

Table S1. Conserved domain analysis of AQPs identified from *Aquilegia coerula* using CDD tool from NCBI.

Query	Hit type	PSSM-ID	E-Value	Bitscore	Accession	Short name	Superfamily
AqcNIP1-1	superfamily	294134	6.35E-125	357.024	cl00200	MIP superfamily	-
AqcNIP1-2	superfamily	294134	4.39E-134	380.906	cl00200	MIP superfamily	-
AqcNIP1-3	superfamily	294134	1.74E-77	236.842	cl00200	MIP superfamily	-
AqcNIP2-1	superfamily	294134	1.20E-76	235.574	cl00200	MIP superfamily	-
AqcNIP3-1	Specific	177663	1.17E-161	452.009	PLN00026	PLN00026	cl00200
AqcNIP4-1	superfamily	294134	1.78E-132	375.786	cl00200	MIP superfamily	-
AqcNIP4-3	superfamily	294134	2.49E-118	340.296	cl00200	MIP superfamily	-
AqcNIP4-2	superfamily	294134	6.03E-132	374.631	cl00200	MIP superfamily	-
AqcNIP5-1	Specific	177663	3.17E-171	475.891	PLN00026	PLN00026	cl00200
AqcPIP1-1	Specific	278651	8.12E-99	288.832	pfam00230	MIP	cl00200
AqcPIP1-2	Specific	278651	5.09E-98	286.906	pfam00230	MIP	cl00200
AqcPIP2-1	Specific	278651	1.66E-94	277.661	pfam00230	MIP	cl00200
AqcPIP2-2	Specific	278651	1.82E-92	272.654	pfam00230	MIP	cl00200
AqcSIP1-1	superfamily	294134	5.30E-17	76.9086	cl00200	MIP superfamily	-
AqcSIP2-1	superfamily	294134	3.51E-08	52.2558	cl00200	MIP superfamily	-
AqcTIP1-2	Specific	177664	2.25E-146	409.176	PLN00027	PLN00027	cl00200
AqcTIP1-1	Specific	177664	6.59E-119	339.455	PLN00027	PLN00027	cl00200
AqcTIP1-3	Specific	177664	4.11E-155	431.132	PLN00027	PLN00027	cl00200
AqcTIP2-1	superfamily	294134	9.56E-79	237.913	cl00200	MIP superfamily	-
AqcTIP2-3	superfamily	294134	1.10E-120	343.843	cl00200	MIP superfamily	-
AqcTIP2-2	Specific	165733	6.48E-134	377.355	PLN00166	PLN00166	cl00200
AqcTIP3-1	Specific	177664	3.93E-109	314.802	PLN00027	PLN00027	cl00200
AqcTIP4-1	superfamily	294134	2.51E-99	289.764	cl00200	MIP superfamily	-
AqcTIP4-2	superfamily	294134	5.96E-82	245.081	cl00200	MIP superfamily	-
AqcTIP5-1	superfamily	294134	4.44E-121	346.12	cl00200	MIP superfamily	-
AqcXIP1-2	superfamily	294134	2.31E-36	130.066	cl00200	MIP superfamily	-
AqcXIP1-1	superfamily	294134	3.58E-35	126.599	cl00200	MIP superfamily	-
AqcXIP1-4	superfamily	294134	7.22E-40	138.926	cl00200	MIP superfamily	-
AqcXIP1-3	superfamily	294134	4.38E-37	131.607	cl00200	MIP superfamily	-

Table S2. Transmembrane domains and cellular localization of AQPs identified from *Aquilegia coerulea* using TMHMM, Targetp, Cello and wolfsort.

S. No.	Gene ID	Length	TMHMM			Targetp	Cello	Wolfsort
			ExpAA	First60	TMH			
1	AqcNIP1-1	268	130.8	22	6		PlasmaMembrane	PlasmaMembrane
2	AqcNIP1-2	285	129.87	9.3	6		PlasmaMembrane	Vacoule
3	AqcNIP1-3	277	131.03	7.35	6		PlasmaMembrane	PlasmaMembrane
4	AqcNIP2-1	311	132.41	0.19	6		PlasmaMembrane	Vacoule
5	AqcNIP3-1	307	134.45	0.49	6	Chloroplast	PlasmaMembrane	PlasmaMembrane
6	AqcNIP4-1	271	130.66	19.42	6		PlasmaMembrane	PlasmaMembrane
7	AqcNIP4-3	289	129.36	0.05	6		PlasmaMembrane	PlasmaMembrane
8	AqcNIP4-2	278	130.96	14.79	6		PlasmaMembrane	PlasmaMembrane
9	AqcNIP5-1	301	122.52	0.05	6	Chloroplast	PlasmaMembrane	PlasmaMembrane
10	AqcPIP1-1	288	122.45	7.04	6		PlasmaMembrane	PlasmaMembrane
11	AqcPIP1-2	288	120.84	6.36	6		PlasmaMembrane	PlasmaMembrane
12	AqcPIP2-1	284	132.08	21.22	6		PlasmaMembrane	PlasmaMembrane
13	AqcPIP2-2	281	135.72	22.12	6		PlasmaMembrane	PlasmaMembrane
14	AqcSIP1-1	245	130.48	35.98	6		PlasmaMembrane	Vacoule
15	AqcSIP2-1	251	106.1	26.79	5	Mitochondria	PlasmaMembrane	PlasmaMembrane
16	AqcTIP1-2	254	148.75	23.33	7		PlasmaMembrane	PlasmaMembrane
17	AqcTIP1-1	250	128.06	19.87	6		PlasmaMembrane	PlasmaMembrane
18	AqcTIP1-3	253	135.67	24.63	6		PlasmaMembrane	Vacoule
19	AqcTIP2-1	264	143.89	22.04	6		PlasmaMembrane	PlasmaMembrane
20	AqcTIP2-3	249	153.83	29.58	6	Secretory	PlasmaMembrane	PlasmaMembrane
21	AqcTIP2-2	251	152.58	29.14	6		PlasmaMembrane	Vacoule
22	AqcTIP3-1	256	134.16	25.37	6		PlasmaMembrane	PlasmaMembrane
23	AqcTIP4-1	248	138.49	30.41	6		PlasmaMembrane	Vacoule
24	AqcTIP4-2	233	129.69	30.54	6		PlasmaMembrane	Vacoule
25	AqcTIP5-1	275	132.16	19.14	6		PlasmaMembrane	PlasmaMembrane
26	AqcXIP1-2	308	150.74	0	7		PlasmaMembrane	PlasmaMembrane
27	AqcXIP1-1	304	148.85	0.075	7		PlasmaMembrane	PlasmaMembrane
28	AqcXIP1-4	300	140.38	1.07	6		PlasmaMembrane	PlasmaMembrane
29	AqcXIP1-3	304	149.16	0.86	7		PlasmaMembrane	PlasmaMembrane

Footnote: Sequences showing less than six transmembrane domains predicted based on their sequence alignment. ExpAA: The expected number of amino acids in transmembrane helices. First60: The expected number of amino acids in transmembrane helices in the first 60 amino acids of the protein.

Table S3. Molecular weight and average PI of *Aquilegia coerula* Aquaporin.

Gene ID	Molecular weight (kDa)	Average PI
AqcNIP1-1	28.4	8.343
AqcNIP1-2	30	7.381
AqcNIP1-3	29.3	6.35
AqcNIP2-1	33.5	8.512
AqcNIP3-1	31.9	8.201
AqcNIP4-1	28.8	6.067
AqcNIP4-3	30.4	6.364
AqcNIP4-2	29.8	5.956
AqcNIP5-1	31.2	7.337
AqcPIP1-1	30.6	8.522
AqcPIP1-2	30.8	8.535
AqcPIP2-1	30.4	7.726
AqcPIP2-2	29.8	8.992
AqcSIP1-1	25.4	8.243
AqcSIP2-1	27.6	10.49
AqcTIP1-2	25.8	4.931
AqcTIP1-1	26.2	7.552
AqcTIP1-3	25.8	5.635
AqcTIP2-1	27.2	6.118
AqcTIP2-3	25	5.427
AqcTIP2-2	25.1	5.136
AqcTIP3-1	27	7.432
AqcTIP4-1	26	5.819
AqcTIP4-2	24.4	5.836
AqcTIP5-1	28.1	5.628
AqcXIP1-2	32.6	7.627
AqcXIP1-1	32.6	6.435
AqcXIP1-4	32	6.945
AqcXIP1-3	32.3	6.508

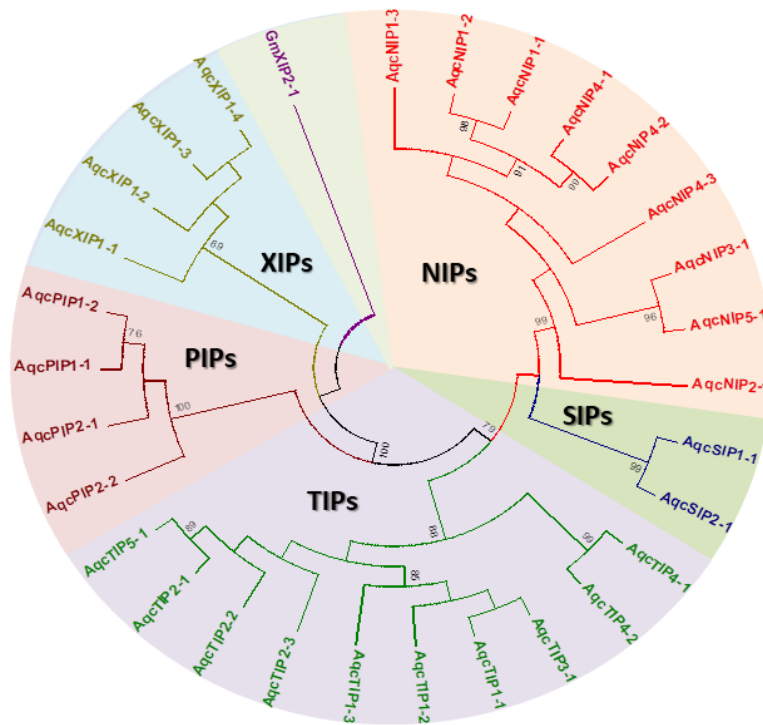


Figure S1. Phylogenetic analysis of *Aquilegia coerulea* aquaporins (AQPs). Phylogenetic tree showing distribution of aquaporins in five different subfamilies namely NOD26-like intrinsic proteins (NIPs), tonoplast intrinsic proteins (TIPs), plasma membrane intrinsic proteins (PIPs), small basic intrinsic proteins (SIPs) and uncharacterized intrinsic proteins (XIPs). The outgroup was taken from *Glycine max* (Gm).

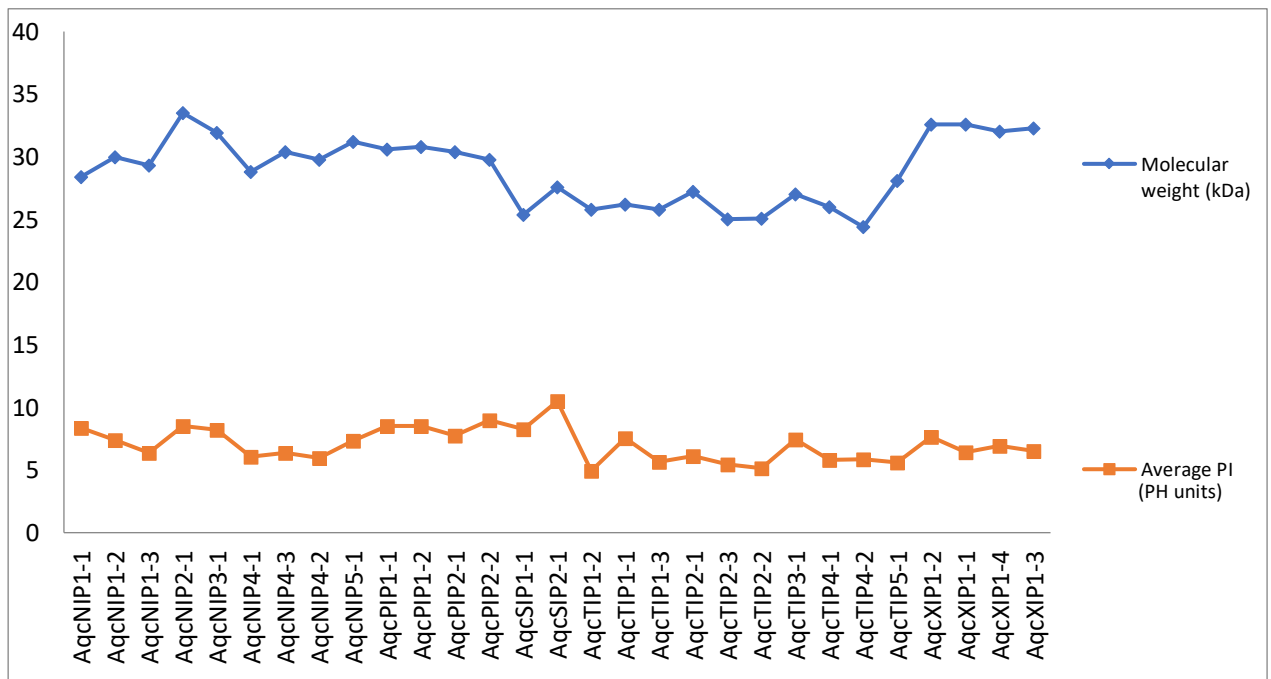


Figure S2. Molecular weight and isoelectric point of *Aquilegia coerulea* aquaporins (AQPs).

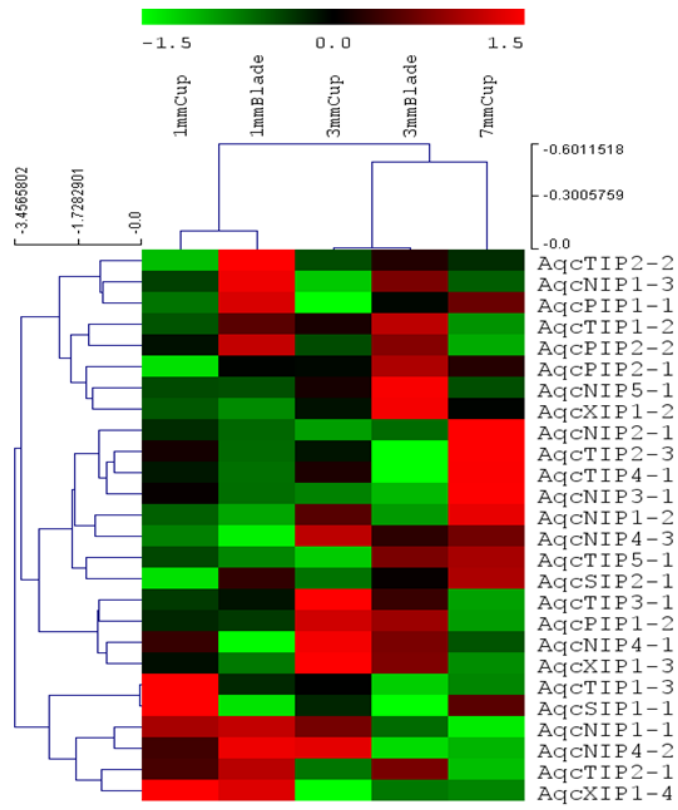


Figure S3. Heatmap showing expression profile of aquaporin genes in petal spur of *Aquilegia coerulea*. Genes with no expression (0 FPKM values) were removed from the heatmap.