Table 1 Suppl. Effects of different NaCl concentrations on the fluorescence parameters of *Carex pumila* determined by the chlorophyll *a* fluorescence induction transient (OJIP) test. Columns marked with different letters indicate significant differences among different salt treatments based on least significant difference tests ($P < 0.05$).

OJIP-test	0 mM	200 mM	300 mM	400 mM	500 mM	Definitions
φP_O	0.784a	0.784a	0.775a	0.740b	0.680c	maximum quantum yield for primary photochemistry, namely F_V/F_M
φE_O	0.301a	0.288a	0.303a	0.240b	0.195c	quantum yield of the electron transport flux from Q_A to Q_B
Ψ_O	0.383a	0.367a	0.391a	0.324b	0.287c	the efficiency with which a trapped exaction can move an electron into the electron transport chain further than Q_A
DI_O/RC	0.687b	0.654b	0.683b	0.857b	1.245a	dissipation energy flux per PSII reaction center (RC) (at t = 0)
ET_O/RC	0.960a	0.872a	0.915a	0.788ab	0.735b	maximum electron transport flux (further than Q_A^-) per PSII reaction center (RC) (at t = 0)
TR_O/CS_O	0.721a	0.758a	0.747a	0.743a	0.680b	phenomenological fluxes for trapping per cross section, approximated by F_M
DI_O/CS_O	0.199c	0.209c	0.218c	0.261b	0.325a	dissipation per cross section, approximated by F_M
PI_{ABS}	0.726a	0.698a	0.732a	0.421b	0.242c	performance index on absorption basis
PI_{CS}	0.667a	0.675a	0.706a	0.421b	0.236c	performance index on cross section basis (at t = 0)

Table 2 Suppl. Changes in metabolites in *Carex pumila* grown under different concentrations of NaCl for 60 h. Means ± SDs, $n = 3$ independent experiments. Columns marked with different letters indicate significant differences based on the least significant difference tests ($P < 0.05$). nd - not detected.

Category	Metabolites	0 mM NaCl	300 mM NaCl	500 mM NaCl
Organic acids	itaconic acid	nd	0.0114±0.0015a	0.0143±0.0033a
	benzoic acid	nd	0.0274±0.0034a	0.0239±0.0001a
	fumaric acid	nd	0.0260±0.0005b	0.0361±0.0036a
	galactaric acid	0.0769±0.0296b	0.0596±0.0132b	0.1509±0.0161a
	gluconic acid	0.0931±0.0125b	0.1071±0.0049b	0.2462±0.0286a
	glutaric acid	0.1165±0.0042b	0.1349±0.0001b	0.1876±0.0239a
	glyceric acid	nd	0.0673±0.0109a	0.0559±0.0145a
	malic acid	2.1335±0.1628b	3.4187±0.0271ab	4.4653±0.9365a
	malonic acid	0.2524±0.0180b	0.2328±0.0116b	0.3276±0.0242a
	succinic acid	0.0694±0.0065a	0.0817±0.0180a	0.0988±0.0168a
	hexacosanoic acid	0.4696±0.0328a	0.3491±0.1027b	0.2135±0.0132b
	hexadecanoic acid	0.5000±0.1380b	1.6840±0.5435a	0.3738±0.0253b
	hydroxycarbamic acid	0.2484±0.0101a	0.1926±0.0723ab	0.1310±0.0545b
	octadecanoic acid	0.4765±0.0083a	0.2647±0.0242b	0.2722±0.0568b
	phosphoric acid	5.8462±0.4352a	4.0546±0.4631b	4.0222±0.2162b
	propanoic acid	0.2000±0.0031a	0.0127±0.0004b	nd
Sugar alcohols	galactinol	0.0121±0.0022b	0.0140±0.0013b	0.2815±0.2133a
	glycerol	nd	0.1981±0.0063b	0.2603±0.0358a
	myo-inositol	0.0934±0.0062b	0.1292±0.0103b	0.2679±0.0347a
Sugars	fructose	0.2625±0.5922b	0.5113±0.2831b	1.9994±0.3762a
	galactopyranose	nd	0.0499±0.0044a	0.0309±0.0113a
	galactose	nd	0.2885±0.1428a	0.0826±0.0425a
	glucopyranose	nd	0.1259±0.0253a	0.0325±0.0026a
	glucose	0.5166±0.0644a	0.0213±0.0008b	0.0289±0.0015b
	mannose	nd	0.0137±0.0016b	2.6077±0.4275a
	sucrose	18.9574±2.2819ab	18.2324±0.1257b	25.6857±4.9571a
	mannobiose	nd	0.0564±0.0151a	0.0746±0.0119a
	allose	nd	1.5551±0.8571a	0.7036±0.1102a
Amino acids	alanine	0.1345±0.2089b	0.1916±0.0270b	0.2909±0.0223a
	asparagine	0.1058±0.0392c	0.4021±0.0556b	1.7143±0.5081a
	aspartic acid	0.0880±0.0209b	0.1015±0.0134b	0.7787±0.2121a
	glycine	nd	0.0676±0.0212a	0.0921±0.0197a
	isoleucine	nd	0.0358±0.0042b	0.2043±0.0655a
	proline	0.2530±0.0234b	0.3325±0.0636b	1.4830±0.1732a
	serine	0.0962±0.0135c	0.2141±0.0078b	0.6050±0.0130a
	threonine	0.0437±0.0016b	0.1230±0.0177b	0.6927±0.0834a
	valine	nd	0.1296±0.0088b	0.5322±0.0812a
Amines	ethanolamine	0.0891±0.0227a	0.0763±0.0181a	0.0351±0.0059b
	hydroxylamine	0.1567±0.0048a	0.0665±0.0062b	0.0369±0.0098c

Table 3 Suppl. The total metabolites of each group under salt stress and its major metabolic pathway. Means ± SDs, n = 3. Columns marked with different letters indicate significant differences based on the least significant difference tests (P < 0.05).

Metabolite		0 mM NaCl	300 mM NaCl	500 mM NaCl	Main pathway
Organic acids	A	1.2601±0.0991a	1.0930±0.1304ab	0.8355±0.0579b	TCA cycle
	B	0.2741±0.0190b	0.4167±0.0030ab	0.5607±0.1051a	fatty acid metabolism
	total	0.6439±0.0313a	0.6703±0.0480a	0.6637±0.0654a	–
Sugar alcohols		0.0352±0.0020b	0.1139±0.0022b	0.2699±0.0921a	galactose metabolism
Sugars		2.3041±0.3366b	2.3172±0.1540b	3.4553±0.5840a	sucrose, starch, and galactose metabolism
Amino acids		0.0801±0.0048b	0.1775±0.0200b	0.7104±0.1231a	amino acid metabolism and synthesis
Amines		0.1229±0.0128a	0.0714±0.0060b	0.0360±0.0078c	nitrogen metabolism

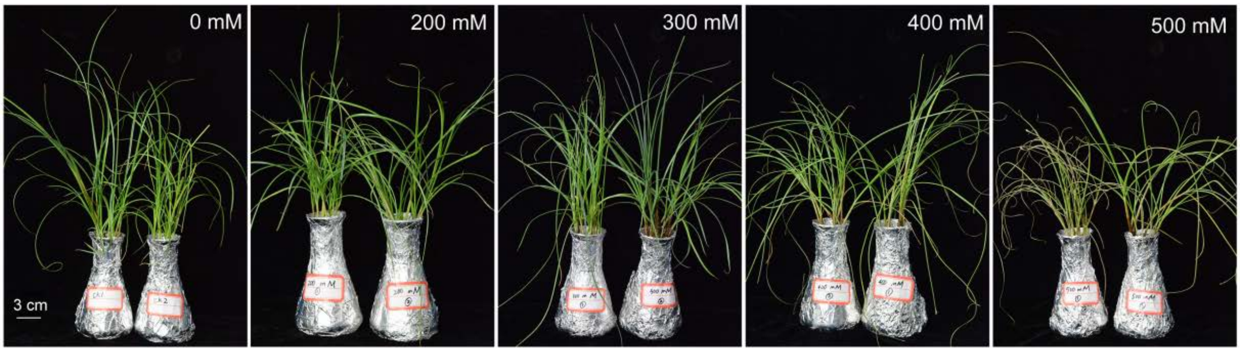

Fig. 1 Suppl. Snapshots showing the effects of salt stress on the morphology of *Carex pumila*. Plants were grown in the nutrient solution with 0, 200, 300, 400, and 500 mM NaCl for 60 h.

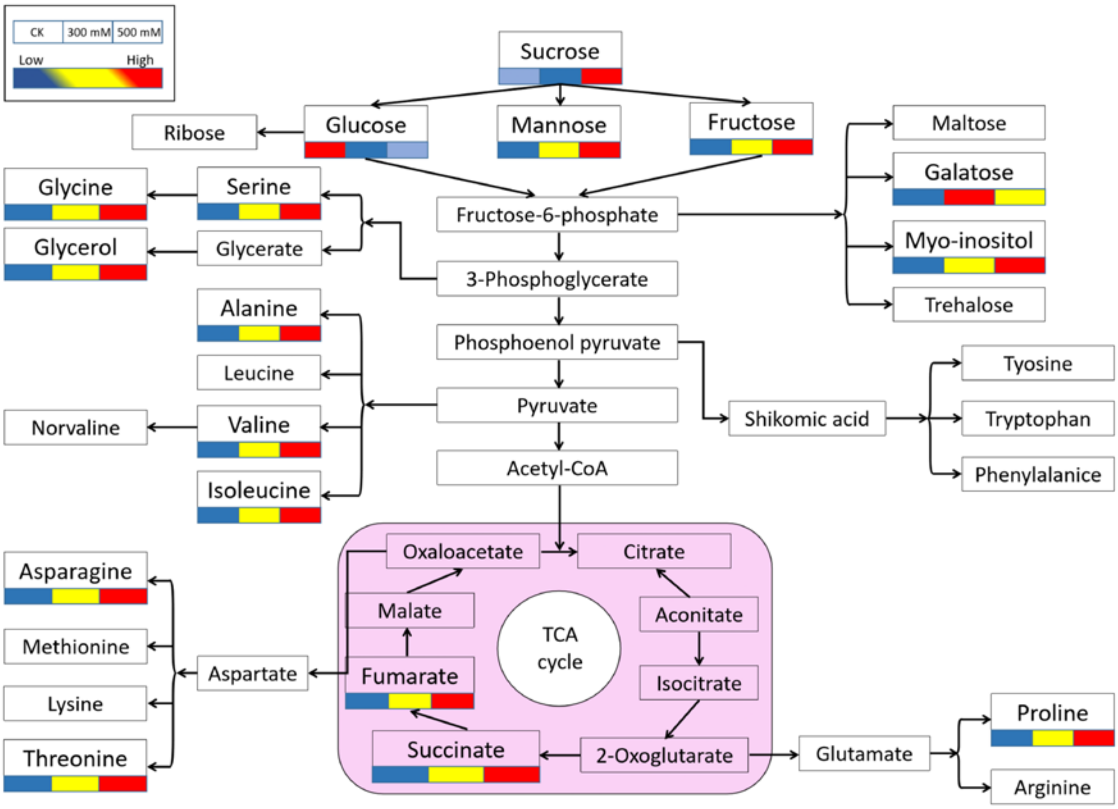

Fig. 2 Suppl. A flow chart showing the effects of salt stress on 17 metabolites from 39 assayed metabolites that were involved in the carbon metabolic pathway. The metabolic status of the control group (0 mM NaCl), 300 mM, and 500 mM NaCl were observed from left to right and compared to their control ($P < 0.05$) The color of the *box* changes from *blue to red* to indicate content from low to high.