Supplementary Tables

Supplemental Table S1: Leaf area (LA) at the start and end of the experiment, water use (WU) and transpiration efficiency (TE) of 8 wild banana genotypes during the Phenodyn phenotyping experiment for well-watered (WW) and water deficit plants (WD). Data represent mean \pm se (n = 7-8). Note that at the start of the experiment plants there was not yet a separation between WW and WD (n=15-16). Additionally, LA at the start were obtained non-destructively by calibrating top and side view images as described in Eq. 1. Different letters indicate significant differences between genotypes and treatments (P < 0.05; A>B>C>D>E>F). G represents the genotype-effect, T the treatment effect and G x T the genotype treatment interaction (*** for P<0.001, NA; not applicable).

genotype	LA at start (m²)	LA at end (m²)		WU (g H₂O/day)		TE (g FW/I H ₂ 0)	
	NA	ww	WD	ww	WD	ww	WD
Balbisiana	0.020±0.001(E)	0.24±0.01(G)	0.15±0.01(HI)	178.3±6.6(D)	92.3±7.6(I)	85.3±4.3(DEF)	101.5±3.9(CDE)
Banksii_11	0.052±0.002(B)	0.53±0.02(B)	0.34±0.01(E)	365.4±15.2(A)	160.9±6.6(DEF)	87.1±3(DEF)	117.7±4.3(BC)
Banksii_17	0.062±0.002(A)	0.62±0.02(A)	0.36±0.01(E)	359.8±19.4(A)	147.7±8.8(DEF)	90.8±4.4(DEF)	113±5.9(BC)
Burmannicoides	0.066±0.002(A)	0.54±0.02(B)	0.35±0.01(E)	335.2±8.8(AB)	173.7±12.9(DE)	72.2±2.4(F)	88.7±2.6(DEF)
Errans	0.03±0.001(D)	0.18±0.02(H)	0.12±0.01(I)	113.3±9(GHI)	46.9±6.2(J)	100±4.1(CDE)	169.4±18.8(A)
Malaccensis_33	0.042±0.002(C)	0.43±0.01(D)	0.29±0.01(F)	239.3±16.8(C)	104±6.4(HI)	90.6±4.9(DEF)	123.4±6.8(B)
Malaccensis_ITC0074	0.065±0.002(A)	0.47±0.02(C)	0.32±0.01(EF)	267.7±10.2(C)	143.4±7.5(EFG)	86.4±2.4(DEF)	104.6±4.1(BCD)
Microcarpa	0.032±0.002(D)	0.47±0.02(CD)	0.29±0.01(F)	312.2±14.6(B)	129±9.7(FGH)	82.5±2.4(EF)	119.1±7.4(BC)
G	***	***		***		***	
Т	NA	***		***		***	
GxT	NA	***		***		***	

Supplemental Table S2: Leaf area (LA) at the start and end of the experiment, water use (WU) and transpiration efficiency (TE) of 3 wild banana genotypes during the second phenotyping experiment for well-watered (WW) and water deficit plants (WD). Data of LA represent mean \pm se of the second set of plants put on the balances ($n_{WW} = 4 \& n_{WD} = 4$), data of WU and TE represent mean \pm se of the all plants included in the experiment ($n_{WW} = 4 \& n_{WD} = 8$). Note that at the start of the experiment plants there was not yet a separation between WW and WD. Additionally, LA at the start were obtained non-destructively by calibrating top and side view images as described in Eq. 1.Different letters indicate significant differences between genotypes and treatments (P < 0.05; A>B>C). G represents the genotype-effect, T the treatment effect and G x T the genotype treatment interaction (n.s. for not significant, ** for P < 0.01, *** for P < 0.001; NA; not applicable).

genotype	LA at start (m²)	LA at end (m²)		WU (g H₂O/day)		TE (g FW/I H₂0)	
	NA	ww	WD	ww	WD	ww	WD
Balbisiana	0.037±0.002 (B)	0.60 ±0.06 (B)	0.50±0.03 (B)	175.1±16.9 (B)	114.9±8.6 (C)	70.1±2.8 (A)	57.3±7 (A)
Banksii_11	0.059±0.003 (A)	1.26±0.14 (A)	0.67±0.04 (B)	335.4±30.1 (A)	125±8 (C)	79.2±5 (A)	72.5±11.5 (A)
Malaccensis_33	0.069±0.007 (A)	1.33±0.10 (A)	0.71±0.07 (B)	325.6±15.9 (A)	127.1±11.1 (C)	84.6±1.4 (A)	67.3±12.2 (A)
G	***	***		***		n.s.	
Т	NA	***		***		n.s.	
GxT	NA	**		***		n.s.	

Supplemental Table S3: Parameter estimates of the Jarvis-Stewart model for both phenotyping experiments (Eq 9-12). Data represent the optimal parameter value and the 95% confidence interval within brackets. E_{max} represents the maximum transpiration rate; SWC_{crit} ; critical soil water content threshold at which transpiration rate starts to decrease; SWC_{slope} ; slope of transpiration rate decrease with decreasing soil water content after SWC_{crit} ; SWC_{wilt} , the soil water content at which water uptake and consequently transpiration is halted; k_1 , parameter describing the sensitivity of the light response; k_2 , parameter describing the sensitivity of the vapour pressure deficit response.

genotype	E _{max} (g cm ⁻² h ⁻¹)	SWC _{crit} (g g ⁻¹)	SWC _{slope} (g cm ⁻² h ⁻¹)	SWC _{wilt} (g g ⁻¹)	k ₁	k ₂		
High-throughput phenotyping experiment								
Balbisiana	0.024 [0.023;0.026]	1.10 [1.08;1.13]	0.030 [0.028;0.32]	0.29 [0.26;0.30]	58.22 [51.62;65.37]	0.31 [0.28;0.33]		
Banksii_11	0.020 [0.019;0.021]	1.18 [1.17;1.19]	0.023 [0.022;0.024]	0.31 [0.30;0.33]	48.79 [43.34;54.33]	0.29 [0.27;0.31]		
Banksii_17.8.1	0.022 [0.021;0.023]	1.20 [1.19;1.21]	0.026 [0.025;0.028]	0.38 [0.36;0.39]	95.29 [85.79;104.55]	0.27 [0.24;0.29]		
Burmannicoides	0.020 [0.019;0.021]	1.21 [1.21;1.22]	0.021 [0.020;0.022]	0.28 [0.26;0.29]	45.91 [39.01;52.54]	0.24 [0.21;0.26]		
Errans	0.021 [0.020;0.022]	1.38 [1.35;1.40]	0.030 [0.029;0.032]	0.68 [0.67;0.69]	53.21 [46.56;59.88]	0.24 [0.21;0.26]		
Malaccensis_33	0.015 [0.015;0.016]	1.28 [1.27;1.28]	0.016 [0.016;0.017]	0.34 [0.33;0.36]	28.21 [23.14;33.08]	0.26 [0.24;0.29]		
Malaccensis_ITC0074	0.018 [0.018;0.019]	1.23 [1.21;1.25]	0.018 [0.017;0.020]	0.22 [0.20;0.24]	41.96 [33.16;51.51]	0.20 [0.18;0.22]		
Microcarpa	0.024 [0.023;0.025]	1.20 [1.19;1.21]	0.028 [0.027;0.030]	0.37 [0.36;0.38]	54.56 [48.90;60.41]	0.23 [0.21;0.26]		
Validation phenotyping experiment								
Balbisiana	0.033 [0.032;0.035]	1.82 [1.77;1.88]	0.023 [0.021;0.024]	0.35 [0.29;0.29]	109.61 [94.43;129.82]	0.08 [0.07;0.10]		
Banksii_11	0.027 [0.026;0.028]	2.14 [2.11;2.17]	0.017 [0.016;0.017]	0.53 [0.51;0.51]	75.69 [68.22;84.38]	0.13 [0.12;0.14]		
Malaccensis_33	0.023 [0.022;0.024]	2.06 [2.03;2.09]	0.015 [0.015;0.016]	0.57 [0.54;0.54]	164.45 [133.34;203.50]	0.11 [0.08;0.13]		