Defining soil water regimes for screening waterlogging tolerance in tropical forage grasses

SUPPLEMENTARY TABLES

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Table S1. Analysis of variance for green, yellow, and total leaf numbers of *Megathyrsus maximus* genotypes subjected to different soil water availability levels.

Trait	Source of variation	df	MS	F-value	p-value
Green leaf number	Blocks	3	1.5458	0.5134	0.67466
	Genotypes (G)	4	1773.6250	589.0983	<0.00001
	Soil water availability (W)	3	419.2125	139.2388	<0.00001
	G × W	12	35.3583	11.7440	<0.00001
	Residual	57	3.0108	—	—
Yellow leaf number	Blocks	3	1.5125	1.8261	0.15268
	Genotypes (G)	4	19.8938	24.0179	<0.00001
	Soil water availability (W)	3	2.8458	3.4358	0.02274
	G × W	12	0.6688	0.8074	0.64157
	Residual	57	0.8283	—	—
Total leaf number	Blocks	3	3.0833	0.7820	0.50891
	Genotypes (G)	4	2065.8938	523.9419	<0.00001
	Soil water availability (W)	3	373.6500	94.7633	<0.00001
	G × W	12	31.9500	8.1029	<0.00001
	Residual	57	3.9430	—	—

Note: df = degrees of freedom; MS = mean square; F-value = calculated F statistic; p-value = probability associated with the F-test; G × W = genotype × soil water availability interaction. Significance was assessed at $p < 0.05$.

Table S2. Treatment means and standard errors for green, yellow, and total leaf numbers in *Megathyrsus maximus* genotypes under different soil water availability levels.

Genotype	Soil water availability (%)	Green leaf Number	Yellow leaf number	Total leaf number
Mombaça	60	13.25 ± 0.25	1.50 ± 0.29	14.75 ± 0.48
	80	12.75 ± 0.63	1.75 ± 0.25	14.50 ± 0.50
	100	15.00 ± 0.41	1.75 ± 0.25	16.75 ± 0.63
	120	7.75 ± 0.63	1.25 ± 0.25	9.00 ± 0.71
BRS Tamani	60	35.75 ± 1.25	3.25 ± 1.31	39.00 ± 1.29
	80	38.75 ± 1.11	2.75 ± 0.48	41.50 ± 1.55
	100	36.50 ± 1.19	3.50 ± 0.87	40.00 ± 1.87
	120	30.25 ± 1.38	4.25 ± 0.25	34.50 ± 1.32
BRS Zuri	60	16.50 ± 0.96	0.50 ± 0.29	17.00 ± 1.08
	80	18.25 ± 0.85	0.00 ± 0.00	18.25 ± 0.85
	100	15.00 ± 0.41	1.00 ± 0.41	16.00 ± 0.71
	120	5.00 ± 0.00	1.00 ± 0.41	6.00 ± 0.41
PM18	60	14.00 ± 0.91	1.25 ± 0.25	15.25 ± 0.75
	80	12.75 ± 0.85	0.75 ± 0.25	13.50 ± 0.96
	100	12.00 ± 0.91	1.25 ± 0.25	13.25 ± 0.85
	120	9.00 ± 0.41	1.25 ± 0.48	10.25 ± 0.85
PM21	60	28.00 ± 0.71	0.25 ± 0.25	28.25 ± 0.85
	80	33.25 ± 0.85	0.25 ± 0.25	33.50 ± 0.65
	100	31.25 ± 1.11	1.50 ± 0.29	32.75 ± 1.18
	120	13.75 ± 0.85	1.75 ± 0.48	15.50 ± 0.87

Note: Values are presented as mean ± standard error (SE), calculated from four independent replicates (n = 4) per genotype × soil water availability combination. SE was calculated as the sample standard deviation divided by the square root of the number of replicates. Soil water availability is expressed as a percentage of pot water capacity.

Table S3. Analysis of variance for tiller number, leaf elongation rate, and SPAD index of *Megathyrsus maximus* genotypes subjected to different soil water availability levels.

Trait	Source of variation	df	MS	F-value	p-value
Tiller number	Blocks	3	1.246	1.392	0.25451
	Genotype (G)	4	247.419	276.459	<0.00001
	Soil water availability (W)	3	28.246	31.561	<0.00001
	G × W	12	4.194	4.686	0.00003
	Residual	57	0.895	—	—
Leaf elongation rate	Blocks	3	0.676	0.786	0.50653
	Genotype (G)	4	63.995	74.426	<0.00001
	Soil water availability (W)	3	21.867	25.431	<0.00001
	G × W	12	3.516	4.089	0.00014
	Residual	57	0.860	—	—
SPAD index	Blocks	3	18.27	1.2493	0.300447
	Genotype (G)	4	330.04	22.5712	<0.000001
	Soil water availability (W)	3	102.65	7.0205	0.000424
	G × W	12	30.97	2.1178	0.029760
	Residual	57	14.62	—	—

df = degrees of freedom; MS = mean square; F-value = calculated F statistic; p-value = probability associated with the F-test; G × W = genotype × soil water availability interaction. Significance was assessed at $p < 0.05$.

Table S4. Treatment means and standard errors for tiller number, leaf elongation rate, and SPAD index in *Megathyrsus maximus* genotypes under different soil water availability levels.

Genotype	Soil water availability (%)	Tiller number	Leaf elongation rate	SPAD index
Mombaça	60	3.25 ± 0.25	8.69 ± 0.25	27.02 ± 1.38
	80	3.00 ± 0.41	11.09 ± 0.30	28.30 ± 1.32
	100	3.75 ± 0.48	10.88 ± 0.67	27.65 ± 1.88
	120	2.00 ± 0.41	9.87 ± 0.30	30.17 ± 1.87
BRS Tamani	60	11.75 ± 0.85	6.77 ± 0.71	25.80 ± 1.98
	80	11.00 ± 0.41	6.51 ± 0.52	26.93 ± 1.50
	100	12.00 ± 0.41	7.37 ± 0.58	25.60 ± 2.27
	120	10.50 ± 0.65	5.56 ± 0.22	23.12 ± 0.60
BRS Zuri	60	4.25 ± 0.48	11.81 ± 0.65	31.58 ± 3.00
	80	5.25 ± 0.48	12.74 ± 0.24	35.90 ± 1.63
	100	4.25 ± 0.25	11.89 ± 0.80	35.08 ± 2.31
	120	1.00 ± 0.00	9.86 ± 0.10	28.88 ± 2.60
PM18	60	2.50 ± 0.29	10.04 ± 0.65	30.75 ± 2.48
	80	2.75 ± 0.48	11.95 ± 0.48	36.52 ± 2.52
	100	3.00 ± 0.41	11.69 ± 0.50	35.00 ± 2.33
	120	2.00 ± 0.41	9.46 ± 0.27	28.85 ± 1.06
PM21	60	9.25 ± 0.48	10.02 ± 0.26	41.83 ± 2.04
	80	10.75 ± 0.63	9.84 ± 0.13	40.67 ± 1.39
	100	10.00 ± 0.71	8.68 ± 0.34	35.82 ± 1.33
	120	5.00 ± 0.41	5.58 ± 0.29	30.05 ± 1.00

Note: Values are presented as mean ± standard error (SE), calculated from four independent replicates (n = 4) per genotype × soil water availability combination. SE was calculated as the sample standard deviation divided by the square root of the number of replicates. Soil water availability is expressed as a percentage of pot water capacity.

Table S5. Analysis of variance for green, yellow, senescent, and total leaf numbers in *Urochloa* spp. genotypes subjected to different soil water availability levels.

Trait	Source of variation	df	MS	F-value	p-value
Green leaf number	Blocks	3	4.8125	1.1559	0.33457
	Genotype (G)	4	3087.9375	741.6905	<0.00001
	Soil water availability (W)	3	676.2458	162.4272	<0.00001
	G × W	12	30.3708	7.2948	<0.00001
	Residual	57	4.1634	—	—
Yellow leaf number	Blocks	3	0.0792	1.4979	0.22485
	Genotype (G)	4	0.0813	1.5373	0.20364
	Soil water availability (W)	3	0.6125	11.5892	0.000005
	G × W	12	0.0813	1.5373	0.13777
	Residual	57	0.0529	—	—
Senescent leaf number	Blocks	3	0.0125	0.3220	0.80940
	Genotype (G)	4	0.9688	24.9576	<0.00001
	Soil water availability (W)	3	15.3125	394.4915	<0.00001
	G × W	12	0.9688	24.9576	<0.00001
	Residual	57	0.0388	—	—
Total leaf number	Blocks	3	4.5125	1.0280	0.38711
	Genotype (G)	4	2961.4250	674.6315	<0.00001
	Soil water availability (W)	3	455.0458	103.6623	<0.00001
	G × W	12	27.7750	6.3273	<0.00001
	Residual	57	4.3897	—	—

Note: df = degrees of freedom; MS = mean square; F-value = calculated F statistic; p-value = probability associated with the F-test; G × W = genotype × soil water availability interaction. Significance was assessed at $p < 0.05$.

Table S6. Treatment means and standard errors for green, yellow, senescent, and total leaf numbers in *Urochloa* spp. genotypes under different soil water availability levels.

Genotype	Soil water availability (%)	Green leaf number	Yellow leaf number	Senescent leaf number	Total leaf number
U. humidicola	60	49.25 ± 2.29	0.00 ± 0.00	0.00 ± 0.00	49.25 ± 2.29
	80	53.50 ± 1.26	0.00 ± 0.00	0.00 ± 0.00	53.50 ± 1.26
	100	55.75 ± 1.93	0.00 ± 0.00	0.00 ± 0.00	55.75 ± 1.93
	120	45.00 ± 1.08	0.00 ± 0.00	0.00 ± 0.00	45.00 ± 1.08
Marandu	60	23.00 ± 1.08	0.00 ± 0.00	0.00 ± 0.00	23.00 ± 1.08
	80	27.00 ± 0.71	0.00 ± 0.00	0.00 ± 0.00	27.00 ± 0.71
	100	26.50 ± 0.65	0.00 ± 0.00	0.00 ± 0.00	26.50 ± 0.65
	120	11.50 ± 0.65	0.25 ± 0.25	3.00 ± 0.41	14.75 ± 0.95
Xaraés	60	29.50 ± 0.65	0.00 ± 0.00	0.00 ± 0.00	29.50 ± 0.65
	80	31.25 ± 0.85	0.00 ± 0.00	0.00 ± 0.00	31.25 ± 0.85
	100	30.75 ± 1.11	0.00 ± 0.00	0.00 ± 0.00	30.75 ± 1.11
	120	14.50 ± 0.65	0.25 ± 0.25	1.25 ± 0.25	16.00 ± 0.58
Mulato II	60	20.50 ± 0.65	0.00 ± 0.00	0.00 ± 0.00	20.50 ± 0.65
	80	22.50 ± 0.65	0.00 ± 0.00	0.00 ± 0.00	22.50 ± 0.65
	100	19.75 ± 0.85	0.00 ± 0.00	0.00 ± 0.00	19.75 ± 0.85
	120	12.00 ± 0.41	0.75 ± 0.25	2.25 ± 0.25	15.00 ± 0.41
Ub001	60	23.25 ± 1.11	0.00 ± 0.00	0.00 ± 0.00	23.25 ± 1.11
	80	16.75 ± 0.48	0.00 ± 0.00	0.00 ± 0.00	16.75 ± 0.48
	100	18.25 ± 0.63	0.00 ± 0.00	0.00 ± 0.00	18.25 ± 0.63
	120	8.25 ± 0.63	0.50 ± 0.29	2.00 ± 0.00	10.75 ± 0.85

Note: Values are presented as mean ± standard error (SE), calculated from four independent replicates (n = 4) per genotype × soil water availability combination. SE was calculated as the sample standard deviation divided by the square root of the number of replicates. Total leaf number was calculated as the sum of green, yellow, and senescent leaves.

Table S7. Analysis of variance for tiller number, leaf elongation rate, and SPAD index in *Urochloa* spp. genotypes under different soil water availability levels.

Trait	Source of variation	df	MS	F-value	p-value
Tiller number	Blocks	3	1.2333	0.9398	0.42749
	Genotype (G)	4	106.4813	81.1421	<0.00001
	Soil water availability (W)	3	31.3000	23.8516	<0.00001
	G × W	12	8.3729	6.3804	<0.00001
	Residual	57	1.3123	—	—
Leaf elongation rate	Blocks	3	0.3324	0.6010	0.61673
	Genotype (G)	4	23.9975	43.4180	<0.00001
	Soil water availability (W)	3	24.0994	43.6030	<0.00001
	G × W	12	0.9626	1.7420	0.08160
	Residual	57	0.5527	—	—
SPAD index	Blocks	3	3.2552	0.6286	0.59950
	Genotype (G)	4	85.2308	16.4597	<0.00001
	Soil water availability (W)	3	979.8045	189.2191	<0.00001
	G × W	12	23.1116	4.4633	0.00005
	Residual	57	5.1781	—	—

Note: df = degrees of freedom; MS = mean square; F-value = calculated F statistic; p-value = probability associated with the F-test; G × W = genotype × soil water availability interaction. Significance was assessed at $p < 0.05$.

Table S8. Treatment means and standard errors for tiller number, leaf elongation rate, and SPAD index in *Urochloa* spp. genotypes under different soil water availability levels.

Genotype	Soil water availability (%)	Tiller number	Leaf elongation rate	SPAD index
U. humidicola	60	10.25 ± 0.75	4.25 ± 0.40	41.20 ± 0.98
	80	11.75 ± 0.63	4.05 ± 0.52	40.72 ± 1.05
	100	9.25 ± 0.63	4.37 ± 0.16	40.60 ± 1.30
	120	12.00 ± 0.91	3.33 ± 0.18	33.52 ± 1.73
Marandu	60	6.00 ± 0.41	7.01 ± 0.37	48.00 ± 1.44
	80	7.50 ± 0.65	6.53 ± 0.38	46.55 ± 0.60
	100	7.25 ± 0.63	7.19 ± 0.32	47.85 ± 1.18
	120	2.75 ± 0.25	4.31 ± 0.04	30.45 ± 1.27
Xaraés	60	9.25 ± 0.63	5.49 ± 0.15	47.75 ± 1.35
	80	8.50 ± 0.65	5.47 ± 0.41	48.92 ± 0.84
	100	8.50 ± 0.29	5.49 ± 0.20	47.55 ± 1.22
	120	3.50 ± 0.29	2.99 ± 0.10	34.88 ± 0.51
Mulato II	60	5.75 ± 0.75	7.76 ± 0.66	48.68 ± 0.79
	80	6.00 ± 0.41	7.19 ± 0.30	45.20 ± 1.10
	100	5.50 ± 0.65	6.68 ± 0.75	50.50 ± 0.79
	120	3.25 ± 0.25	4.24 ± 0.16	31.28 ± 0.52
Ub001	60	5.00 ± 0.71	4.08 ± 0.44	46.85 ± 1.34
	80	4.25 ± 0.48	4.32 ± 0.43	49.72 ± 1.36
	100	5.00 ± 0.41	4.70 ± 0.21	47.62 ± 1.45
	120	2.75 ± 0.48	2.38 ± 0.21	32.50 ± 0.72

Note: Values are presented as mean ± standard error (SE), calculated from four independent replicates (n = 4) per genotype × soil water availability combination. SE was calculated as the sample standard deviation divided by the square root of the number of replicates. Soil water availability is expressed as a percentage of pot water capacity.

Table S9. Analysis of variance for leaf blade, stem, root, and total dry mass of *Megathyrsus maximus* genotypes subjected to different soil water availability levels.

Trait	Source of variation	df	MS	F-value	p-value
Leaf blade dry mass	Blocks	3	0.2215	2.150	0.10393
	Genotype (G)	4	31.0199	301.057	<0.00001
	Soil water availability (W)	3	22.7008	220.317	<0.00001
	G × W	12	2.3370	22.682	<0.00001
	Residual	57	0.1030	—	—
Stem dry mass	Blocks	3	0.109	1.05	0.37874
	Genotype (G)	4	45.484	436.52	<0.00001
	Soil water availability (W)	3	6.571	63.06	<0.00001
	G × W	12	3.438	33.00	<0.00001
	Residual	57	0.104	—	—
Root dry mass	Blocks	3	0.233	3.50	0.021049
	Genotype (G)	4	35.939	539.49	<0.00001
	Soil water availability (W)	3	29.399	441.32	<0.00001
	G × W	12	1.076	16.16	<0.00001
	Residual	57	0.067	—	—
Total dry mass	Blocks	3	0.362	0.89	0.45106
	Genotype (G)	4	298.017	734.58	<0.00001
	Soil water availability (W)	3	161.868	398.99	<0.00001
	G × W	12	9.157	22.57	<0.00001
	Residual	57	0.406	—	—

Note: df = degrees of freedom; MS = mean square; F-value = calculated F statistic; p-value = probability associated with the F-test; G × W = genotype × soil water availability interaction. Significance was assessed at $p < 0.05$.

Table S10. Treatment means and standard errors for leaf, stem, root, and total dry mass in *Megathyrsus maximus* genotypes under different soil water availability levels.

Genotype	Soil water availability (%)	Leaf dry mass	Stem dry mass	Root dry mass	Total dry mass
Mombaça	60	8.12 ± 0.20	6.10 ± 0.08	5.59 ± 0.20	19.81 ± 0.42
	80	7.42 ± 0.26	5.00 ± 0.18	5.38 ± 0.19	17.80 ± 0.53
	100	7.50 ± 0.07	5.59 ± 0.23	5.57 ± 0.17	18.67 ± 0.24
	120	4.88 ± 0.12	4.91 ± 0.17	2.95 ± 0.11	12.75 ± 0.12
BRS Tamani	60	6.75 ± 0.20	4.84 ± 0.11	6.02 ± 0.19	17.61 ± 0.27
	80	6.49 ± 0.22	5.00 ± 0.21	6.78 ± 0.14	18.27 ± 0.48
	100	5.73 ± 0.14	5.12 ± 0.13	4.77 ± 0.09	15.62 ± 0.26
	120	5.84 ± 0.12	6.06 ± 0.13	3.14 ± 0.08	15.03 ± 0.22
BRS Zuri	60	6.31 ± 0.15	4.42 ± 0.17	4.10 ± 0.14	14.84 ± 0.17
	80	6.40 ± 0.24	4.90 ± 0.09	3.48 ± 0.09	14.78 ± 0.38
	100	6.53 ± 0.21	4.55 ± 0.17	3.68 ± 0.14	14.76 ± 0.20
	120	2.48 ± 0.20	2.60 ± 0.08	2.01 ± 0.12	7.08 ± 0.37
PM18	60	7.21 ± 0.09	9.50 ± 0.21	6.35 ± 0.17	23.05 ± 0.32
	80	7.09 ± 0.13	8.16 ± 0.24	5.94 ± 0.15	21.18 ± 0.17
	100	6.22 ± 0.19	6.85 ± 0.20	5.74 ± 0.15	18.81 ± 0.52
	120	5.55 ± 0.14	6.50 ± 0.14	2.82 ± 0.13	14.87 ± 0.12
PM21	60	3.34 ± 0.05	3.09 ± 0.11	2.09 ± 0.11	8.53 ± 0.20
	80	4.41 ± 0.22	4.55 ± 0.20	2.21 ± 0.09	11.17 ± 0.45
	100	4.08 ± 0.06	3.86 ± 0.15	2.38 ± 0.09	10.31 ± 0.22
	120	1.92 ± 0.06	1.66 ± 0.08	0.44 ± 0.04	4.02 ± 0.11

Note: Values are presented as mean ± standard error (SE), calculated from four independent replicates (n = 4) per genotype × soil water availability combination. SE was calculated as the sample standard deviation divided by the square root of the number of replicates. Soil water availability is expressed as a percentage of pot water capacity.

Table S11. Analysis of variance for leaf blade, stem, root, and total dry mass in *Urochloa* spp. genotypes under different soil water availability levels.

Trait	Source of variation	df	MS	F-value	p-value
Leaf blade dry mass	Blocks	3	1.1043	2.058	0.115936
	Genotype (G)	4	23.6096	44.002	<0.00001
	Soil water availability (W)	3	17.2864	32.217	<0.00001
	G × W	12	1.3518	2.519	0.009837
	Residual	57	0.5366	—	—
Stem dry mass	Blocks	3	0.5373	2.854	0.045073
	Genotype (G)	4	0.9410	4.998	0.001595
	Soil water availability (W)	3	14.4154	76.577	<0.00001
	G × W	12	1.0401	5.525	0.000004
	Residual	57	0.1882	—	—
Root dry mass	Blocks	3	3.520	1.8252	0.152837
	Genotype (G)	4	38.540	19.9814	<0.00001
	Soil water availability (W)	3	38.168	19.7889	<0.00001
	G × W	12	5.850	3.0330	0.002373
	Residual	57	1.929	—	—
Total dry mass	Blocks	3	8.800	1.883	0.142704
	Genotype (G)	4	108.241	23.161	<0.00001
	Soil water availability (W)	3	191.019	40.873	<0.00001
	G × W	12	17.696	3.786	0.000307
	Residual	57	4.673	—	—

Note: df = degrees of freedom; MS = mean square; F-value = calculated F statistic; p-value = probability associated with the F-test; G × W = genotype × soil water availability interaction. Significance was assessed at $p < 0.05$.

Table S12. Treatment means and standard errors for leaf, stem, root, and total dry mass in *Urochloa* spp. genotypes under different soil water availability levels.

Genotype	Soil water availability (%)	Leaf dry mass	Stem dry mass	Root dry mass	Total dry mass
U. humidicola	60	11.86 ± 0.24	13.05 ± 0.33	8.83 ± 0.20	33.75 ± 0.66
	80	12.11 ± 0.26	13.37 ± 0.33	9.26 ± 0.35	34.73 ± 0.93
	100	12.18 ± 0.36	14.34 ± 0.13	8.00 ± 1.56	34.52 ± 2.02
	120	12.01 ± 0.27	13.26 ± 0.19	9.45 ± 0.29	34.72 ± 0.61
Marandu	60	13.82 ± 0.47	13.17 ± 0.34	12.25 ± 0.94	39.24 ± 1.68
	80	15.05 ± 0.20	14.25 ± 0.20	13.20 ± 0.63	42.50 ± 0.84
	100	14.90 ± 0.19	14.35 ± 0.18	12.35 ± 0.76	41.61 ± 0.91
	120	12.37 ± 0.23	11.92 ± 0.21	8.80 ± 0.20	33.09 ± 0.61
Xaraés	60	14.74 ± 0.20	13.37 ± 0.15	14.80 ± 1.04	42.91 ± 1.27
	80	14.86 ± 0.31	13.20 ± 0.25	14.63 ± 0.68	42.68 ± 0.51
	100	15.09 ± 0.20	13.80 ± 0.10	13.47 ± 0.37	42.35 ± 0.57
	120	12.38 ± 0.18	11.80 ± 0.27	9.21 ± 0.31	33.39 ± 0.65
Mulato II	60	15.71 ± 0.27	14.11 ± 0.21	12.66 ± 0.61	42.48 ± 0.83
	80	15.89 ± 0.36	14.28 ± 0.14	12.93 ± 0.62	43.09 ± 1.06
	100	15.19 ± 0.52	13.87 ± 0.18	11.21 ± 0.44	40.26 ± 0.90
	120	13.16 ± 0.23	12.04 ± 0.08	8.71 ± 0.09	33.90 ± 0.30
Ub001	60	12.92 ± 0.71	13.66 ± 0.18	10.57 ± 1.10	37.15 ± 1.84
	80	13.19 ± 0.85	13.67 ± 0.09	10.57 ± 0.96	37.44 ± 1.76
	100	13.25 ± 0.39	13.59 ± 0.35	10.91 ± 0.48	37.74 ± 1.17
	120	11.21 ± 0.16	11.45 ± 0.29	9.11 ± 0.61	31.77 ± 0.85

Note: Values are presented as mean ± standard error (SE), calculated from four independent replicates (n = 4) per genotype × soil water availability combination. SE was calculated as the sample standard deviation divided by the square root of the number of replicates. Total dry mass corresponds to the sum of leaf, stem, and root dry mass for each replicate. Soil water availability is expressed as a percentage of pot water capacity.

Table S13. Analysis of variance for photosynthesis, transpiration, stomatal conductance, and intercellular CO_2 concentration in *Megathyrsus maximus* genotypes subjected to different soil water availability levels.

Trait	Source of variation	df	MS	F-value	p-value
Photosynthesis (Pn)	Blocks	3	0.3479	0.3775	0.76959
	Genotype (G)	4	519.3399	563.4513	<0.00001
	Soil water availability (W)	3	251.9794	273.3819	<0.00001
	G × W	12	96.9691	105.2056	<0.00001
	Residual	57	0.9217	—	—
Transpiration (E)	Blocks	3	0.1509	0.7528	0.52526
	Genotype (G)	4	15.2011	75.8220	<0.00001
	Soil water availability (W)	3	6.0408	30.1308	<0.00001
	G × W	12	3.3102	16.5110	<0.00001
	Residual	57	0.2005	—	—
Stomatal conductance (gs)	Blocks	3	0.0001133	0.8660	0.46411
	Genotype (G)	4	0.0284438	217.3320	<0.00001
	Soil water availability (W)	3	0.0155833	119.0680	<0.00001
	G × W	12	0.0080812	61.7470	<0.00001
	Residual	57	0.0001309	—	—
Intercellular CO_2 concentration (Ci)	Blocks	3	1.2943	1.3199	0.27681
	Genotype (G)	4	32.1652	32.8027	<0.00001
	Soil water availability (W)	3	9.1060	9.2864	0.000043
	G × W	12	13.1393	13.4000	<0.00001
	Residual	57	0.9806	—	—

Note: df = degrees of freedom; MS = mean square; F-value = calculated F statistic; p-value = probability associated with the F-test; G × W = genotype × soil water availability interaction; Pn = net photosynthetic rate; E = transpiration rate; gs = stomatal conductance; Ci = intercellular CO_2 concentration. Significance was assessed at $p < 0.05$.

Table S14. Treatment means and standard errors for net photosynthetic rate, transpiration rate, stomatal conductance, and internal CO_2 concentration in *Megathyrsus maximus* genotypes under different soil water availability levels.

Genotype	Soil water availability (%)	Net photosynthetic rate (Pn)	Transpiration rate (E)	Stomatal conductance (gs)	Internal CO_2 concentration (Ci)
Mombaça	60	15.62 ± 0.38	3.77 ± 0.15	0.118 ± 0.011	14.27 ± 0.75
	80	17.46 ± 0.27	4.59 ± 0.09	0.150 ± 0.004	18.32 ± 0.47
	100	17.81 ± 0.83	4.67 ± 0.32	0.160 ± 0.004	17.75 ± 0.71
	120	16.21 ± 0.43	5.08 ± 0.05	0.165 ± 0.003	21.00 ± 0.61
BRS Tamani	60	14.36 ± 0.46	3.92 ± 0.18	0.125 ± 0.006	17.01 ± 0.28
	80	15.37 ± 0.50	4.21 ± 0.21	0.140 ± 0.004	18.15 ± 0.61
	100	16.39 ± 0.37	3.82 ± 0.14	0.120 ± 0.004	16.60 ± 0.48
	120	13.05 ± 0.44	3.01 ± 0.08	0.088 ± 0.003	14.73 ± 0.51
BRS Zuri	60	24.78 ± 0.68	6.02 ± 0.24	0.218 ± 0.005	17.76 ± 0.38
	80	27.68 ± 0.48	6.65 ± 0.50	0.253 ± 0.005	18.70 ± 0.58
	100	20.29 ± 0.35	5.09 ± 0.16	0.173 ± 0.006	18.34 ± 0.67
	120	17.23 ± 0.49	5.07 ± 0.10	0.165 ± 0.006	18.90 ± 0.59
PM18	60	16.46 ± 0.50	4.18 ± 0.34	0.150 ± 0.004	17.37 ± 0.40
	80	19.66 ± 0.33	5.37 ± 0.20	0.193 ± 0.009	16.19 ± 0.31
	100	23.84 ± 0.44	5.43 ± 0.15	0.193 ± 0.005	19.84 ± 0.44
	120	14.63 ± 0.30	4.08 ± 0.09	0.145 ± 0.006	20.32 ± 0.56
PM21	60	39.99 ± 0.46	8.12 ± 0.29	0.330 ± 0.004	16.34 ± 0.35
	80	34.60 ± 0.63	6.79 ± 0.33	0.248 ± 0.005	13.36 ± 0.28
	100	27.53 ± 0.44	5.97 ± 0.13	0.215 ± 0.006	15.36 ± 0.32
	120	14.76 ± 0.28	3.90 ± 0.12	0.105 ± 0.006	15.42 ± 0.21

Note: Values are presented as mean ± standard error (SE), calculated from four independent replicates (n = 4) per genotype × soil water availability combination. SE was calculated as the sample standard deviation divided by the square root of the number of replicates. Soil water availability is expressed as a percentage of pot water capacity.

Table S15. Analysis of variance for carboxylation efficiency and water use efficiency in *Megathyrsus maximus* genotypes under different soil water availability levels.

Trait	Source of variation	df	MS	F-value	p-value
Carboxylation efficiency (CE)	Blocks	3	0.00916	1.63	0.19316
	Genotype (G)	4	2.97953	529.06	<0.00001
	Soil water availability (W)	3	1.27227	225.91	<0.00001
	G × W	12	0.38500	68.36	<0.00001
	Residual	57	0.00563	—	—
Water use efficiency (WUE)	Blocks	3	0.07397	0.8151	0.49083
	Genotype (G)	4	1.79115	19.7379	<0.00001
	Soil water availability (W)	3	1.35337	14.9137	<0.00001
	G × W	12	0.58548	6.4518	<0.00001
	Residual	57	0.09075	—	—

Note: df = degrees of freedom; MS = mean square; F-value = calculated F statistic; p-value = probability associated with the F-test; G × W = genotype × soil water availability interaction; CE = carboxylation efficiency; WUE = water use efficiency. Significance was assessed at $p < 0.05$.

Table S16. Treatment means and standard errors for carboxylation efficiency and water use efficiency in *Megathyrsus maximus* genotypes under different soil water availability levels.

Genotype	Soil water availability (%)	Carboxylation efficiency (CE)	Water use efficiency (WUE)
Mombaça	60	1.102 ± 0.043	4.158 ± 0.110
	80	0.958 ± 0.035	3.808 ± 0.110
	100	1.002 ± 0.029	3.843 ± 0.196
	120	0.775 ± 0.038	3.188 ± 0.106
BRS Tamani	60	0.845 ± 0.026	3.682 ± 0.172
	80	0.850 ± 0.017	3.665 ± 0.097
	100	0.990 ± 0.036	4.305 ± 0.123
	120	0.890 ± 0.046	4.338 ± 0.048
BRS Zuri	60	1.392 ± 0.021	4.123 ± 0.070
	80	1.482 ± 0.030	4.222 ± 0.272
	100	1.110 ± 0.037	3.995 ± 0.099
	120	0.915 ± 0.032	3.407 ± 0.130
PM18	60	0.950 ± 0.027	3.995 ± 0.256
	80	1.212 ± 0.013	3.675 ± 0.123
	100	1.205 ± 0.034	4.405 ± 0.181
	120	0.722 ± 0.032	3.585 ± 0.080
PM21	60	2.450 ± 0.059	4.948 ± 0.199
	80	2.595 ± 0.087	5.123 ± 0.180
	100	1.792 ± 0.038	4.612 ± 0.083
	120	0.960 ± 0.012	3.792 ± 0.125

Note: Values are presented as mean ± standard error (SE), calculated from four independent replicates (n = 4) per genotype × soil water availability combination. SE was calculated as the sample standard deviation divided by the square root of the number of replicates. Soil water availability is expressed as a percentage of pot water capacity.

Table S17. Analysis of variance for photosynthesis, transpiration, stomatal conductance, and intercellular CO_2 concentration in *Urochloa* spp. genotypes under different soil water availability levels.

Trait	Source of variation	df	MS	F-value	p-value
Photosynthesis (Pn)	Blocks	3	0.01861	0.0398	0.98930
	Genotype (G)	4	131.51547	281.2579	<0.00001
	Soil water availability (W)	3	884.45106	1891.4799	<0.00001
	G × W	12	29.37892	62.83	<0.00001
	Residual	57	0.46760	—	—
Transpiration (E)	Blocks	3	0.00045	0.0068	0.99922
	Genotype (G)	4	3.70799	55.9992	<0.00001
	Soil water availability (W)	3	17.69549	267.2429	<0.00001
	G × W	12	0.6723	10.154	<0.00001
	Residual	57	0.06622	—	—
Stomatal conductance (gs)	Blocks	3	0.000168	1.7622	0.16467
	Genotype (G)	4	0.010199	106.7638	<0.00001
	Soil water availability (W)	3	0.039125	409.5730	<0.00001
	G × W	12	0.001906	19.96	<0.00001
	Residual	57	0.000096	—	—
Intercellular CO_2 concentration (Ci)	Blocks	3	1.91971	8.1064	0.00014
	Genotype (G)	4	14.99165	63.3055	<0.00001
	Soil water availability (W)	3	6.62764	27.9867	<0.00001
	G × W	12	6.0895	25.714	<0.00001
	Residual	57	0.23681	—	—

Note: df = degrees of freedom; MS = mean square; F-value = calculated F statistic; p-value = probability associated with the F-test; G × W = genotype × soil water availability interaction. Significance was assessed at $p < 0.05$.

Table S18. Treatment means and standard errors for net photosynthetic rate, transpiration rate, stomatal conductance, and internal CO_2 concentration in *Urochloa* spp. genotypes under different soil water availability levels.

Genotype	Soil water availability (%)	Net photosynthetic rate (Pn)	Transpiration rate (E)	Stomatal conductance (gs)	Internal CO_2 concentration (Ci)
U. humidicola	60	31.12 ± 0.23	5.65 ± 0.16	0.225 ± 0.014	13.25 ± 0.21
	80	28.90 ± 0.60	4.86 ± 0.19	0.180 ± 0.004	10.16 ± 0.07
	100	30.04 ± 0.31	5.01 ± 0.03	0.188 ± 0.005	10.61 ± 0.14
	120	23.22 ± 0.17	4.25 ± 0.13	0.155 ± 0.003	12.55 ± 0.28
Marandu	60	32.99 ± 0.17	5.45 ± 0.19	0.237 ± 0.005	12.34 ± 0.38
	80	30.57 ± 0.37	5.33 ± 0.07	0.208 ± 0.005	12.20 ± 0.27
	100	32.49 ± 0.25	5.16 ± 0.10	0.198 ± 0.005	9.87 ± 0.10
	120	14.26 ± 0.47	2.84 ± 0.14	0.100 ± 0.004	13.15 ± 0.40
Xaraés	60	31.66 ± 0.14	5.28 ± 0.16	0.210 ± 0.004	11.56 ± 0.23
	80	31.91 ± 0.27	5.42 ± 0.11	0.217 ± 0.003	12.44 ± 0.35
	100	26.63 ± 0.34	4.67 ± 0.11	0.175 ± 0.003	12.40 ± 0.27
	120	12.52 ± 0.24	2.54 ± 0.02	0.070 ± 0.004	11.34 ± 0.12
Mulato II	60	24.64 ± 0.25	4.15 ± 0.07	0.152 ± 0.003	10.13 ± 0.25
	80	24.74 ± 0.35	4.24 ± 0.07	0.152 ± 0.005	11.05 ± 0.24
	100	21.74 ± 0.27	3.89 ± 0.06	0.133 ± 0.005	10.83 ± 0.18
	120	13.96 ± 0.55	2.83 ± 0.13	0.090 ± 0.004	13.45 ± 0.53
Ub001	60	29.01 ± 0.32	4.54 ± 0.10	0.163 ± 0.003	8.01 ± 0.31
	80	26.79 ± 0.21	4.61 ± 0.19	0.165 ± 0.003	10.16 ± 0.35
	100	26.07 ± 0.23	4.39 ± 0.17	0.160 ± 0.004	10.18 ± 0.10
	120	13.42 ± 0.47	2.50 ± 0.07	0.077 ± 0.002	10.07 ± 0.38

Note: Values are presented as mean ± standard error (SE), calculated from four independent replicates (n = 4) per genotype × soil water availability combination. SE was calculated as the sample standard deviation divided by the square root of the number of replicates. Soil water availability is expressed as a percentage of pot water capacity.

Table S19. Analysis of variance for carboxylation efficiency and water use efficiency in Urochloa spp. genotypes under different soil water availability levels.

Trait	Source of variation	df	MS	F-value	p-value
Carboxylation efficiency (CE)	Blocks	3	0.09023	6.9434	0.00046
	Genotype (G)	4	1.03067	79.3115	<0.00001
	Soil water availability (W)	3	9.27911	714.0370	<0.00001
	G × W	12	0.5792	44.57	<0.00001
	Residual	57	0.01300	—	—
Water use efficiency (WUE)	Blocks	3	0.00721	0.0641	0.97860
	Genotype (G)	4	0.25528	2.2694	0.07285
	Soil water availability (W)	3	2.98905	26.5726	<0.00001
	G × W	12	0.24877	2.2115	0.02302
	Residual	57	0.11249	—	—

Note: df = degrees of freedom; MS = mean square; F-value = calculated F statistic; p-value = probability associated with the F-test; G × W = genotype × soil water availability interaction; CE = carboxylation efficiency; WUE = water use efficiency. Significance was assessed at $p < 0.05$.

Table S20. Treatment means and standard errors for carboxylation efficiency and water use efficiency in *Urochloa* spp. genotypes under different soil water availability levels.

Genotype	Soil water availability (%)	Carboxylation efficiency (CE)	Water use efficiency (WUE)
U. humidicola	60	2.350 ± 0.039	5.523 ± 0.150
	80	2.850 ± 0.076	5.972 ± 0.238
	100	2.833 ± 0.062	5.995 ± 0.100
	120	1.850 ± 0.029	5.478 ± 0.147
Marandu	60	2.683 ± 0.097	6.075 ± 0.253
	80	2.510 ± 0.060	5.735 ± 0.150
	100	3.293 ± 0.010	6.300 ± 0.072
	120	1.087 ± 0.047	5.045 ± 0.225
Xaraés	60	2.740 ± 0.043	6.020 ± 0.212
	80	2.575 ± 0.085	5.895 ± 0.076
	100	2.150 ± 0.051	5.705 ± 0.105
	120	1.103 ± 0.010	4.923 ± 0.080
Mulato II	60	2.433 ± 0.038	5.938 ± 0.060
	80	2.243 ± 0.075	5.840 ± 0.064
	100	2.013 ± 0.057	5.588 ± 0.137
	120	1.045 ± 0.058	4.948 ± 0.144
Ub001	60	3.633 ± 0.128	6.402 ± 0.209
	80	2.647 ± 0.088	5.848 ± 0.255
	100	2.562 ± 0.023	5.962 ± 0.195
	120	1.340 ± 0.083	5.380 ± 0.144

Note: Values are presented as mean ± standard error (SE), calculated from four independent replicates (n = 4) per genotype × soil water availability combination. SE was calculated as the sample standard deviation divided by the square root of the number of replicates. Soil water availability is expressed as a percentage of pot water capacity.