

**Growth-inducing effects of argon plasma on soybean sprouts via the regulation of  
demethylation levels of energy metabolism-related genes**

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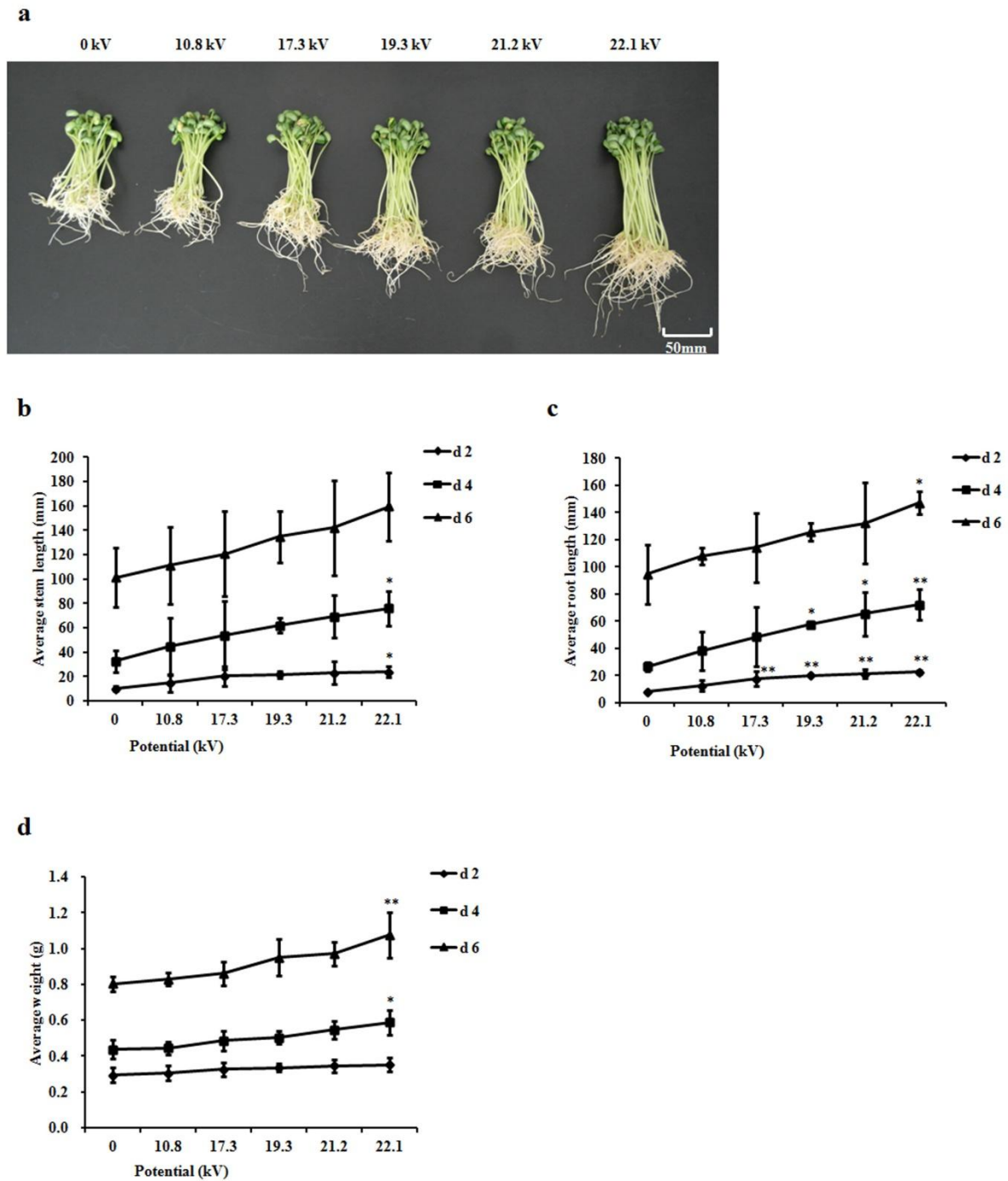
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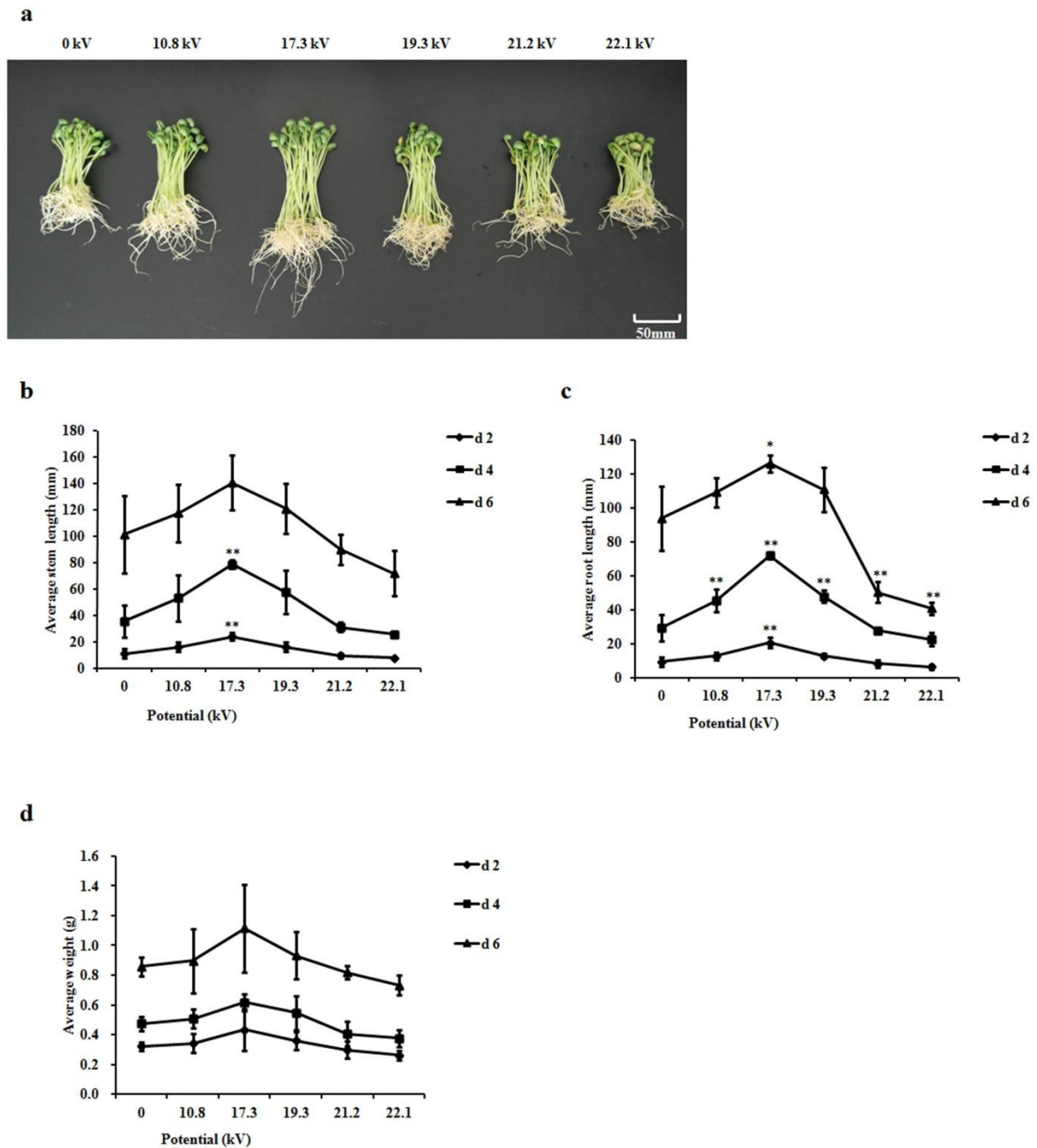
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Supplementary Figure S1. Effects of plasma at different potentials for 1 min on (a) 6-day-old soybean sprouts appearance, (b) average stem length, (c) average root length, and (d) average weight of soybean sprouts on days 2, 4, and 6. Error bars indicated standard error ( $n = 3$ ). \*,  $p < 0.05$  versus control; \*\*,  $p < 0.01$  versus control, according to LSD test.



Supplementary Figure S2. Effects of plasma at different potentials for 2 min on (a) 6-day-old soybean sprouts appearance, (b) average stem length, (c) average root length, and (d) average weight of soybean sprouts on days 2, 4, and 6. Error bars indicated standard error ( $n = 3$ ). \*,  $p < 0.05$  versus control; \*\*,  $p < 0.01$  versus control, according to LSD test.



**Supplementary Table S3. Effects of plasma at different potentials and exposure durations on germination and production rates of soybean sprouts**

Potential (kV)	Germination rate (%)		Production rate (%)	
	Exposure duration		Exposure duration	
	1 min	2 min	1 min	2 min
0	80.44 ± 2.03	81.42 ± 2.77	4.72 ± 0.51	5.11 ± 0.35
10.8	80.42 ± 1.22	86.42 ± 1.94*	4.81 ± 0.24	5.88 ± 0.67
17.3	83.36 ± 3.05	88.33 ± 1.96**	5.28 ± 0.33	7.82 ± 0.41**
19.3	83.55 ± 1.97	84.38 ± 4.20	5.93 ± 0.57*	5.93 ± 0.39*
21.2	86.54 ± 2.20**	78.60 ± 1.03	6.12 ± 0.65*	4.72 ± 0.52
22.1	90.42 ± 1.93**	74.60 ± 2.13**	6.80 ± 1.06**	4.13 ± 0.24*

Within a column: \*,  $p < 0.05$  versus control; \*\*,  $p < 0.01$  versus control, according to LSD test.

**Supplementary Table S4. Primer sequences for RT-PCR**

Gene	Sequence number	Sequence position	Product length (bp)	Sequence (5'to3')
$\beta$ -actin	CA937380.1	248-377	130	F: CTACTGGGTTTAGAGGCTCATGG R: AACCTGCCATAGAAGAAGTGCC
ATP a1	XM_003540456.2	397-534	138	F: CCTGCTCCCGGTATTATTTCG R: TGCTGTTTTACCCGTTTGTCTG
ATP a2	XM_006588217.1	184-347	164	F: GGCATTGCTTTGAATTTGGAA R: ATTGGTTTAGCCAGGGCATTTA
ATP b1	XM_003536602.2	396-492	97	F: AGGCGTTGTCCGAACCATT R: ACCAACTGGAACGGTAATAGGG
ATP b2	XM_003555884.2	603-706	104	F: TGAGCAAGAAACCGCACAGC R: CAGCACCACCAAACAACCCA
ATP b3	XM_006584177.1	211-399	189	F: GTTGGAGAACGAACCCGAGAA R: AGCATCACGGAAGTGTTTAGCC
ATP MI25	XM_003550048.2	419-545	127	F: CTCCTGTTCGCATCCGTCTTC R: ACCACCAAGCTCTCTCGAATGA
TOR	XM_003517543.2	182-293	112	F: TGGGCAAATCATCCACAGG R: ATGCTGCCGAACCTTTGTCAAC
GRF 1	XM_003534897.2	849-1007	159	F: CCACTCAAAGCAGCAGCAACA R: TCATCCAAATCAAGCCAAGACC
GRF 2	XM_003518751.2	176-316	141	F: TGAACAGACCAAGTGAGAAGCG R: AATCAGCAGTGAAAGCCAACG
GRF 3	XM_003542518.2	743-854	112	F: AGCCTGACAATGGTGAAAGCA R: CCAGTGGACAATTTCAACGACA
GRF 4	XM_003537618.2	609-702	94	F: GGAGCCACAGATGGACAACACT R: ATCACCTTGCAACATGGAATTAT
GRF 5	XM_003547671.2	100-294	195	F: ACAGGAACACCTATCCCACCAG R: TGCCTCCTTTGAACATCTCCAT
GRF 6	XM_003549320.2	662-835	174	F: ACAGCACAGACCCTGAGCCA R: TGTTAGTGGTGGTGAGGGCAT

ATP a1, Glycine max ATP synthase subunit alpha, chloroplastic-like (LOC100815582). ATP a2, Glycine max ATP synthase subunit alpha, chloroplastic-like (LOC102661828). ATP b1, Glycine max ATP synthase subunit beta, mitochondrial-like (LOC100797948). ATP b2, Glycine max ATP synthase subunit beta, mitochondrial-like (LOC100789705). ATP b3, Glycine max ATP synthase subunit beta, mitochondrial-like (LOC100783395). ATP MI25, Glycine max ATP synthase protein MI25-like (LOC100816723). TOR, Glycine max serine/threonine-protein kinase TOR-like (LOC100816558). GRF 1, Glycine max growth-regulating factor

1-like (LOC100814271). GRF 2, Glycine max root meristem growth factor 2-like (LOC100818175). GRF 3, Glycine max growth-regulating factor 3-like (LOC100817197). GRF 4, Glycine max growth-regulating factor 4-like (LOC100817313). GRF 5, Glycine max growth-regulating factor 5-like (LOC100814760). GRF 6, Glycine max growth-regulating factor 6-like (LOC100819396).

**Supplementary Table S5. Primer sequences for bisulfite-sequencing PCR**

Gene	Sequence number	Sequence position	Product length (bp)	Sequence (5'to3')	Expected No. of CpGs
ATP a1	XM_003540456.2	123-423	301	F: TGAATAGTTGGAAAAAGTTTAAGTT R: CATACCAATATTAACACTAACAATAC	13
ATP b1	XM_003536602.2	42-408	367	F: TTTTTTTTGAAGATGGTTTTA R: AATAATCCAAAACCTCCAAC	38
TOR	XM_003517543.2	324-612	289	F: TTGAAGAAGTATTTAGAGGAAGAAGTT R: CCCCAACCCTAACAAAATAAC	17
GRF 5	XM_003547671.2	1279-1590	312	F: AGGTTAAGTAAAGAGAAAGAAGTTGAGATA R: AACACAAATCCTACTATAATCCCCTAC	4
GRF 6	XM_003549320.2	987-1162	176	F: GGAGGTTTTTATTTGGGATTTTTTA R: CCTAATTAACCTTCCACAACTTTCT	6