

S8 Table. Transmembrane domain analysis of aquaporins in pearl millet.

Gene	TMHMM		TMPred				Phyre2				
	Exp. AA	First 60	N-ter	C-ter	TM	N-ter	C-ter	TM	N-ter	C-ter	TM
Plasma membrane intrinsic proteins (PIP)											
PgPIP1-1	130.8	5.35	in	in	6	in	in	6	in	in	6
PgPIP1-3	129.6	5.40	in	in	6	in	in	6	in	in	6
PgPIP1-4	132.9	0.25	in	in	6	in	in	6	in	in	6
PgPIP2-1	141.4	17.92	out	out	6	in	in	6	in	in	6
PgPIP2-2	135.3	18.48	in	in	6	in	in	6	in	in	6
PgPIP2-3	133.3	17.67	in	in	6	in	in	6	in	in	6
PgPIP2-5	136.9	20.82	in	in	6	in	in	6	in	in	6
PgPIP2-6	139.3	20.81	out	in	7	in	in	6	in	in	6
PgPIP2-7	140.9	17.23	in	in	6	in	in	6	in	in	6
PgPIP2-8	132.8	21.99	in	in	6	in	in	6	in	in	6
Tonoplast intrinsic proteins (TIP)											
PgTIP1-1	137.1	26.29	in	in	6	in	in	6	in	in	6
PgTIP2-3	136.7	28.76	out	out	6	in	in	6	in	in	6
PgTIP2-1	137.0	29.24	out	out	6	in	in	6	in	in	6
PgTIP4-1	133.0	25.54	in	in	6	in	in	6	in	in	6
PgTIP3-1	134.4	20.98	in	in	6	in	out	6	in	in	6
PgTIP2-2	142.1	26.95	in	in	6	in	in	6	in	in	6
PgTIP4-3	132.9	29.79	in	in	6	in	out	6	in	in	6
PgTIP4-2	138.1	33.59	in	in	6	in	out	6	in	in	6
PgTIP5-1	132.56	21.99	in	in	6	out	out	6	in	in	6
Noduline-26 like intrinsic proteins (NIP)											
PgNIP1-2	122.1	9.84	out	in	5	in	in	6	in	in	6
PgNIP1-1	128.3	16.10	in	in	6	in	in	6	in	in	6
PgNIP1-4	131.4	0.40	in	in	6	in	in	6	in	in	6
PgNIP2-2	129.4	4.75	in	in	6	in	in	6	in	in	6
PgNIP2-1	132.9	9.80	in	in	6	in	in	6	in	in	6
PgNIP3-1	122.3	0.11	out	in	5	in	in	6	in	in	6
PgNIP3-2	127.3	9.76	in	in	6	in	in	6	in	in	6
PgNIP3-3	129.6	9.98	in	in	6	in	in	6	in	in	6
PgNIP3-4	129.82	20.04	in	in	6	in	in	6	in	in	6
PgNIP4-1	130.3	3.05	in	in	6	in	out	7	in	in	6
PgNIP3-5	125.11	0.006	in	in	6	in	in	6	in	in	6
Small intrinsic proteins (SIPs)											
PgSIP1-1	133.1	41.61	in	in	6	in	out	7	in	in	6
PgSIP1-2	130.1	29.71	in	in	6	out	in	7	out	out	6
PgSIP2-1	131.4	26.07	out	in	5	in	out	7	in	in	6

Cytosolic (in) or extra-cellular (out) location of the N-terminal (N-ter) and C-terminal (C-ter) ends of the different aquaporin isoforms as well as the number of transmembrane domains (TM) were predicted using TMHMM, TMPred and Phyre2 software. TMHMM provided information on the expected total number of amino-acids in the transmembrane domains (Exp. AA) and the number of amino-acids of the N-ter region (First 60).