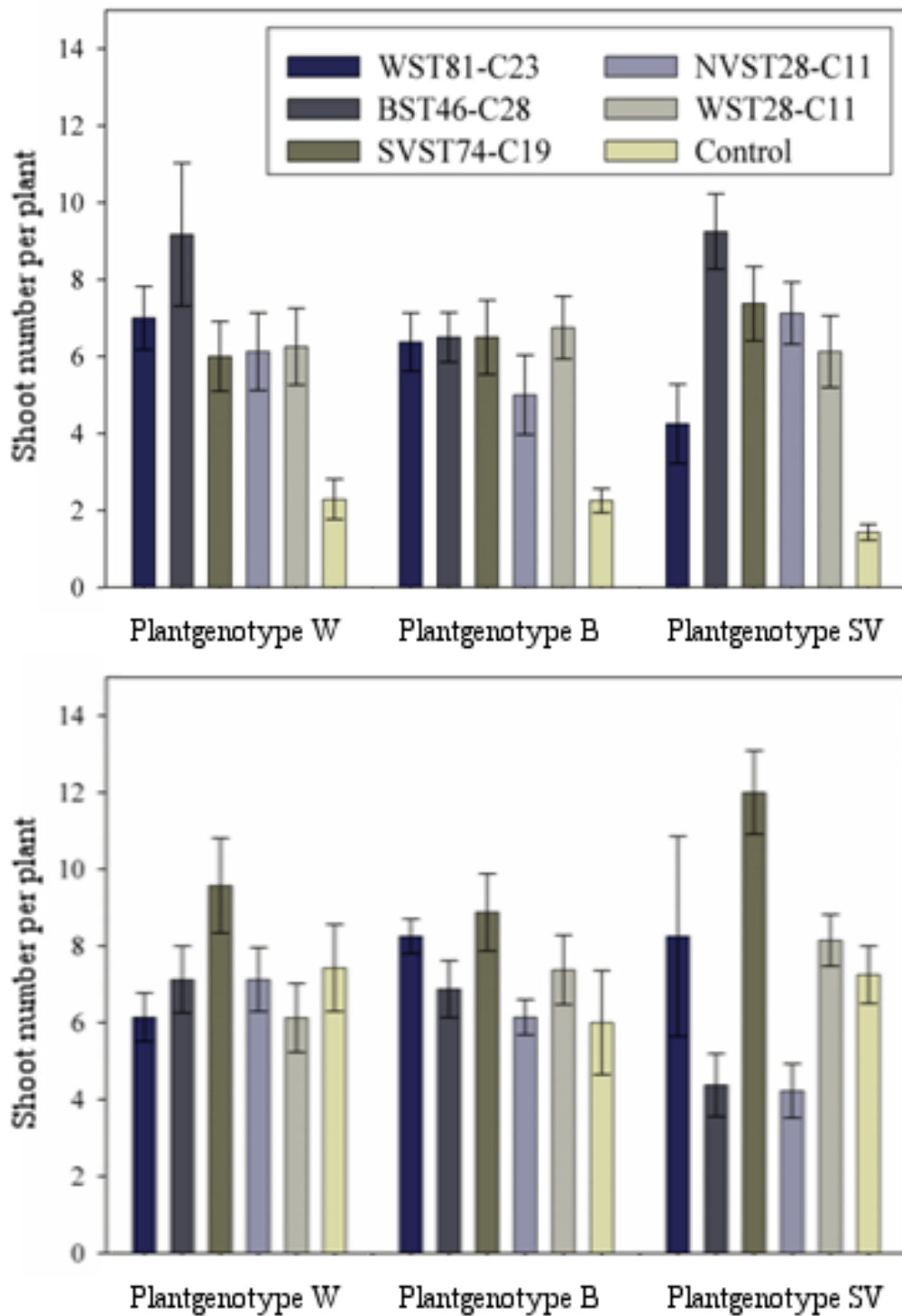


Figure A5. Mean (\pm SE) root dry weight (g) from *V. cracca* genotypes from populations W, B and SV, either uninoculated (control) or in association with *R. leguminosarum* biovar *viciae* genotypes W_ST81-C23, B_ST46-C28, SV_ST74-C19, NV_ST28-C11 or W_ST28-C11 in soils with low (upper plot) and high (lower plot) N conditions.

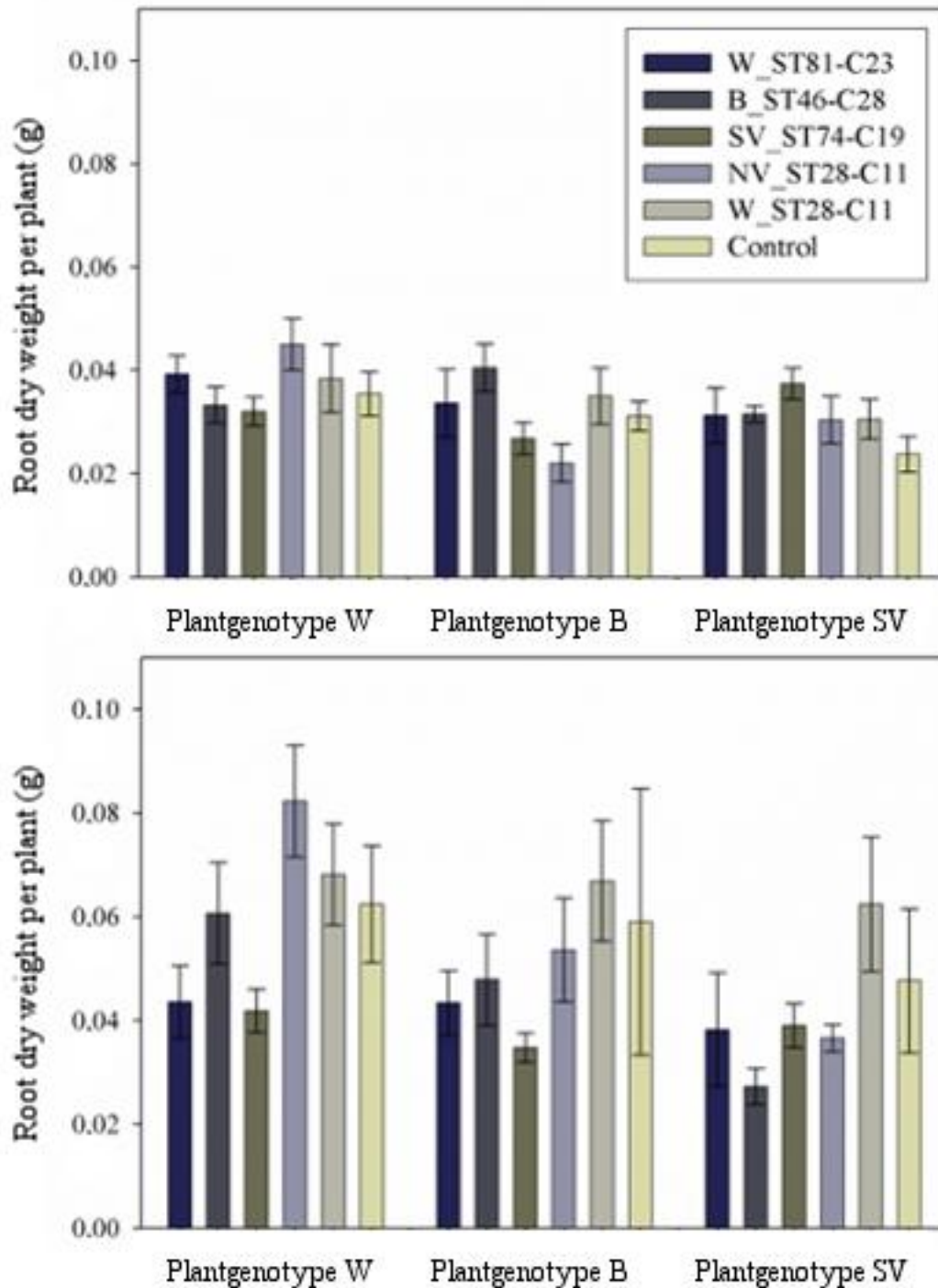


Figure A6. Mean (\pm SE) shoot length (cm) measured from *V. cracca* genotypes from populations W, B and SV, either uninoculated (control) or in association with *R. leguminosarum* biovar *viciae* genotypes W_ST81-C23, B_ST46-C28, SV_ST74-C19, NV_ST28-C11 or W_ST28-C11 in soils with low (upper plot) and high (lower plot) N conditions.

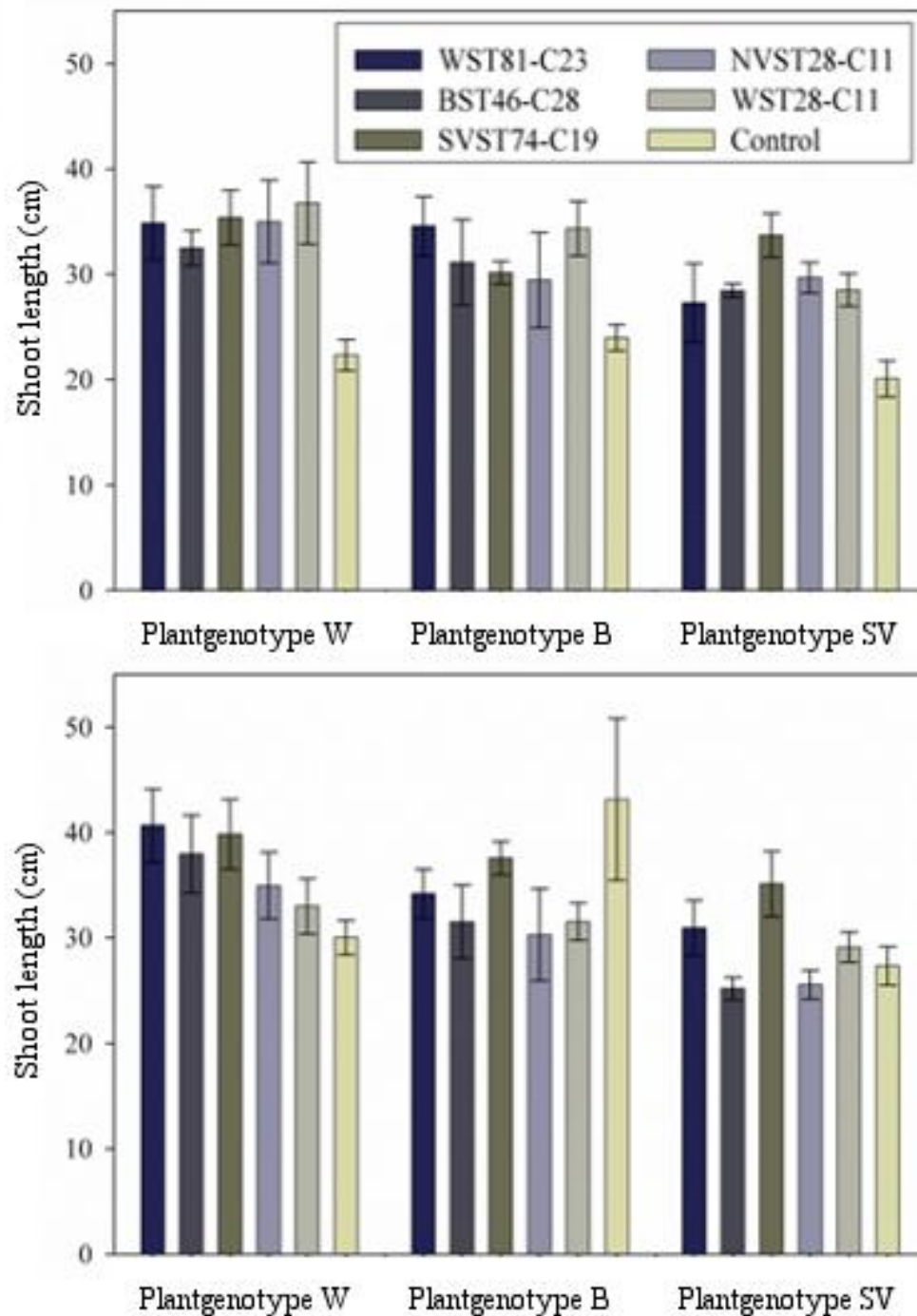


Figure A7. Mean (\pm SE) plant N content (%) in *V. cracca* genotypes from populations W, B and SV, either uninoculated (control) or in association with *R. leguminosarum* biovar *viciae* genotypes W_ST81-C23, B_ST46-C28, SV_ST74-C19, NV_ST28-C11 or W_ST28-C11 in soils with low (upper plot) and high (lower plot) N conditions.

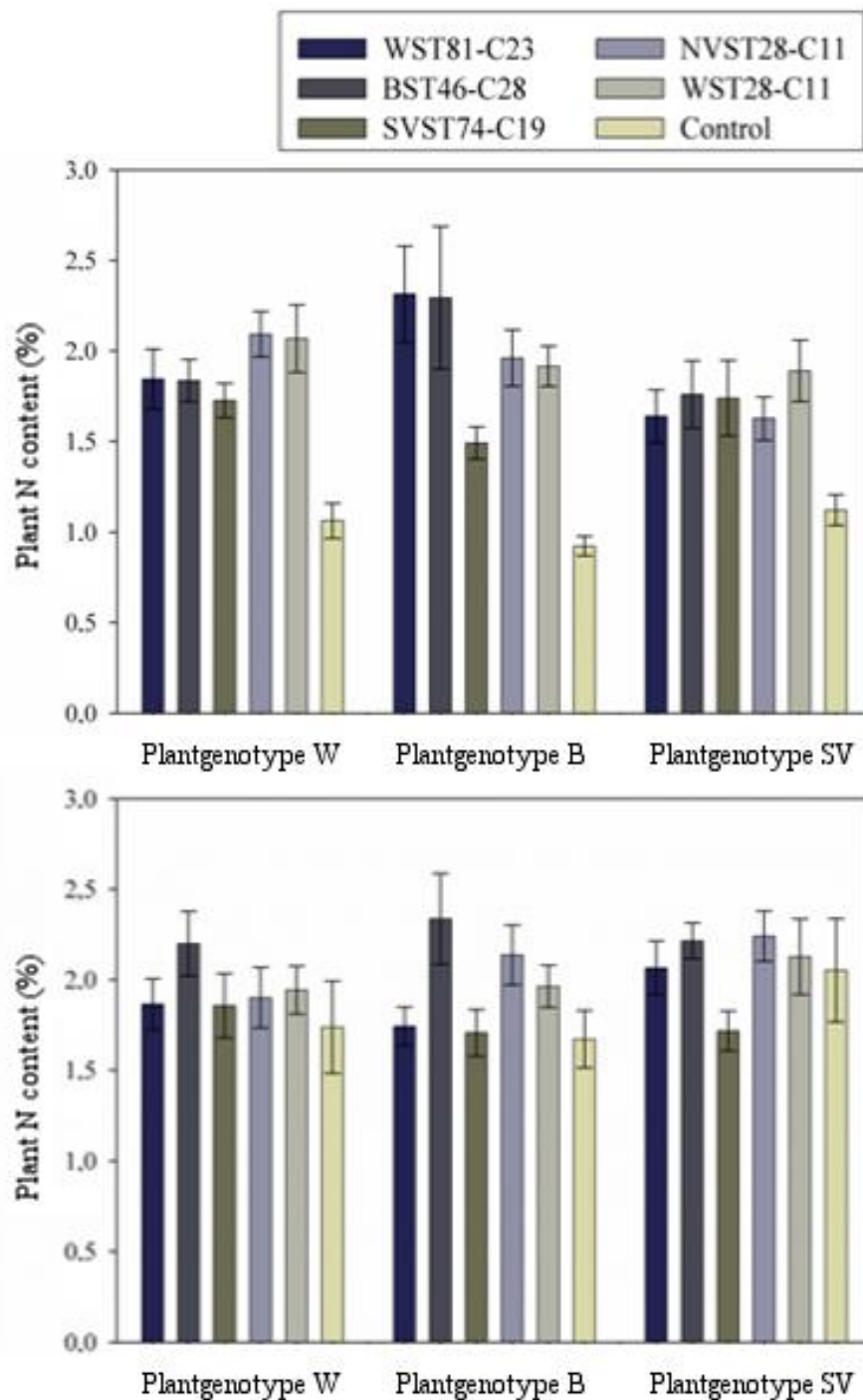


Figure A8. Mean (\pm SE) plant C content (%) in *V. cracca* genotypes from populations W, B and SV, either uninoculated (control) or in association with *R. leguminosarum* biovar *viciae* genotypes W_ST81-C23, B_ST46-C28, SV_ST74-C19, NV_ST28-C11 or W_ST28-C11 in soils with low (upper plot) and high (lower plot) N conditions.

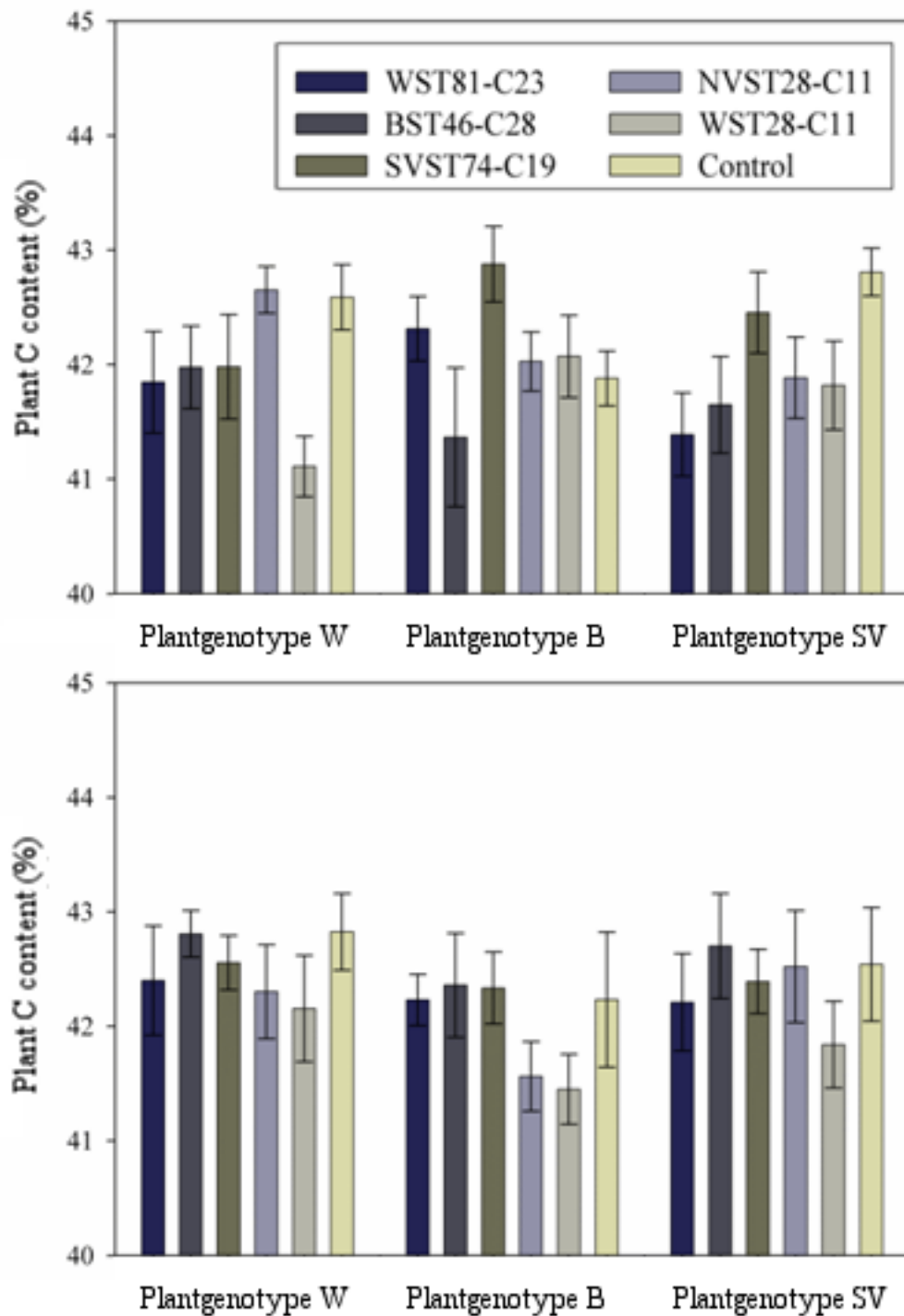


Figure A9. Mean (\pm SE) plant P content (%) in *V. cracca* genotypes from populations W, B and SV, either uninoculated (control) or in association with *R. leguminosarum* biovar *viciae* genotypes W_ST81-C23, B_ST46-C28, SV_ST74-C19, NV_ST28-C11 or W_ST28-C11 in soils with low (upper plot) and high (lower plot) N conditions. No data on plant P content was collected for uninoculated plants due to the lack of material needed for an accurate analysis.

