1 Supplementary material



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Supplementary Figure S1. Nitrogen derived from the atmosphere (Ndfa, %) estimated using
unfertilized corn or non-nodulating soybeans (Lee genotype) as the reference plant. Unfertilized
corn was growing in an eight-row strip by the side of the experiments, while the non-nodulating
soybeans was randomized along with the four tested genotypes in 2019 (A) and 2020 (B)
(Manhattan, KS). Soybean samplings occurred at similar days after emergence in both site-year
experiments. Targeted stages were the seventh leaf (V7), full flowering (R2), pod setting (R4),

9 beginning of seed filling (R5), full seed (R6), and physiological maturity (R7).



Supplementary Figure S2. Gaussian growth model describing changes on nitrogen derived 11 12 from the atmosphere (Ndfa, %) over time (days after emergence). Model parameters are the 13 maximum predicted value (m), timing of the maximum (t), and a third parameter which controls 14 growth and decay rates (c). Prior distributions were non-restrictive but introduced biological 15 knowledge to the model fitting, with black triangles representing the 95% probability intervals 16 (A). Within the high probability intervals, each individual parameter could produce contrasting 17 seasonal Ndfa shapes (B). When sampled simultaneously, non-linear parameter priors proved 18 flexible to describe Ndfa throughout the season (C). Besides the Ndfa true state (z), first (z') and 19 second (z'') derivatives were used to calculate secondary parameters of interest (D).

20 Supplementary Table S1. Soybean seed yield, seed size, seed number, protein, and oil

21 concentration for each genotype during the 2019 and 2020 growing seasons (site-years).

22 Values represent the median of estimated marginal means (emmeans) posterior distributions,

and letters represent Tukey test results (p < 0.05) within the Bayesian statistical framework.

24 Uppercase letters compare site-years within genotypes, while lowercase letters compare the

25 genotypes within site-years. Letters were omitted when treatment levels did not differ.

Genotype	Yield	Seed size ^a	Seed number ^b	Protein	Oil
	Mg ha ⁻¹	mg seed ⁻¹	seed m ⁻²	g kg ⁻¹	g kg⁻¹
2019					
Williams 82 P34T43R2 P35T75X P37T51PR	2.90 2.99 3.11 2.95	122 B 132 A 124 B 125 B	2360 2250 2500 2320	435 Aa 432 Aab 420 Abc 406 Ac	206 B 199 B 201 B 202 B
2020					
Williams 82 P34T43R2 P35T75X P37T51PR	3.24 3.52 3.43 3.63	137 A 142 A 137 A 144 A	2370 2460 2500 2500	410 Ba 400 Bab 399 Bab 392 Bb	228 A 223 A 220 A 222 A

^a Soybean seed weight; ^b Seed number was calculated based on seed yield and seed size.

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Supplementary Table S2. Logistic non-linear model parameters and means comparison for dry
matter (Mg ha⁻¹) accumulation over time (days after emergence). Uppercase letters compare the
site-years in 2019 and 2020 (Manhattan, KS), while lowercase letters compare the genotypes.
Primary model parameters are the asymptote (*m*), timing of maximum growth (*g*), and a third
parameter controlling the growth rate (*k*). Secondary model parameters are the maximum
growth rate (*r*), and the predicted value at physiological maturity (R7 stage) (*f*). Values represent

33 the median of estimated marginal means (emmeans) posterior distributions, and letters

Genotype	m	g	k	r ^a	f ^a
2019					
Williams 82	6.98 Aa	65 Aa	0.09 Aa	0.157 Aa	6.57 Ba
P34T43R2	7.74 Aa	71 Aa	0.08 Aa	0.149 Aa	6.78 Ba
P35T75X	8.10 Aa	71 Aa	0.09 Aa	0.192 Aa	7.47 Ba
P37T51PR	7.95 Aa	72 Aa	0.08 Aa	0.170 Aa	7.09 Ba
2020					
Williams 82	8.55 Aa	56 Aa	0.08 Aa	0.173 Aa	8.20 Aa
P34T43R2	9.54 Aa	60 Aa	0.08 Aa	0.202 Aa	9.06 Aa
P35T75X	9.77 Aa	62 Aa	0.08 Aa	0.188 Aa	9.10 Aa
P37T51PR	10.14 Aa	62 Aa	0.07 Aa	0.188 Aa	9.31 Aa

represent Tukey test results (p < 0.05) within the Bayesian statistical framework.

Supplementary Table S3. Logistic non-linear model parameters for total nitrogen (N) uptake, 36 uptake from the soil supply, and from the symbiotic N fixation process (kg ha⁻¹). Uppercase 37 38 letters compare the site-years (2019 and 2020, Manhattan, KS), while lowercase letters 39 compare the genotypes. Primary model parameters are *m* (asymptote), *g* (timing of maximum 40 growth in days after emergence), and k (which controls the growth rate). Secondary parameters 41 are r (maximum growth rate), and f (predicted value at physiological maturity, R7 stage). Values 42 are the median of estimated marginal means (emmeans) posterior distributions, and letters 43 represent Tukey test results (p < 0.05) within the Bayesian statistical framework.

Uptake	Genotype	m	g	k	r ^a	f ^a
Total	2019					
	Williams 82 P34T43R2 P35T75X P37T51PR	160.3 Aa 204.0 Aa 229.6 Aa 181.5 Aa	55 Aa 66 Aa 68 Aa 65 Aa	0.11 Aa 0.07 Aa 0.08 Aa 0.07 Aa	4.47 Aa 3.59 Aa 4.62 Aa 3.43 Aa	157.7 Aa 182.9 Aa 209.2 Aa 165.6 Ba
	2020					
	Williams 82 P34T43R2 P35T75X P37T51PR	181.4 Aa 221.6 Aa 224.7 Aa 228.0 Aa	48 Aa 54 Aa 54 Ba 58 Aa	0.11 Aa 0.11 Aa 0.10 Aa 0.08 Aa	5.08 Aa 5.99 Aa 5.33 Aa 4.49 Aa	179.8 Aa 218.8 Aa 220.2 Aa 216.3 Aa
Soil	2019					
	Williams 82 P34T43R2 P35T75X P37T51PR	96.2 Aa 93.3 Aa 109.8 Aa 111.4 Aa	49 Aa 49 Aa 57 Aa 58 Aa	0.16 Aa 0.11 Aa 0.10 Aa 0.07 Aa	3.80 Aa 2.40 Aa 2.76 Aa 2.02 Aa	95.9 Aa 90.8 Aa 106.1 Aa 102.2 Aa
	2020					
	Williams 82 P34T43R2 P35T75X P37T51PR	67.1 Ba 81.0 Aa 89.7 Aa 86.8 Aa	32 Ba 38 Aa 39 Ba 41 Aa	0.14 Aa 0.11 Aa 0.12 Aa 0.09 Aa	2.33 Aa 2.20 Aa 2.52 Aa 1.82 Aa	66.5 Ba 79.6 Aa 88.4 Aa 83.8 Aa
Fixation	2019					
	Williams 82 P34T43R2 P35T75X P37T51PR	101.6 Aa 117.9 Aa 134.3 Aa 76.7 Aa	83 Aa 82 Aa 83 Aa 79 Aa	0.08 Ba 0.11 Ba 0.10 Aa 0.10 Aa	2.05 Ba 3.18 Ba 3.58 Aa 2.04 Aa	76.8 Bbc 100.3 Bab 111.6 Aa 66.7 Bc
	2020					
	Williams 82 P34T43R2 P35T75X P37T51PR	112.2 Aa 133.9 Aa 120.0 Aa 122.9 Aa	55 Ba 58 Ba 57 Ba 61 Ba	0.23 Aa 0.25 Aa 0.20 Aa 0.12 Aa	6.31 Aab 8.20 Aa 5.87 Aab 3.65 Ab	112.1 Aa 133.9 Aa 119.8 Aa 119.9 Aa

45 Supplementary Table S4. Gaussian growth non-linear model parameters describing seasonal 46 changes on nitrogen derived from the atmosphere (Ndfa, %). Primary model parameters are the 47 maximum predicted value (m), timing of the maximum (t, days after emergence), and a third 48 parameter controlling growth and decay rates (c). Secondary parameters were g (timing of 49 maximum growth), r (maximum growth rate), f (predicted value at physiological maturity, R7 50 stage), and AUC (area under the curve). Values are the median of estimated marginal means 51 (emmeans) posterior distributions, and letters represent Tukey test results (p < 0.05) within the 52 Bayesian statistical framework. Uppercase letters compare the site-year from 2019 and 2020 53 (Manhattan, KS) while lowercase letters compare the four soybean genotypes.

Genotype	m	t	С	g ^a	r ^a	f ^a	AUC ^a
2019							
Williams 82 P34T43R2 P35T75X P37T51PR	46 Ba 57 Aa 51 Aa 41 Ba	110 Aa 116 Aa 110 Aa 107 Aa	7.2 Aa 6.7 Aa 7.7 Aa 6.8 Aa	60 Aa 67 Aa 58 Aa 61 Aa	0.96 Ba 1.18 Ba 1.04 Aa 0.90 Ba	44 Ba 53 Aa 49 Aa 39 Aa	15.9 Ba 16.3 Ba 18.2 Ba 13.9 Ba
2020							
Williams 82 P34T43R2 P35T75X P37T51PR	67 Aa 67 Aa 62 Aa 61 Aa	87 Aa 88 Ba 87 Aa 82 Aa	6.4 Aa 5.9 Aa 6.5 Aa 6.9 Aa	46 Aa 51 Aa 46 Aa 41 Aa	1.74 Aa 1.75 Aa 1.59 Aa 1.63 Aa	64 Aa 64 Aa 59 Aa 57 Aa	31.3 Aa 29.0 Aa 28.5 Aa 30.9 Aa

55 Supplementary Table S5. Gaussian peak non-linear model parameters for the seasonal 56 changes on soil nitrate (NO₃) and ammonia (NH₄). Both soil nitrogen forms were expressed in mg dm⁻³ and assessed over time (days after emergence). Gaussian peak primary parameters 57 58 are the baseline concentration (b), concentration at the peak (m), timing of the peak (t), and a 59 fourth parameter controlling the growth and decay rates, or width of the peak (w). Only the area 60 under the curve (AUC) was calculated as a secondary parameter. Values are the median of 61 estimated marginal means (emmeans) posterior distributions, and letters represent Tukey test 62 results (p < 0.05) within the Bayesian framework. Uppercase letters compare the site-year from 63 2019 and 2020 (Manhattan, KS), while lowercase letters compare the four genotypes.

Form	Genotype	b	m	t	w	AUC ^a
NO ₃	2019					
	Williams 82 P34T43R2 P35T75X P37T51PR	0.07 Aa 0.07 Aa 0.07 Aa 0.07 Aa	23.81 Aa 14.82 Ab 17.13 Aab 19 28 Aab	50 Aa 48 Aa 48 Aa 48 Aa	18.1 Aa 21.7 Aa 20.4 Aa 21 5 Aa	749 Aa 574 Aa 611 Aa 731 Aa
	2020		10.207.00	10714	2110710	rorra
	Williams 82 P34T43R2 P35T75X P37T51PR	0.07 Aa 0.07 Aa 0.07 Aa 0.07 Aa	13.98 Ba 19.75 Aa 22.72 Aa 26.71 Aa	11 Ba 7 Ba 5 Ba 5 Ba	27.7 Aa 28.0 Aa 27.0 Aa 24.9 Aa	487 Aa 635 Aa 660 Aa 700 Aa
NH ₄	2019					
	Williams 82 P34T43R2 P35T75X P37T51PR	6.31 Aa 5.88 Aa 5.84 Aa 5.89 Aa	8.07 Aa 10.34 Aa 8.70 Aa 6.16 Aa	123 Aa 122 Aa 128 Aa 117 Aa	32.2 Aa 26.8 Aa 31.9 Aa 37.4 Aa	693 Aa 641 Aa 624 Aa 684 Aa
	2020					
	Williams 82 P34T43R2 P35T75X P37T51PR	4.37 Ba 4.44 Ba 4.22 Ba 4 20 Ba	7.50 Aa 6.69 Aa 6.55 Aa 8 29 Aa	34 Ba 33 Ba 34 Ba 34 Ba	10.0 Ba 10.4 Ba 11.7 Ba 9 0 Ba	559 Ba 557 Ba 546 Ba 544 Ba



Supplementary Figure S3. Dilution curves for total nitrogen (N) (A-D) and fixed N (E-H) 66 67 concentration in the aboveground dry matter (shoot). Panel columns represent the four soybean genotypes and colors represent the site-year from 2019 and 2020 (Manhattan, KS). Exponential 68 69 non-linear model parameters are presented and compared within each panel. The first value 70 represents u (N concentration when dry matter equals to one) and the second value represents 71 k (which controls exponential growth or decay). Values are the median of estimated marginal 72 means (emmeans) posterior distributions, and letters represent Tukey test results (p < 0.05). 73 Uppercase letters compare site-years and lowercase letters compare genotypes. The last 74 sampling (at the R7 stage) was removed to avoid potential variation due to leaf senescence. 75 Coefficient of determination (R²) and root mean squared errors (RMSE) were presented.



Supplementary Figure S4. Database from Ciampitti and Salvagiotti (2018) showing the
relationship between nitrogen (N) uptake (kg ha⁻¹) and aboveground dry matter (Mg ha⁻¹) at
physiological maturity (R7 stage). Boundary functions were fitted over the 10th and 90th
percentiles for total N uptake and fixed N (A). Nitrogen derived from the atmosphere (Ndfa, %)
is presented across different levels of N uptake (B) and fixed N (C). Observations with lower
Ndfa are located close to the lower boundary of fixed N and vice-versa, reasonably explaining a
wider range of variation for fixed N than for total N uptake across similar dry matter levels.