MS08 P01

Neutron Crystallographic studies on the *Rb.sphaeroides 2.4.1* Reaction Centre. Susana Teixeira[a,b], Trevor Forsyth[a,b], Michael Haertlein[a], Peter Timmins[a], Alistair Gardiner[c], Richard Cogdell[c], Neil Isaacs[c] [a]*Deuteration Laboratory, Institut Laue Langevin, Grenoble, France. bSchool of Physical and Geographical Sciences,Keele University, Keele, UK* [c]*Department of Chemistry, University of Glasgow, Glasgow,uk.*
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Keywords: Neutron, X-ray, Crystallography

The aim of these studies is to identify and characterise the interactions between the intra-membrane surface of an integral membrane protein and the acyl chains of neighbouring lipids. Lipids such as cardiolipin provide the immediate environment for catalisys of photosynthetic and respiratory energy transduction, by affecting the activity of a number of major integral membrane proteins [1]. Previous studies at Glasgow University determined a protocol to express, purify and crystallise the reaction center (RC) from *Rhodobacter sphaeroides 2.4.1.* [2]. The structure was obtained and a specific interaction with cardiolipin was observed. Further solvent molecules may be present but the full interpretation of the electron density maps could not be done unambiguosly. We have now obtained crystals suitable for neutron diffraction studies and have collected data on a deuterated crystal of the RC at the DB21 instrument of the ILL. The data is currently being analysed and will be compared with X-ray data collected on BM14 at the ESRF, along with a Mass Spectrometry analysis of the lipid content of the crystal.

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[2] McAuley *et al., FEBS Letters*, 2000, 467, 285-290.

MS08 P02

Crystallisation of purple bacterial LH2 antenna complexes. Aleksander W. Roszak[a], Alastair T. Gardiner[b], Mads Gabrielsen[b], June Southall[b], Neil W. Isaacs[a] and Richard J. Cogdell[b], [a]*Department of Chemistry and* [b]*Division of Biochemistry and Molecular Biology, IBLS, Glasgow Biomedical Research Centre, University of Glasgow, Glasgow G12 8TA, UK.*
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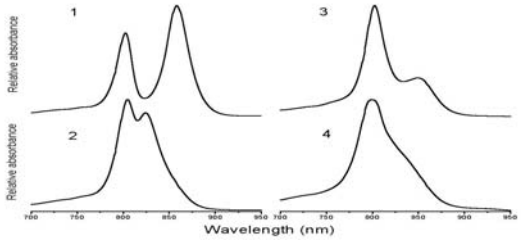
At the present time only two distinctly different light-harvesting (LH) 2 high-resolution structures are available: the complex from *Rhodopseudomonas* (*Rps*.) *acidophila* 10050 [1] and the complex from *Rhodospirillum (Rs.*) *molischianum* [2]. Both complexes are organised in a ring form made of repeating α/β-apoprotein heterodimeric units with the associated molecules of pigments, bacteriochlorophyl Bchl*a* and carotenoid, however the former one forms a nonameric ring while the latter is octameric. Depending on their growth conditions, certain species and strains of bacteria are able to produce alternative forms of LH2, which have different peptide composition and/or different symmetry (number of units), and display altered spectral (i.e. also light-harvesting) characteristics. Near infra-red (NIR) spectra shown below are for LH2 from (**1)** high-light (HL) *Rps*. *acidophila,* strain 10050, (**2)** low-light (LL) *Rps*. *acidophila,* strain 7050, (**3)** LL form of *Rps. palustris*, and (**4)** LL form of *Chromatium* (*Chr.*) *vinosum*.



3-D structure of **2** [3] compared to **1** [1] has revealed rather subtle differences in the H-bonding pattern but the differences between the HL (NIR-spectra similar to **1**) and the LL forms of LH2 from *Rps. palustris* are expected to be more dramatic, for example, the HL form is thought to be nonameric and the LL form octameric [4]. We have obtained preliminary crystals of LH2 for HL and LL forms from *Rps. palustris*, LL form from *Chr. vinosum* and HL form from *Rps. cryptolactis.* We are working towards optimisation of crystallisation conditions for these various LH2 complexes in order to determine their crystal structures and explain the observed spectral differences. Results of this work will be presented. The authors are members of the membrane protein structure initiative (MPSI), and funding of this work by the BBSRC is acknowledged.

[1] McDermott, G., *et al.* (1995) *Nature* 374, 517-521.
[2] Koepke, J., *et al.* (1996) *Structure* 4, 581-597.
[3] McLuskey, *et al.* (2001) *Biochemistry* 40, 8783-8789.
[4] Scheuring, S., *et al.* (2006) *J. Mol. Biol.* 358, 83-96.