**SMALP Conference** 

**October 1, 2021** 

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High resolution CryoEM structures of the E. coli respiratory O<sub>2</sub> reductase cytoch in SMALPS and in MSP nanodiscs.

See Li et al PNAS(2021)118 No. 34

# Thanks to ...

ryoEM SMALPS	Nanjing University of Chinese Medicine, Nanjing, China Jiao Li, Yanmei Luo, Bin Liu, Jiapeng Zhu
cryoEM SMALPS	Yale University, New Haven Long Han, Kai Zhang
cryoEM MSP nanodiscs	Columbia University, New York Francesca Vallese, Oliver Clarke
University of Illinois at Urbana–Champaign   Mol. Dynamics Chun Kit Chan, Emad Tajkhorshid	
Protein characterization	Sangjin Hong, Ziqiao Ding, Sylvia K. Choi

An essential role of the aerobic respiratory chain is to generate a proton electrochemical gradient  $(\Delta \Psi + \Delta pH)$ across the membrane to drive ATP synthesis and active transport processes



#### The mitochondrial respiratory chain has one oxygen reductase



#### The *E. coli* respiratory chain has 3 different oxygen reductases and no cytochrome c



## What is common to all heme-copper oxygen reductases?

- 1. Homologous subunit I.
- 2. One low spin heme
- 3. High spin heme-Cu binuclear site
- 4. Six histidine ligands for metals





# All quinol oxidases have a unique "extra" transmembrane helix at the N-terminus of subunit I compared to the cytochrome c oxidases.



JBC(1990) 265, 1185-1192

#### **Preparation of cytochrome bo<sub>3</sub>**

Cyt bo<sub>3</sub> has a natural affinity for the "his-tag" Ni-NTA column and has been purified in many laboratories by accident. This was the case in the current work.

1. Laboratory of Jiapeng Zhu: solubilized *E. coli* membranes with 1% SMA 3:1 styrene/maleic acid 3000HNA free sample from Cray Valley/Total Petroleum Chemicals and Refinery

2. Laboratory of Oliver Clarke: solubilized *E. coli* membranes with 1% DDM (dodecylmaltoside)

**Reconstituted into Membrane Scaffold Protein (1D1) nanodiscs in POPG** 

POPG: (C16)(C18:1)-phosphatidylglycerol

The two protein structures are virtually identical

cyt bo<sub>3</sub>-SMALP: 2.55 Å

cyt bo<sub>3</sub>-MSP/POPG nanodiscs: 2.19 Å

### cryoEM of cyt bo<sub>3</sub>-SMALP

#### 563,000 particles were used to obtain the class averages shown below



# Local resolution map of cyt bo<sub>3</sub>-SMALP

## average resolution 2.55 Å





#### Four subunits surrounded by native phospholipids



## The four subunits of cyt bo<sub>3</sub>



5 native phospholipids are well resolved in the cyt bo<sub>3</sub>-SMALP

#### all are di-stearoyl-PE

2 are located in a groove in subunit I between TM0, TM1 and TM2



3 are located in a crevice between subunits I and III

## Cyt bo<sub>3</sub>-SMALP has one ubiquinone-8 molecule sandwiched between TM0, TM1 and TM2 in subunit I



# Surface representation of cyt bo<sub>3</sub>-SMALP shows the hydrophobic tail of ubiquinone-8 held against TM1 and TM2 by the "extra" TM0



#### **Ubiquinone-8 headgroup is hydrogen bonded to Asp75, Arg71 and His98**



His98 has two conformations conf. 1: hydrogen bonded to ubiquinone

conf. 2: hydrogen bonded to Glu14

Likely functional role of His98 is to help shuttle protons from quinol to the periplasm upon oxidation

 $QH_2 \stackrel{e^{-1}}{\searrow} Q^{-\bullet} \stackrel{e^{-1}}{\rightarrow} Q$ 

## Headgroup of ubiquinone-8 is 14 Å from heme b



#### **B-factor distribution of cyt bo<sub>3</sub> in the MSP nanodiscs indicates TM0 is dynamic**



Consistent with the need for turnover of ubiquinol-8 every few milliseconds.

# Thanks

# Questions