NMR spectroscopy reveals functional diversity among a family of *Geobacter* multiheme cytochromes

L. Morgado[1], M. Bruix[2], Y.Y. Londer[3], P.R. Pokkuluri[3], M. Schiffer[3], C.A. Salgueiro[1]

[1]Requimte-CQFB, Departamento de Química, Faculdade de Ciências e Tecnologia, Universidade Nova de Lisboa, Campus Caparica, 2829-516 Caparica, Portugal
[2] Departamento de Espectroscopía y Estructura Molecular, Instituto de Química-Física "Rocasolano", CSIC, Serrano 119, 28006 Madrid, Spain
[3] Biosciences Division, Argonne National Laboratory, Argonne, Illinois 60439, USA

Multiheme *c*-type cytochromes play a fundamental role in the metabolism of many bacteria such as *Geobacter* [1]. The close spatial proximity of the redox centers in these proteins establishes controlled electron and proton networks that drive important cellular responses. These networks can be decoded by 2D-NMR spectroscopy [2]. In this work, we describe for the first time the microscopic redox characterization of a family composed of five triheme cytochromes isolated from the same microorganism (*G. sulfurreducens*). For four proteins, partially oxidized samples were studied by mapping the individual behavior of the redox centers by 2D-NMR. The results obtained for the most abundant member of this family (PpcA) showed that it is involved in the bacterial energy transduction mechanism. Although, sequence and structurally homologous to PpcA [3], the data obtained for the other family members showed that the e^-/H^+ networks are different suggesting that their function might be different from PpcA but could be involved in complementary pathways in the *G. sulfurreducens* metabolism.

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