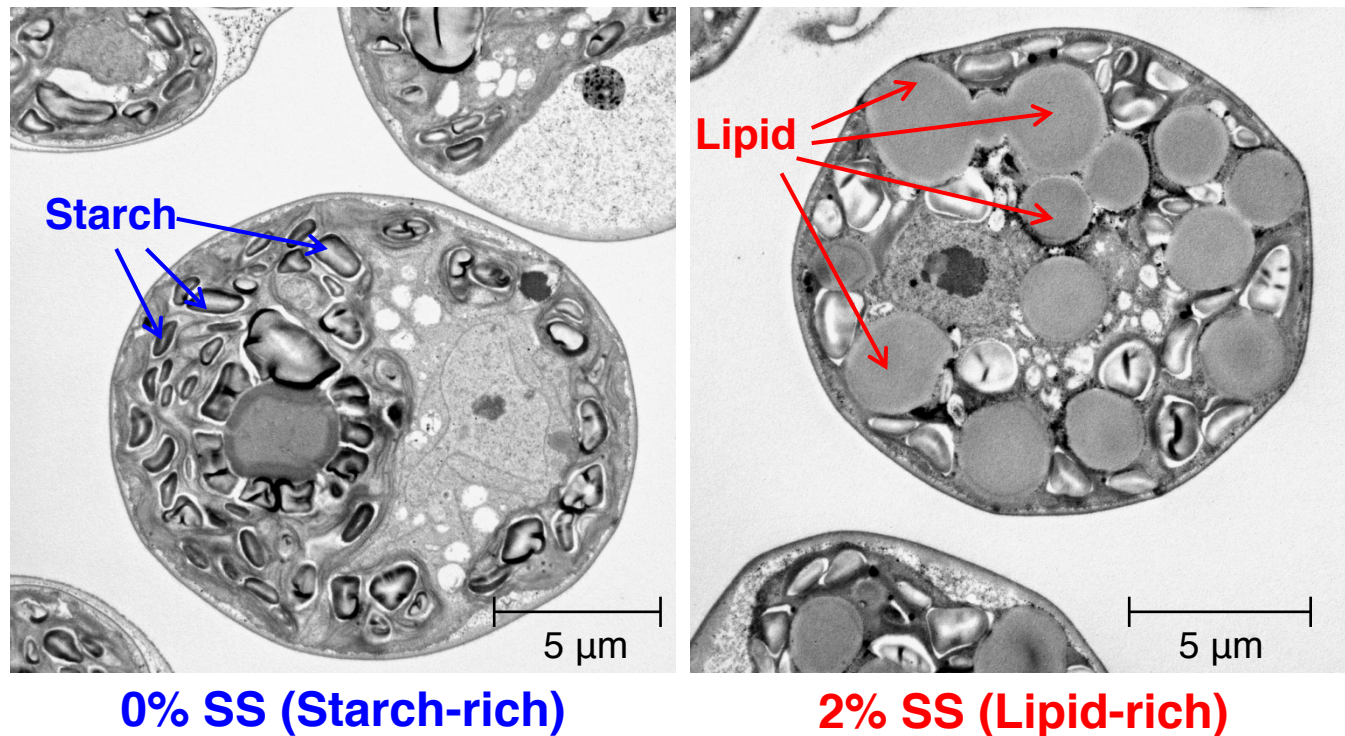


Dynamic metabolic profiling together with transcription analysis reveals salinity-induced starch-to-lipid biosynthesis in alga *Chlamydomonas* sp. JSC4

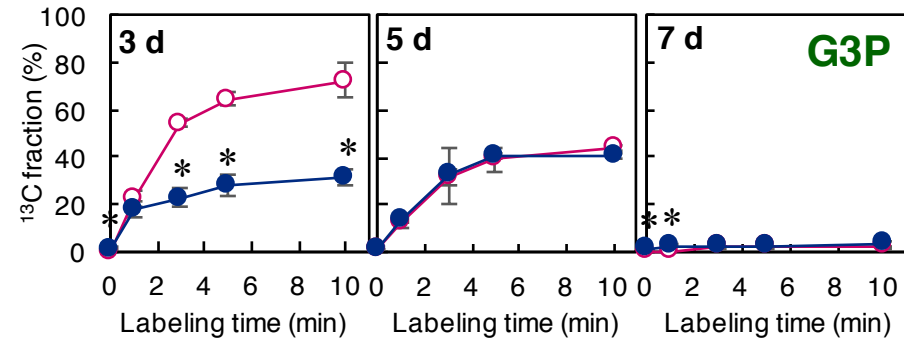
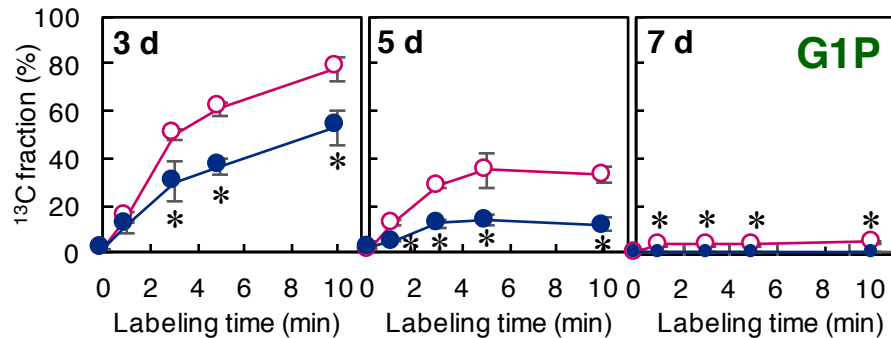
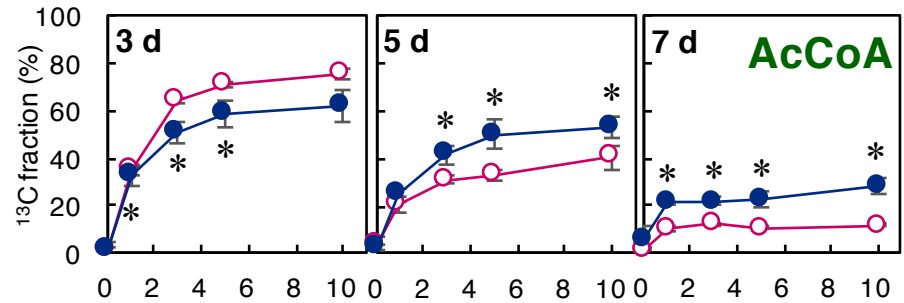
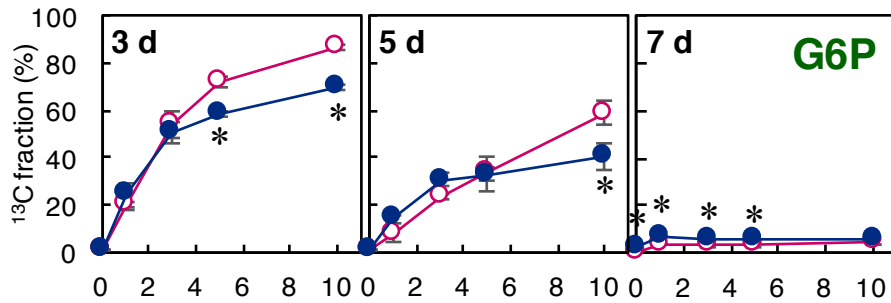
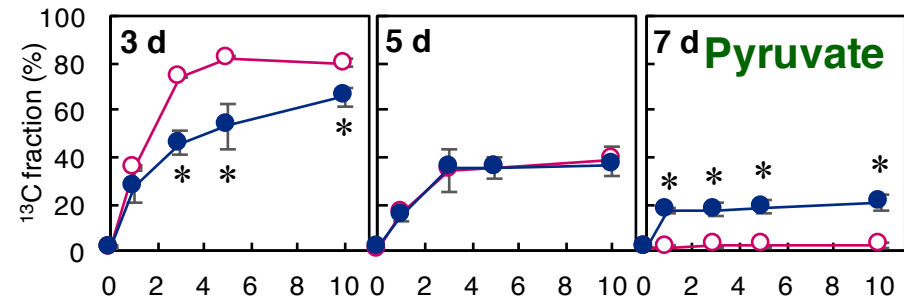
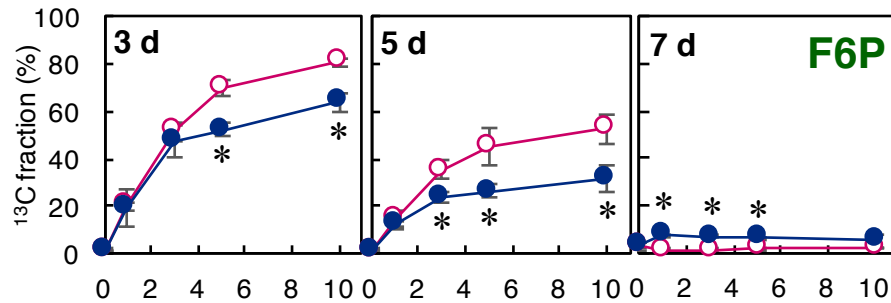
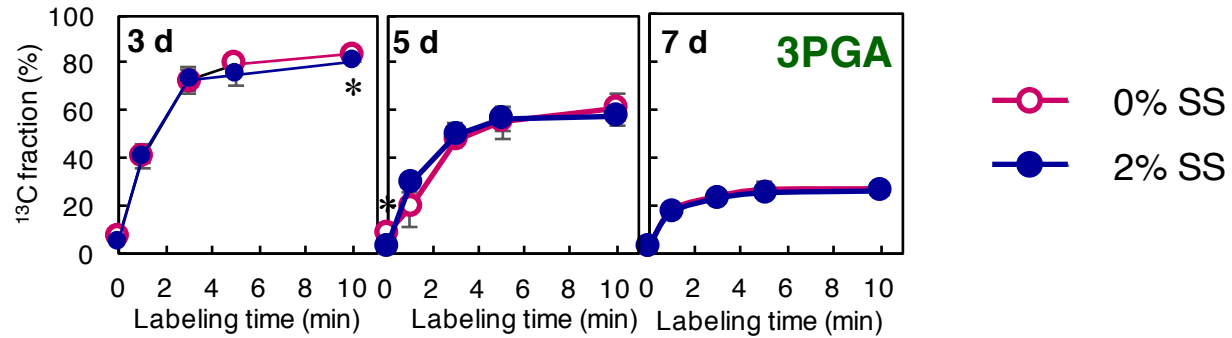
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Supplementary Figure S1. TEM micrographs of JSC4 cultivated under 0% and 2% SS.



Supplementary Figure S2. Time course of ^{13}C fraction under different SS concentrations (0% and 2%) at Days 3, 5, and 7.

○ (pink) and ● (blue) indicate 0% SS and 2% SS, respectively. Error bars indicate the SD of three replicate experiments (*: $p < 0.05$ by Student's t-test).



Supplementary Table S1. Comparison of lipid productivity of *Chlamydomonas* sp. JSC4 with those of other green algae, as reported in the literature.

Strain	Biomass productivity (mg L ⁻¹ d ⁻¹)	Lipid productivity (mg L ⁻¹ d ⁻¹)	Reference
<i>Nannochloropsis</i> sp. F&M-M24	180	55	1
<i>Dunaliella tertiolecta</i> ATCC30929	100	70	2
<i>Isochrysis zhangjiangensis</i>	345	141	3
<i>Nannochloropsis oculata</i> NCTU-3	480	142	4
<i>Chlorella vulgaris</i>	358	167	5
<i>Chlorella sorokiniana</i>	246	189	6
<i>Chlamydomonas</i> sp. JSC4 (1% SS)	775	358	This study

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Supplementary Table S2.

Sequences of primers used for qPCR.

Primer name	Definition	Primer sequence (5' to 3')
RPL32 F	Ribosomal protein L32	acaagaagactcgccacacg
RPL32 R		cgttgatgacgcagatgtg
PGI F	Phosphoglucose isomerase	cacgaccatacaccccaatc
PGI R		gccttgttccacaccatcc
PGM F	Phosphoglucomutase	tcagccgctacgactacgag
PGM R		cggacagggcggaaaatg
AGPP F	ADP-glucose phosphorylase	aactccacctgctcaacc
AGPP R		ctcgatggccctgttctg
SP1 F	Starch phosphorylase 1	tctacttctgcccgactacaac
SP1 R		gaacacgaacacctcctccac
SP2 F	Starch phosphorylase 2	aacaccaccacctcaacaac
SP2 R		gatttcatgcaccaagccatac
AMY1 F	α -Amylase 1	tcagcgtcggaaatcaaacc
AMY1 R		taaacacctccgtccatctcacc
AMY2 F	α -Amylase 2	catcaagatcaacggcaagg
AMY2 R		cgcaacagcacatacacagg
PFOR F	Pyruvate ferredoxin oxidoreductase	cgtggcgggtgttgaga
PFOR R		ggtgttgctggcgatga
PDH F	Pyruvate dehydrogenase	acctgccccttatcgtcacc
PDH R		gtggttcgctcttgcgtacc
PDC F	Pyruvate decarboxylase	acgcgtatgggtaagatacag
PDC R		atagcgcgagaaaaccgttg
ALDH F	Aldehyde dehydrogenase	tcgtgcacgagtctgtatacag
ALDH R		ttgttgactggcgcgtgc
ACS1 F	AcCoA synthetase 1	caccctgcctcaatagtgtcc
ACS1 R		atggctcggcttcttctcc
ACS2 F	AcCoA synthetase 2	cccgtcaacatccagttcttc
ACS2 R		tctggcggatgtgattgtg
ACS3 F	AcCoA synthetase 3	ctggagcaagccatatacaac
ACS3 R		ccctcccagtagaacgcaac
GPDH F	Glycerol 3-phosphate dehydrogenase	aacacgctgcacgaaaacac
GPDH R		ttgctgacgcagatgatgg
BCCP F	Biotin carboxyl carrier protein	aaatgcagctcaacctgacg
BCCP R		cgtcgaacgccatcatgttc
BC F	Biotin carboxylase	tggagatgaacaccgcacc
BC R		acacgatgtctctctgcttg
α CT F	carboxyl transferase α subunit	aacctcatcatgcagaacgc
α CT R		tccatgacgccgaacttgac
β CT F	carboxyl transferase β subunit	caagatggccaaggctgttg
β CT R		ttgcagccaagcagatgtg