The CopC Protein from *Pseudomonas syringae*: Intermolecular Transfer of Copper Occurs from Both the Copper(I) and Copper(II) Sites

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The CopC protein from *Pseudomonas syringae* pathovar *tomato* is expressed as one of four proteins encoded by the operon CopABCD that is responsible for copper resistance.[1] It is a small soluble molecule (10.5 kDa) with a β-barrel structure and features two distinct copper binding sites (see Figure[2]) which are highly specific for Cu^{I} ($K_D \sim 10^{-13}$) and Cu^{II} ($K_D < 10^{-15}$), respectively. These dissociation constants were estimated via ligand competition experiments monitored by electronic spectral and fluorescence probes.

The chemistries of the two copper sites are inter-dependent. When the Cu^{II} site is empty, the Cu^{I} ion is oxidized by air but when both sites are occupied, the molecule is stable in air. The availability of an unoccupied site of higher affinity induces intermolecular transfer of *either* Cu^{I} or Cu^{II} while maintaining free copper ion concentrations in solution at sub-*pico* molar levels.

This intriguing copper chemistry is consistent with the proposed role of CopC as a copper carrier in the oxidizing periplasmic space. These properties would allow it to exchange *either* Cu^{I} or Cu^{II} with its putative partners CopA, CopB and CopD, contrasting with the role of the Cu^{I} (only) chaperones found in the reducing cytoplasm.

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