s7.m26.o5 **High-Pressure Recrystallisation - a Route to New Polymorphs and Solvates of Small Molecules.** F.P.A. Fabbiani, D.R. Allan, S. Parsons, and C.R. Pulham, *School of Chemistry, The University of Edinburgh, King's Buildings, West Mains Road, Edinburgh, EH9 3JJ, Scotland, UK. E-mail: F.P.A.Fabbiani@ed.ac.uk*

Keywords: Polymorphs; Solvates; High Pressure

The importance of polymorphism in crystallisation processes is widely recognised and is the subject of intense academic and industrial interest. Although the use of high pressure has been shown by physicists and geoscientists to be a powerful method for preparing new polymorphs of metals, alloys, ceramics, and minerals, it is only relatively recently that high pressure has been exploited to modify intermolecular interactions in simple molecular compounds. Thus it has been shown that new polymorphs of simple molecular organic and inorganic compounds such as ketones, alcohols, and mineral acids are readily obtained by cooling the liquid compound contained within a diamond-anvil cell under conditions of high pressure. Spectroscopic and structural characterisation of these new polymorphs can then be performed *in situ.*

Whilst this technique is ideally suited for studying compounds that have normal melting points near or below ambient temperature, it is less useful for compounds with higher melting points, such as pharmaceutical compounds, pigments, or explosives. The problem is exacerbated by the generally steep increase in melting point associated with increasing pressure, with the result that thermal decomposition of the compound occurs well before the onset of melting.

We have overcome this problem by using a solvent so that higher melting compounds are effectively recrystallised from solution at elevated pressures, typically in the range 1-20 kbar. The technique has allowed us to extend greatly the range of compounds that may be studied and has been used successfully to identify and characterise new polymorphs of a range of organic compounds. The high-pressure recrystallisation technique also provides a route for the preparation and structural characterisation of new solvates of organic compounds, e.g. the 1:1 methanol solvate of paracetamol [1]. Its potential as a new method of screening pharmaceutical compounds for polymorphism and solvate formation is currently being explored and will be reported here.

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s7.m26.o6 **Chlorothalonil: Unexpected and Unpredictable Polymorphic Structures**. Maryjane Tremayne[a], Benson M Kariuki[a], Helen H Y Tsui[b], Sarah L Price[b], Julian C Cherryman[c], [a]*School of Chemistry, University of Birmingham, Edgbaston, Birmingham UK,* [b]*Centre for Theoretical and Computational Chemistry, Department of Chemistry, University College London, 20 Gordon Street, London, UK,* [c]*Avecia Limited, POBox 24, Hexagon House, Blackley, Manchester, UK. E-mail: m.tremayne@bham.ac.uk*

Keywords: Polymorphism; Powder Diffraction; Crystal Structure Prediction

Chlorothalonil (2,4,5,6-tetrachloro-1,3-benzenedicarbonitrile) is a general-use pesticide that is used as a broad-spectrum fungicide, and as a biocide in paints and wood preservatives. Although the commercially available form (form 1) had been fully structurally characterised [1], the patent indicated the possibility of another polymorphic form that shows reduced biological activity and undergoes irreversible hardening in production. However, there was no reliable crystallographic information regarding this second form, and hence a simultaneous theoretical prediction and experimental search for new polymorphs was carried out. This was done independently, so that it would be a test of crystal structure prediction methods if all the polymorphs could be characterised independently from powder or single-crystal diffraction data. The result is a prediction study and subsequent Rietveld refinement of three polymorphs of chlorothalonil, with two polymorphs uncharacterised before prediction [2]. In the event, the unexpected complexity of the both the new polymorphic crystal structures of this simple molecule rendered them unpredictable, although related approximations to these structures were located within the constraints of prediction techniques. Form 2 is disordered and is therefore of a type that cannot be predicted by current theoretical methods. The determination of this structure from powder diffraction data also turned out to be more problematical than expected, both at the indexing stage and in structure solution, despite being a seemingly trivial structure in terms of global optimisation direct-space techniques. Refinements based on the hypothetical 'ordered' structures predicted in the theoretical search facilitated an interpretation of this disorder. The presence of multiple molecules in the asymmetric unit of form 3 determined from single-crystal data presents another structure that cannot be predicted by current theoretical methods. However, the theoretical search did locate two hypothetical structures that show significant similarities to the form 3 structure. Rietveld refinement of these predicted structures, which are clearly only approximations to the true structure, warns against over-interpretation of powder diffraction data in such cases.

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