

SENSITIVE TO FREEZING2 is crucial for growth of *Marchantia polymorpha* under acidic conditions

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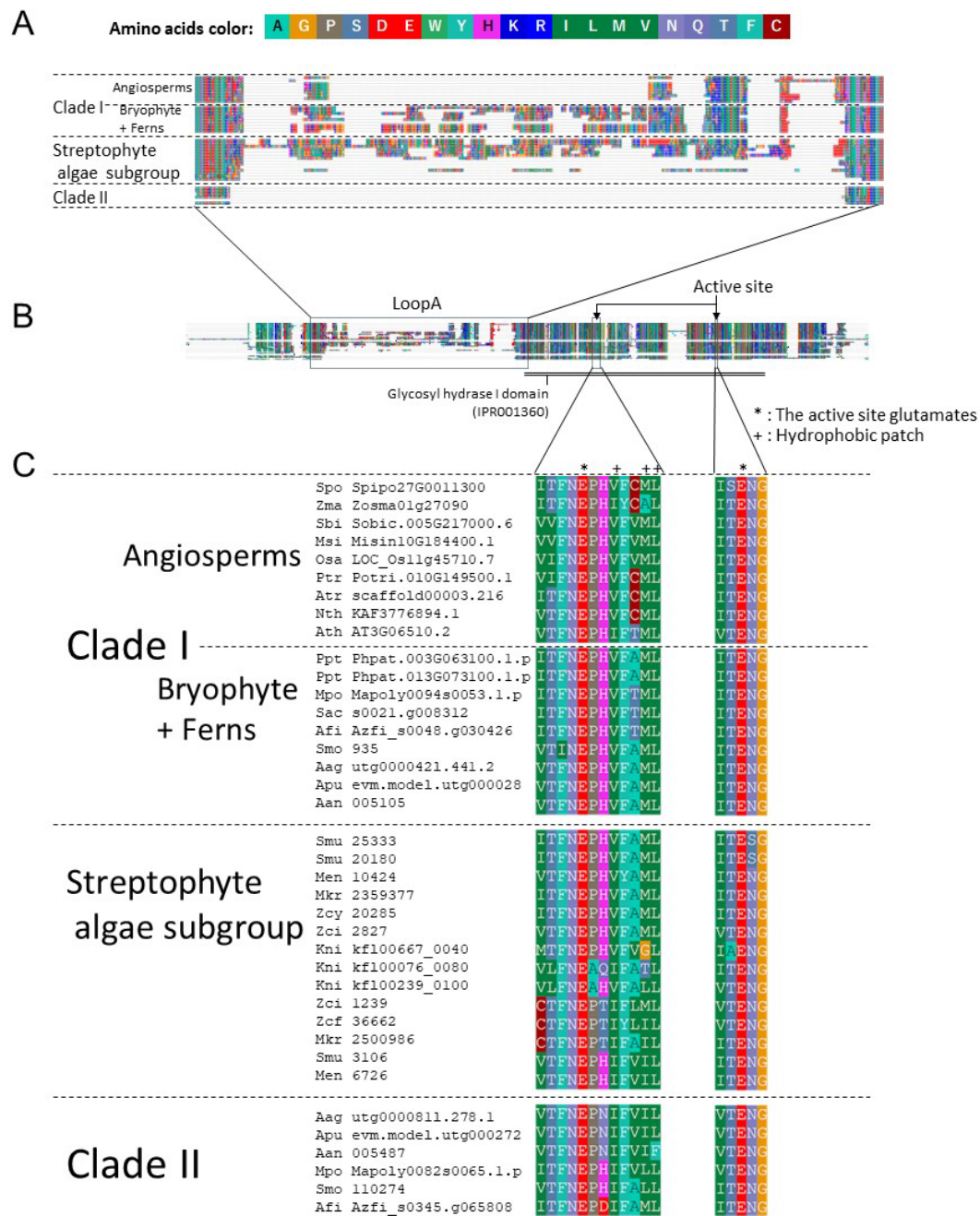


Figure S1. (A) Multiple sequence alignment of the Loop A region in 38 SFR2-like proteins. Amino acids are colored as indicated at the top. (B) Reconstruction of the multiple sequence alignment of the entire region, excluding Azfi_s0048.g030426, Aan 005105, Men 10424, Apu evm.model.utg000272, and Aan 005487, which predicted long insertions. Rectangles denote Loop A and the active site. The horizontal double line denotes the glycosyl hydase I domain (IPR001360). (C) Multiple sequence alignment nearby the active-site glutamates and hydrophobic patch.

Table S1

Classification	Organism	Abbreviation	BLAST site
	Database	Protein ID	
Streptophyte algae			
	<i>Klebsormidium nitens</i>	Kni	PhycoCosm
	Klenit1_1_GeneCatalog_proteins_20230514.aa1		kfl00667_0040 kfl00076_0080 kfl00239_0100
	<i>Mesotaenium endlicherianum</i>	Men	PhycoCosm
	Mesen1_1_GeneCatalog_proteins_20230514.aa		10424 6726
	<i>Mesotaenium kramstae</i> Lemmermann	Mkr	PhycoCosm
	Meskra657_3_GeneCatalog_proteins_20220510.aa		2359377 2500986
	<i>Zygnema</i> cf. <i>cylindricum</i>	Zcy	PhycoCosm
	Zygcy16981a_1_GeneCatalog_proteins_20230203.aa		20285 36662
	<i>Zygnema circumcarinatum</i>	Zci	PhycoCosm
	Zygcir1559_1_GeneCatalog_proteins_20230203.aa		2827 1239
	<i>Spirogloea muscicola</i>	Smu	PhycoCosm
	Spimu1_1_GeneCatalog_proteins_20230519.aa		20180 25333 3106
Bryophyte			
Anthocerotopsida			
	<i>Anthoceros agrestis</i>	Aag	MarpolBase
	Anthoceros agrestis Oxford (v1.0, 2020)		utg0000811.278.1 utg0000421.441.2
	<i>Anthoceros angustus</i>	Aan	MarpolBase
	Anthoceros angustus (v1.0, 2020)		AANG005105 AANG005487
	<i>Anthoceros punctatus</i>	Apu	MarpolBase
	Anthoceros punctatus (v1.0, 2020)		utg0000281.432.1 utg0002721.97.1
Hepatopsida			
	<i>Marchantia polymorpha</i>	Mpo	MarpolBase
	Marchantia polymorpha 'primary' (v3.1, 2015)		Mapoly0094s0053.1.p Mapoly0082s0065.1.p
Bryopsida			
	<i>Physcomitrella patens</i>	Ppa	MarpolBase
	Physcomitrella patens 'primary' (v3.0, 2014)		Phpat.003G063100.1.p Phpat.013G073100.1.p
Ferns			
Lycophytina			
	<i>Selaginella moellendorffii</i>	Smo	MarpolBase
	Selaginella moellendorffii 'primary' (v1.0, 2014)		935 110274
Polypodiopsida			
	<i>Azolla filiculoides</i>	Afi	MarpolBase
	Azolla filiculoides (high_confidence) (v1.1, 2018)		Azfi_s0048.g030426 Azfi_s0345.g065808
	<i>Salvinia cucullate</i>	Scu	MarpolBase
	Salvinia cucullata (high_confidence) (v1.2, 2018)		s0021.g008312
Angiosperms			
	<i>Amborella trichopoda</i>	Atr	MarpolBase
	Amborella trichopoda (v1.0, 2013)		scaffold00003.216

<i>Nymphaea thermarum</i>	Nth	MarpolBase	
Nymphaea thermarum (v1.0, 2020)			KAF3776894.1
Eudicots			
<i>Arabidopsis thaliana</i>	Ath	Phytozome	
Arabidopsis thaliana TAIR10			AT3G06510.2
<i>Populus trichocarpa</i>	Ptr	Phytozome	
Populus trichocarpa v4.1			Phpat.003G063100.1.p Phpat.013G073100.1.p
Monocots			
<i>Zostera marina</i>	Zma	Phytozome	
Zostera marina v3.1			Zosma01g27090
<i>Miscanthus sinensis</i>	Msi	Phytozome	
Miscanthus sinensis v7.1			Misin10G184400.1.p
<i>Sorghum bicolor</i>	Sbi	Phytozome	
Sorghum bicolor v5.1			Sobic.005G217000.6
<i>Oryza sativa</i>	Osa	Phytozome	
Oryza sativa v7.0			LOC_Os11g45710.7
<i>Spirodela polyrhiza</i>	Spo	Phytozome	
Spirodela polyrhiza v2			Spipo27G0011300

Table S2

Primer	sequence
MpGGGT1 Fwd	AAAAAGCAGGCTCAAAAATGGCGCCGTTTTTGTGCTG
MpGGGT1 Rev	AGAAAGCTGGGTATCGGCTGCTGCTGTAGCTCTCT
MpGGGT2 Fwd	AAAAAGCAGGCTCAAAAATGGCGATTCCTTGAGGAAG
MpGGGT2 Rev	AGAAAGCTGGGTATCAACTCCCCGGTCCTAAGTTC
SFR2 Fwd	GGGGACAAGTTTGTACAAAAAGCAGGCTCAATGGAATTATTCGCATTGTTAATTAAGGTCG
SFR2 Rev	GGGGACCACTTTGTACAAGAAAGCTGGGTGGTCAAAGGGTGAGGCTAAAGCAGG
AtRbcs Fwd	AAAAAGCAGGCTCAAAAATGATGATAACTCGCGGTGG
AtRbcs Rev	AGAAAGCTGGGTATCATGATACCCAATTGGAGCTG

Table S3

Primer	sequence
MpGGGT1 sgRNA Fwd 3rd exon 8	CTCGATTCCGTTGAGTGGCTCAAC
MpGGGT1 sgRNA Rev 3rd exon 8	AAACGTTGAGCCACTCAACGGAAT
MpGGGT2 sgRNA Fwd 1st exon	CTCGTGGAGACGGCTCCCGGAGAT
MpGGGT2 sgRNA Rev 1st exon	AAACATCTCCGGGAGCCGTCTCCA