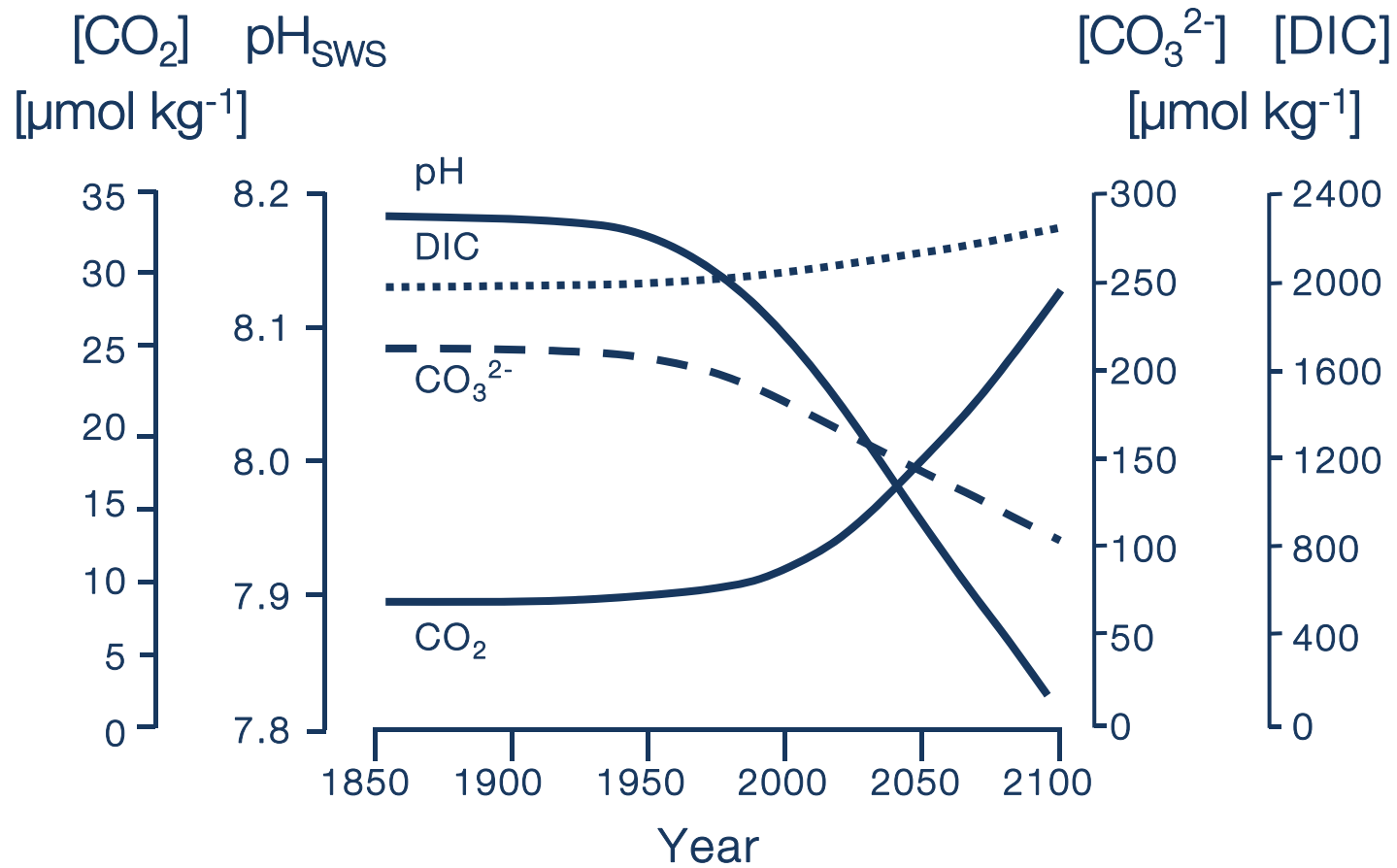# Transcriptomic responses of *Emiliania huxleyi* to Ocean Acidification

Sebastian D. Rokitta, Uwe John and Björn Rost

Ocean Acidifcation

After Wolf-Gladrow et al. (1999)

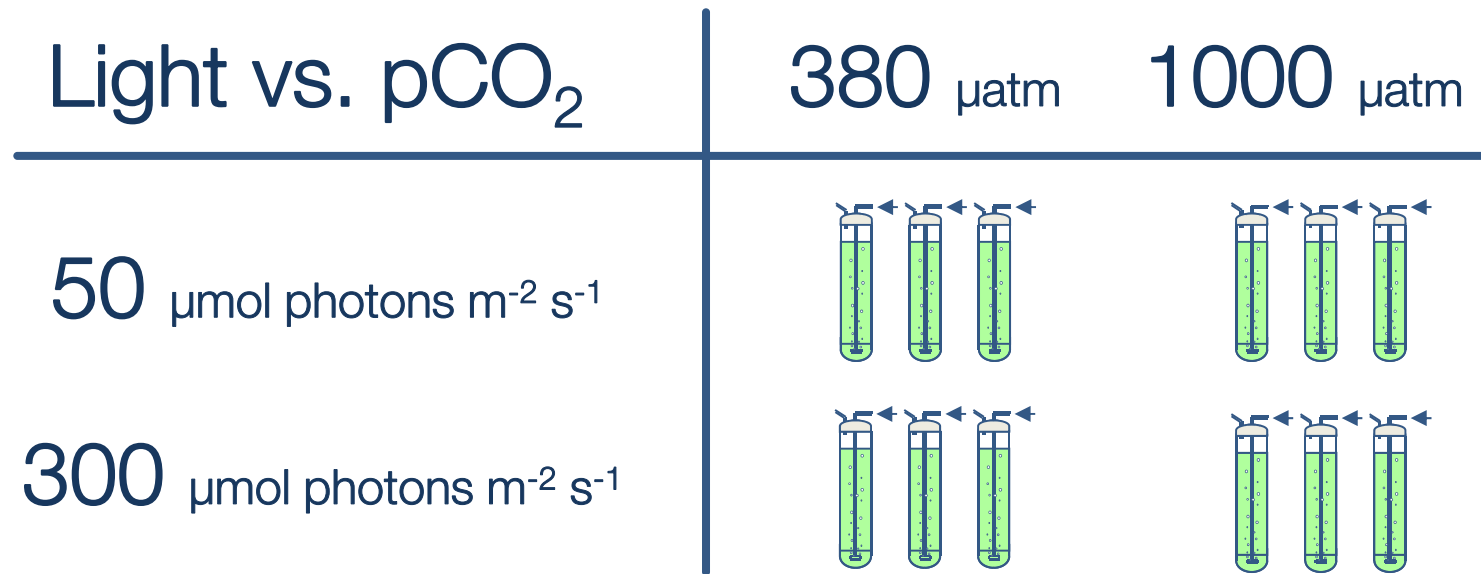# Coccolithophores

Photo: NASA, PML

Biological carbon pumps

OA-responses in *E. huxleyi*

Modified from Hoppe et al. (2011)

Energization?

The matrix approach

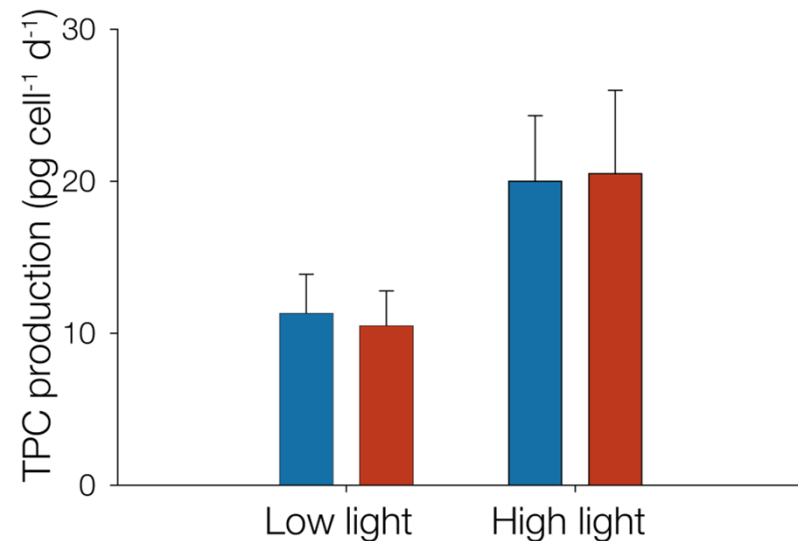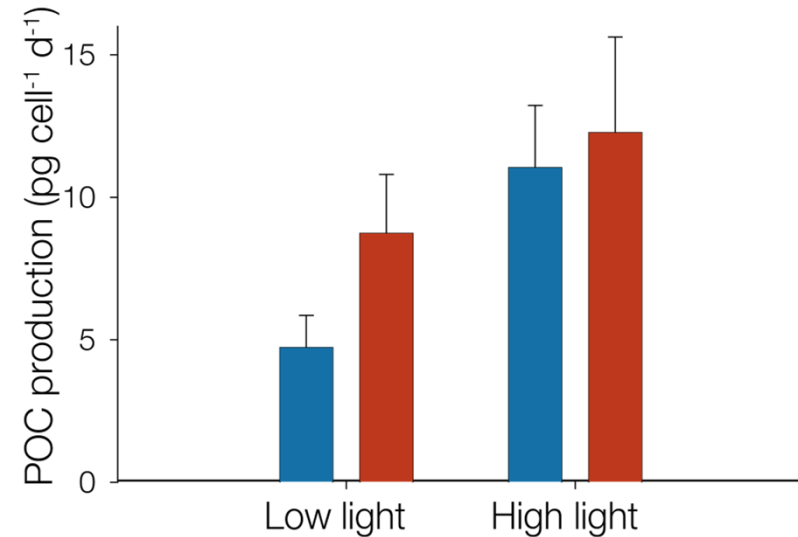| Light vs. pCO_2	380 µatm	1000 µatm
50 µmol photons m^{-2} s^{-1}		
300 µmol photons m^{-2} s^{-1}		

- Acclimation data (µ, POC, PIC)
- Physiology (C_i acquisition, light reactions)
- Transcriptomics (gene expression)

Phenomenology
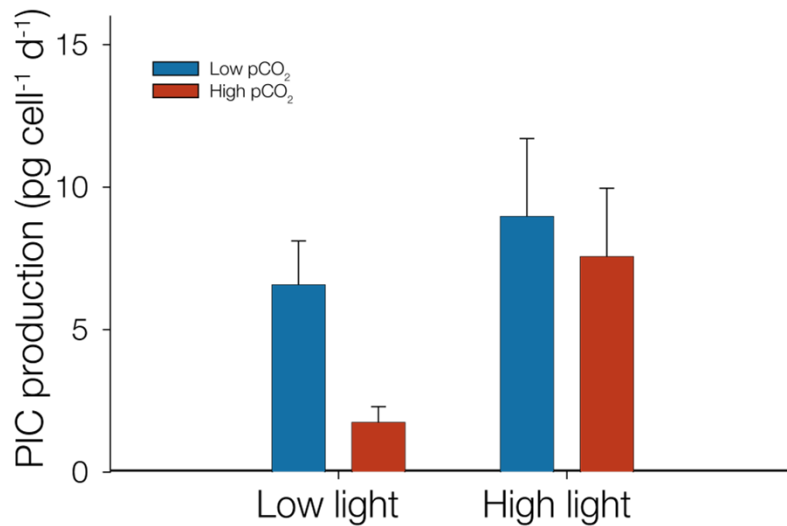
- PIC production drops
  (especially under low light!)

- POC production is boosted
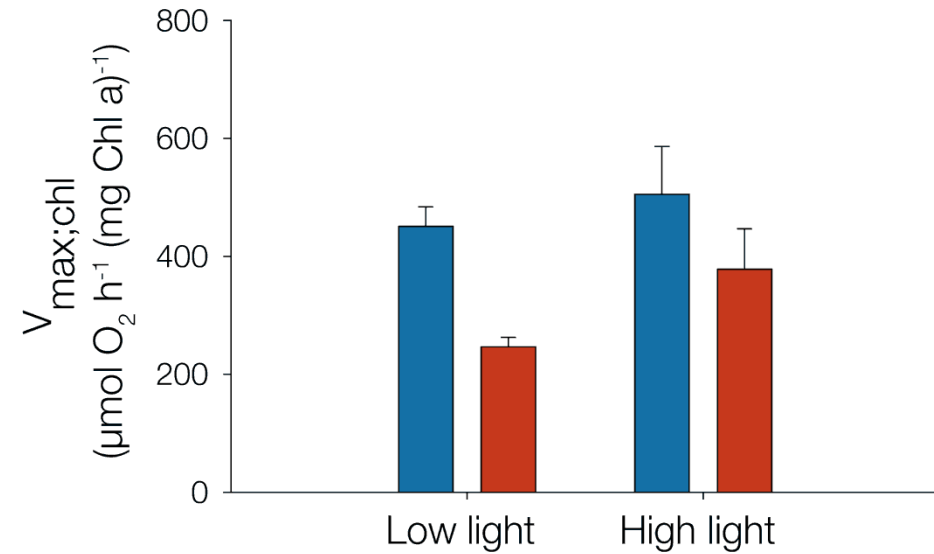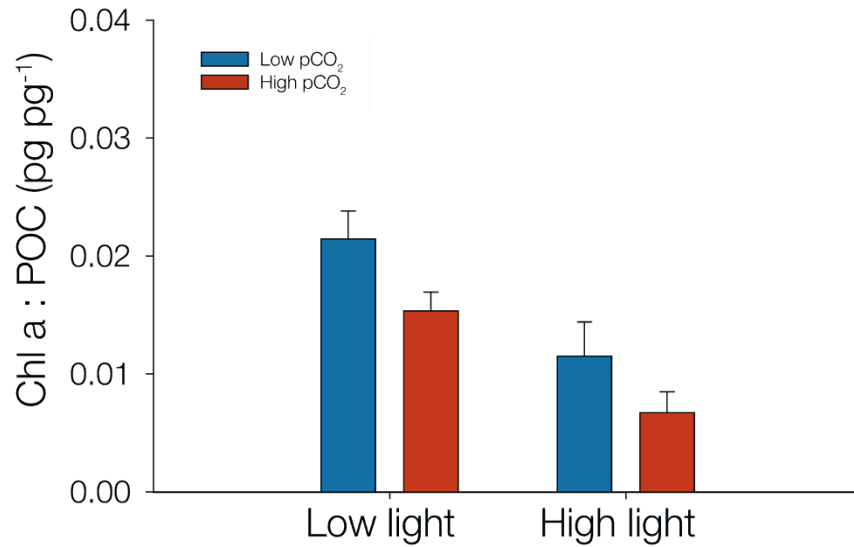 (especially under low light!)

- TPC production is insensitive

Physiology

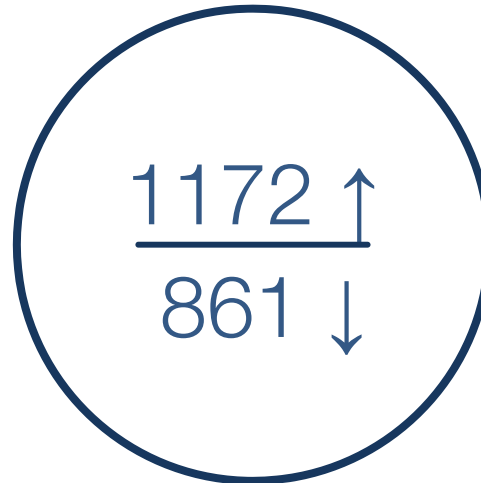- More POC despite less pigmentation and O_2 evolution

  → Improved energy efficiency under OA

Gene expression?
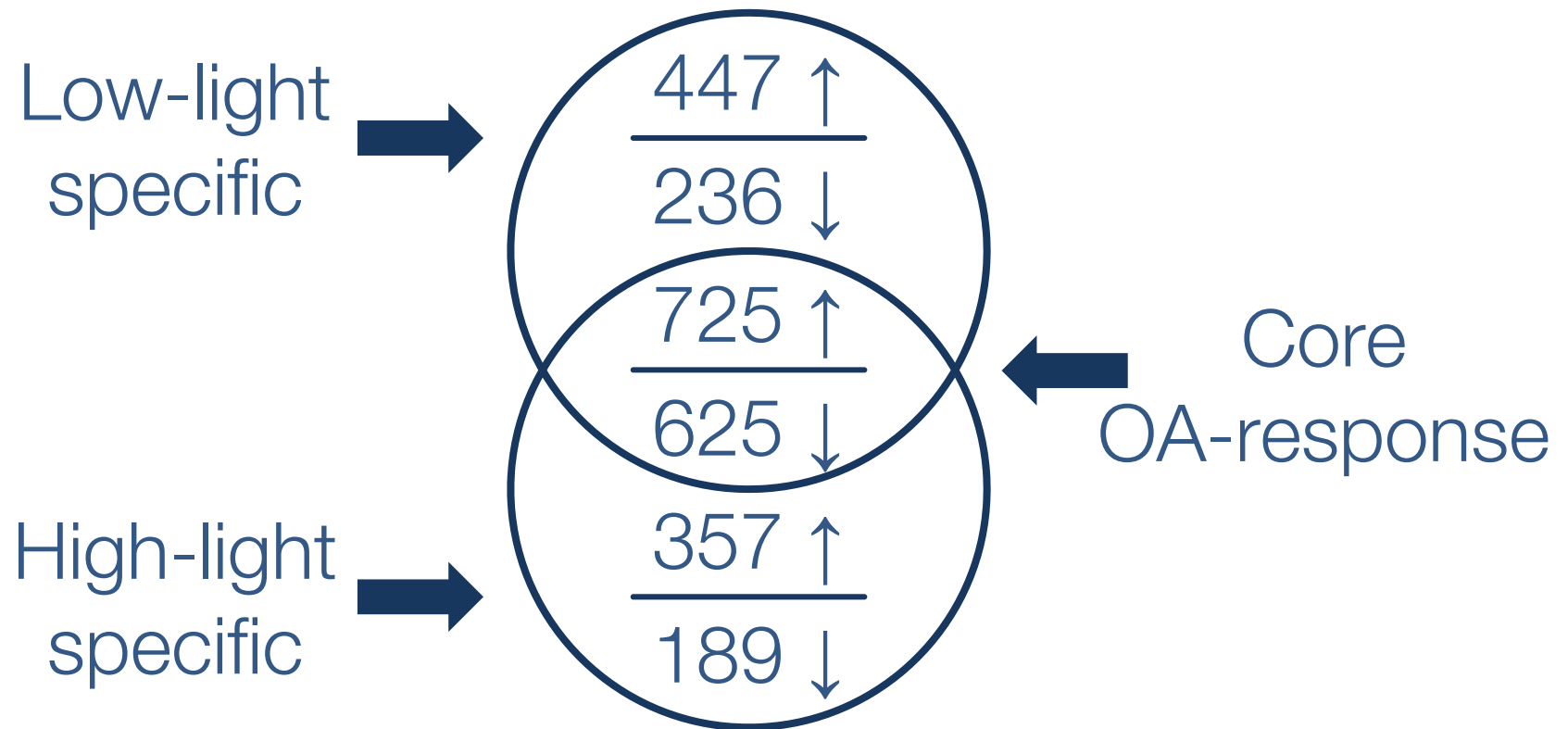
Transcriptomics

OA responsive genes

Low-light
acclimation

1172 ↑
861 ↓

High-light
acclimation

1082↑
814 ↓

Transcriptomics

Low-light specific →

447 ↑ / 236 ↓

725 ↑ / 625 ↓ ← Core OA-response

High-light specific →

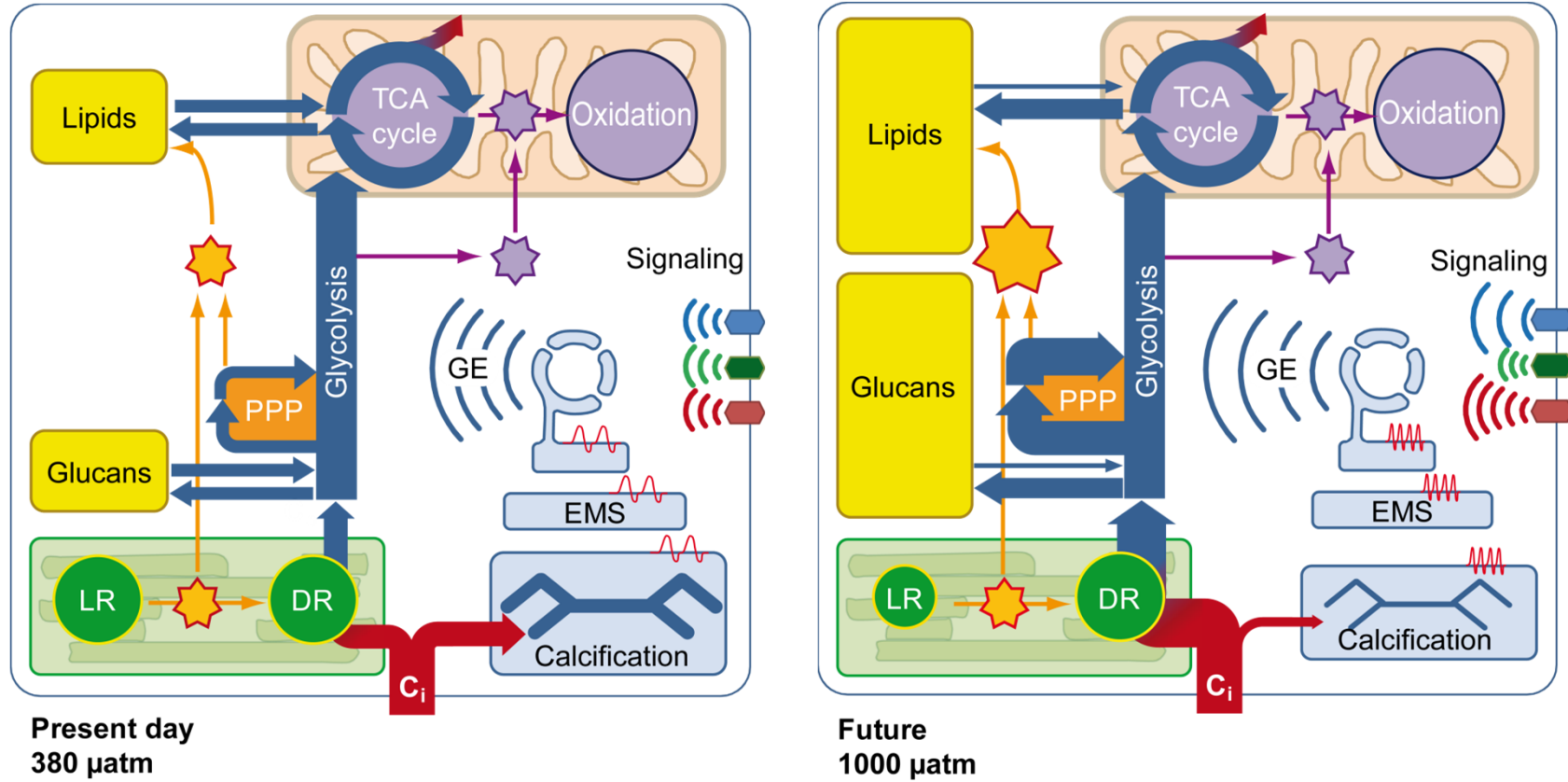357 ↑ / 189 ↓

Transcriptomics

Carbon metabolism
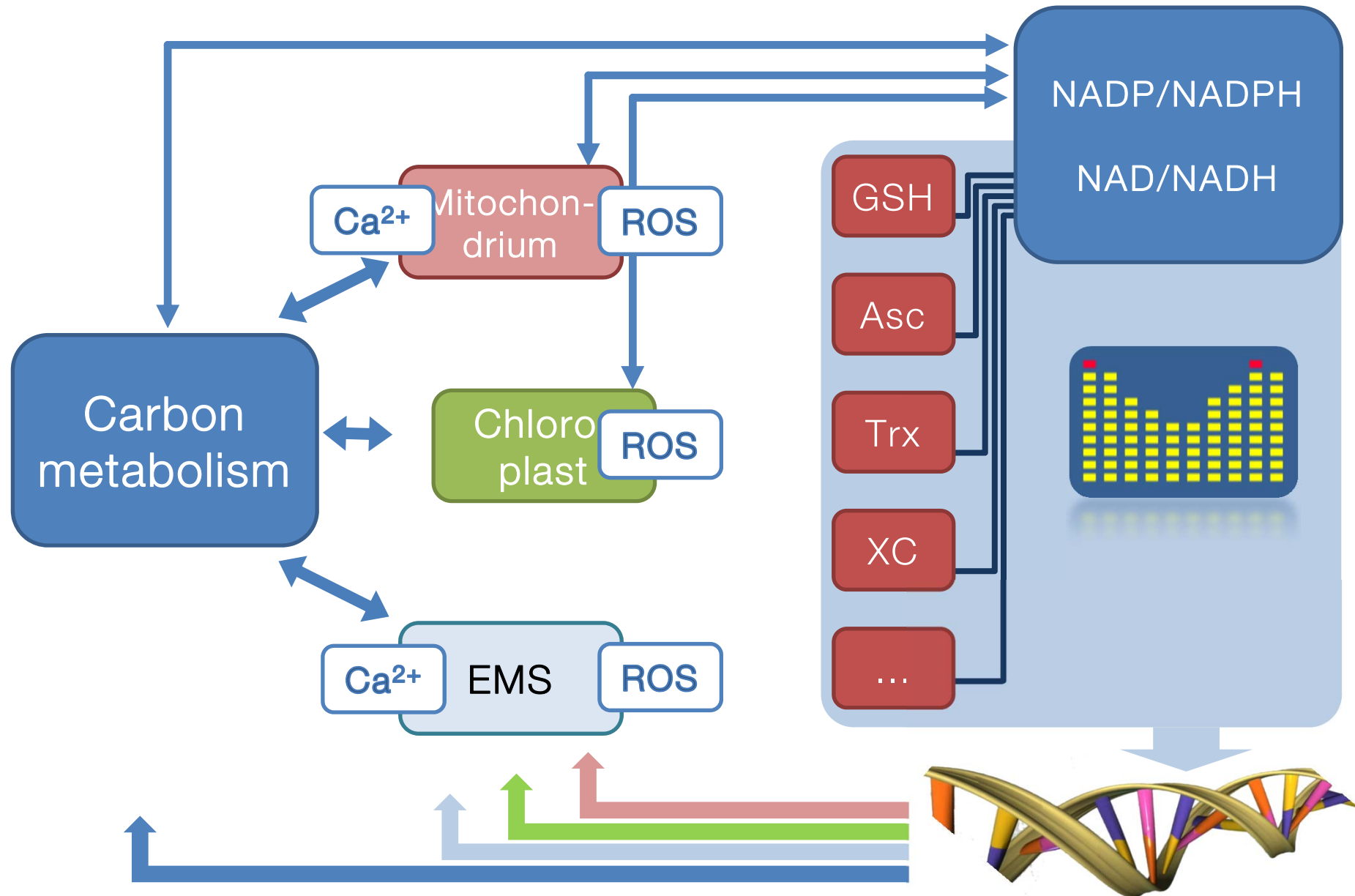
Light physiology

Signalling

Ion fluxes

Pentose phosphate pathway ↑ Glycolysis ↓ Fatty Acid & Glucan anabolism↑	Regulation of C fluxes ↑	Organellar shuttling ↑
Energy dissipation ↑	Energy dissipation ↑	
Lipid and IP$_3$ signaling ↑		
Membrane potentials ↑		

OA re-wires carbon fluxes

Present day
380 µatm

Future
1000 µatm

NADPH   NADH

OA affects the redox hub

Conclusions

- OA causes a shunting of carbon from calcification towards biomass production

- OA-Responses are modulated by energy availability and typically attenuated by high light

- OA affects cellular signaling and the redox hub and thereby re-wires carbon flux networks