

1 **Table S2.** Relative abundance values of differentially abundant protein spots in foxtail millet
2 grains under drought stress (DS) compared with the control treatment (Ctrl).

Spot No.	Ctrl	DS
Storage proteins		
6	0	1.403391392
9	0	-2.14036108
42	0	1.356971236
44	0	-2.22636584
48	0	1.791236985
56	0	-1.285793378
57	0	-2.377695388
58	0	-2.757931806
59	0	-6.26382514
73	0	-2.165308004
74	0	7.480836797
75	0	-4.222069346
82	0	-1.41351558
93	0	2.002677803
97	0	-2.401680389
99	0	2.001703875
101	0	-1.286677671
103	0	1.193348777
Protein folding		
3	0	-1.038577619
4	0	-1.204464001
5	0	1.982836405
11	0	2.329903352
12	0	5.197216693
19	0	3.684925876
20	0	1.364871575
21	0	-3.106041637
23	0	1.250801663
36	0	1.337393849
37	0	2.292198607
67	0	-1.911362091
70	0	-1.217056683
72	0	-7.036147441
81	0	3.17978314
84	0	-1.338123994
Starch and sucrose metabolism		
7	0	1.05507336
8	0	1.515049231

Supplementary table to the article “Proteomic changes in the grains of foxtail millet (Setaria italica (L.) Beau) under drought stress”, by Jing Li, Xia Li, Qinghua Yang, Yan Luo, Xiangwei Gong, Weili Zhang, Yingang Hu, Tianyu Yang, Kongjun Dong and Baili Feng. Spanish Journal of Agricultural Research Vol. 17 No. 2, June 2019
(<https://doi.org/10.5424/sjar/2019172-14300>)

Spot No.	Ctrl	DS
13	0	-4.371391201
17	0	-1.487228011
31	0	1.078344725
34	0	1.142399676
38	0	1.121219053
49	0	-1.911291032
62	0	-1.288731266
63	0	-5.056549749
65	0	-1.830038757
71	0	-2.285920224
86	0	-2.623812241
87	0	-2.433497035
89	0	1.890194395
Glycolysis / Gluconeogenesis		
24	0	2.045919531
33	0	1.631846779
43	0	1.568558498
53	0	1.389737665
76	0	1.452451671
77	0	-3.18420001
78	0	-1.26545176
79	0	-5.541893779
83	0	-4.862341598
85	0	-1.293745148
100	0	-1.746279932
Biosynthesis of amino acids		
47	0	-1.338239496
51	0	1.019835471
52	0	1.21138942
64	0	-1.273460239
69	0	-1.633584743
80	0	-1.698226681
98	0	-3.061236166
Detoxification and defense		
28	0	1.073927643
39	0	1.101740191
40	0	1.415734016
61	0	-3.917466881
92	0	-3.358654534
96	0	4.396183571
102	0	1.056043122

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Spot No.	Ctrl	DS
Protein degradation		
10	0	2.077388912
15	0	1.17794966
26	0	1.147239651
41	0	1.414010343
50	0	-3.661256705
55	0	-1.599877175
95	0	-7.611214815
TCA cycle		
14	0	3.141171887
27	0	1.645139497
46	0	1.035150455
60	0	2.460323548
88	0	-2.538564782
90	0	1.120218632
91	0	1.138364619
Protein synthesis		
1	0	1.651614665
2	0	3.50798763
16	0	1.143974631
25	0	1.189067916
66	0	-1.371165427
68	0	1.218475736
Energy metabolism		
29	0	1.117283821
30	0	1.707363021
32	0	1.930720787
35	0	1.59580331
45	0	1.139732629
Transporter		
18	0	2.025638942
94	0	1.36954963
104	0	1.556394123
Pentose phosphate pathway		
54	0	1.001854761
Signal transduction		
22	0	1.98466252