

Beyond the greenhouse: coupling environmental and salt stress response reveals unexpected global transcriptional regulatory networks in *Salicornia bigelovii*

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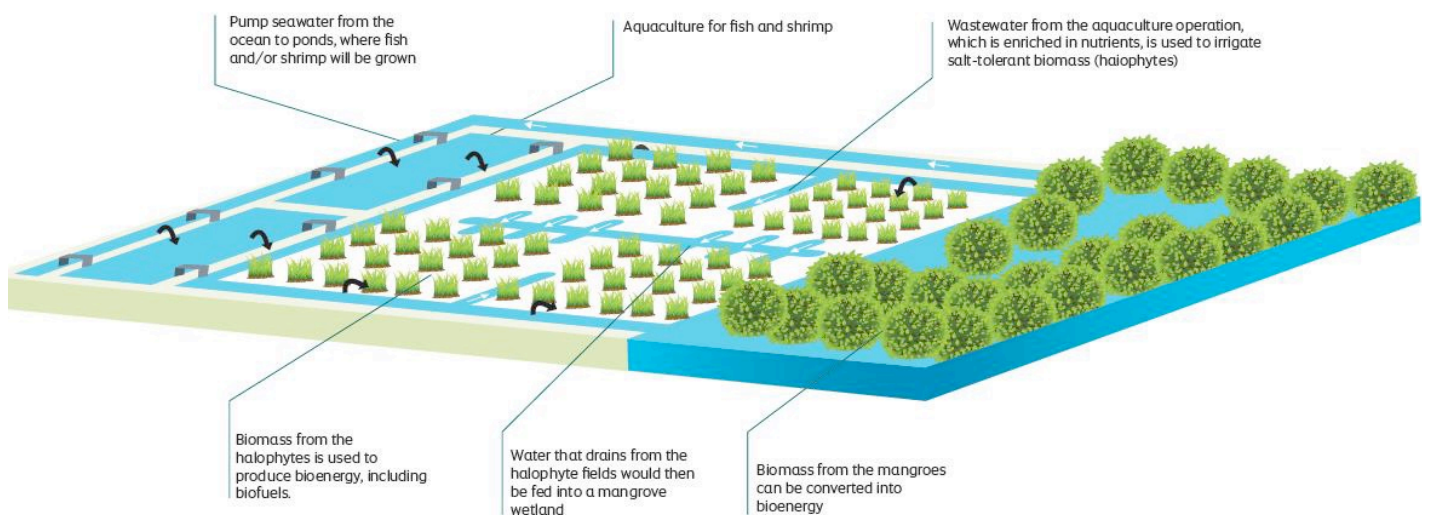


Figure S1. Schematic diagram of the SEAS pilot facility at Masdar Campus, Khalifa University. The pilot facility combines aquaculture, halo-agriculture, and mangrove silviculture for the production of sustainable biofuels for aviation and other high value byproducts such as seafood and animal fodder.



Figure S2. Image showing the different tissues used in the *S. bigelovii* transcriptome analysis. The *S. bigelovii* plant roots extend 20-35 cm into the soil, shoot height ranges from 9-60 cm, flowers are 0.6-0.7 mm, and seeds 1-1.5 mm in length.

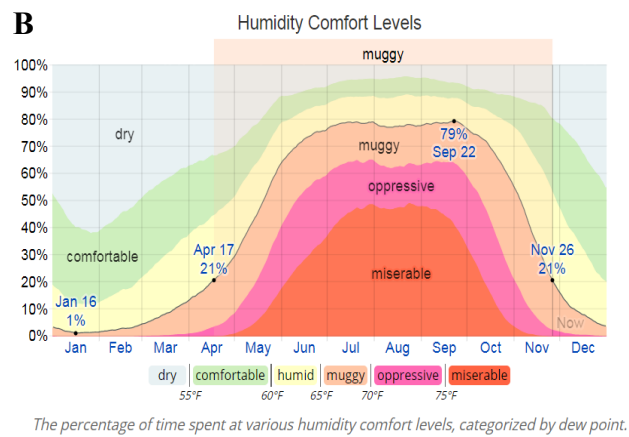
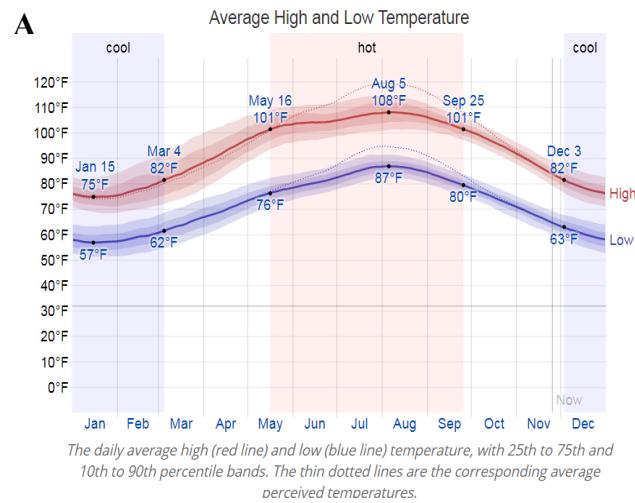


Figure S3. Meteorological data at the SEAS pilot facility as reported by the Abu Dhabi International Airport (24°25'59"N 54°39'04"E). **(A)** Graph represents the average monthly high (red line) and low (blue line) temperatures. **(B)** Image represents the monthly relative humidity levels with average time spent at various comfort levels.

Table S1. Salinity and ion concentration of the effluent water in the Field 1 of SEAS pilot facility measured between March and August 2017.

Ions	March (g L⁻¹)	April (g L⁻¹)	May (g L⁻¹)	June (g L⁻¹)	July (g L⁻¹)	August (g L⁻¹)	Average (g L⁻¹)
Na	11.77	14.57	14.57	16.24	16.63	16.97	15.12 ±1.9
Cl	18.79	20.47	19.47	21.98	21.77	22.00	20.74 ±1.3
Mg	1.16	1.24	1.24	1.35	1.35	1.42	1.29 ±0.09
Ca	0.65	0.70	0.70	0.73	0.73	0.83	0.72 ±0.06
K	0.53	0.52	0.52	0.54	0.54	0.66	0.55 ±0.05
Br	0.06	0.06	0.06	0.07	0.07	0.09	0.07 ±0.01
SO4	0.31	0.32	0.32	0.38	0.38	0.39	0.35 ±0.03
NO2	0.00	0.00	0.00	0.01	0.01	0.01	0.01 ±0.02
Water Salinity	34.57 ±0.76	38.59 ±0.15	36.21 ±0.79	41.45 ±0.83	41.74 ±0.75	42.56 ±1.1	

Table S2. Primer sense and anti-sense primer sequences used in the qRT-PCR assay for validation of differential expression of specific genes.

Transcript ID	Sequence(5'to3')	Reverse	Description
TRINITY_DN119119	CGAACCTTCGAAGATGGAGA	CTTATTTTCGTGTGCCGGTTT	<i>Beta vulgaris</i> subsp. <i>vulgaris</i> probable cation transporter HKT6
TRINITY_DN220726	CGAACCTTCGAAGATGGAGA	CTTATTTTCGTGTGCCGGTTT	<i>Salicornia brachiata</i> salt overly sensitive 1 mRNA, complete CDS
TRINITY_DN207378	TGTACCAATGGCTCCAAACA	GGGGTTGTGATTCTGCTGAT	<i>Salicornia bigelovii</i> Na ⁺ /H ⁺ antiporter (NHX1) mRNA, complete CDS
TRINITY_DN190896	CCTCTCTCCTTGGCTTCCT	ACTTTGGTGAGGTTGGTGCT	<i>Chenopodium quinoa</i> abscisic stress-ripening protein 3-like, mRNA
TRINITY_DN98123	CCCCTCCACAGTGTTCCTTA	ACAAACCAAGCCACACAACA	<i>Beta vulgaris</i> subsp. <i>vulgaris</i> probable aquaporin NIP 5, mRNA
TRINITY_DN231325	AGCACCAGCTTCTGGACCTA	TTCAAAAGCCATGTGCTCAG	<i>Kalidium foliatum</i> betaine aldehyde dehydrogenase protein mRNA, complete CDS
TRINITY_DN218725	CACCCCAATAACATCGGAAC	TGACGACAACGACGAAGAAG	Proline-rich protein PRCC (LOC104883603), transcript variant X2, mRNA
TRINITY_DN223373	TCGCAGCAAGAGAGAGTTCA	CGTATCCAGCTTGTTGAGCA	<i>Beta vulgaris</i> subsp. <i>vulgaris</i> proline-rich protein P5CS
TRINITY_DN206459	TGAATCATCCTGTGCTGCTC	CTGGCTCAATCTCGTTGACA	<i>Salicornia europaea</i> vacuolar H ⁺ -pyrophosphatase mRNA, complete CDS