with growth spirals. At the same time clear microblock features due to of impurity poisoning of growth surface were observed. Thin platelets with smooth {001} crystallized at this stage too. Summary: {001} and {0$\bar{1}$1} faces are growth forms of crystals of RBCO, {100} faces - passive ones. The real symmetry of as-grown bulk crystals is lower than P4/mmm - the horizontal plane of symmetry (001) is usually absent.

MS16.04.07 MORPHOLOGY OF THE EXPLOSIVE COMPOUND RDX. J.H. ter Horst, R.M. Geertman, A.E. van der Heijden*, G.M. van Rosmalen. Delft University of Technology, Laboratory for Process Equipment, Leeghwaterstraat 44, 2628 CA Delft, The Netherlands; *TNO Prins Maurits Laboratory, Pyrotechnics and Energetic Materials, Post office box 45, 2280 AA Rijswijk, The Netherlands

Small scale cooling crystallization experiments in stagnant media show (figure 1 and 2) that the solvent has a strong influence on the crystal morphology of RDX (cyclotrimethylene trinitramine). It is the objective of this study to find an explanation for this behavior.

A PBC (Periodic Bond Chain) Analysis is carried out in order to determine the crystal forms that may contribute to the crystal morphology. Furthermore the growth rates of all geometrically possible faces are calculated by assuming that they are proportional to the attachment energies of these faces. The combination of the PBC analysis and the attachment energy calculations results in an RDX crystal morphology prediction neglecting the influence of the solvent (figure 3). All forms observed experimentally are also present on the calculated morphology.

This calculated morphology gives information about the surface structure on a molecular level and allows an estimation of the influence of the solvents on the crystal morphology e.g. by means of the sorption module of the computer program Cerius^2.

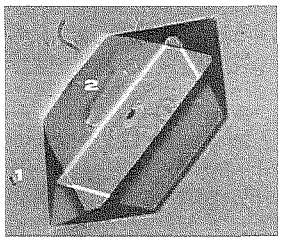

Figure 1: RDX crystal from g-butyrolactone, Σ=0.4

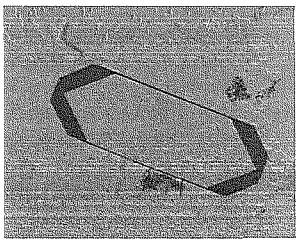

Figure 2: RDX crystal from water waturated cyclohexanon, Σ=0.3

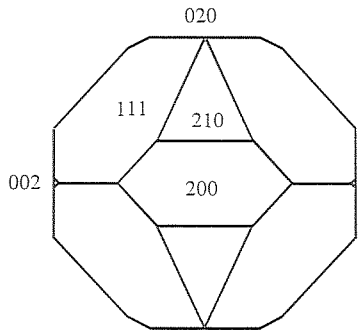

Figure 3: Calculated RDX crystal morphology

Macromolecular Crystal Growth Under Microgravity

PS16.05.01 RECENT ACTIVITIES OF SPACE PROTEIN CRYSTALLIZATION IN CHINA. Ru-Chang Bi, Institute of Biophysics, Academia Sinica, Beijing 100101, P.R.China

Based on encouraging results obtained on the first mission in 1992, the second Chinese mission of protein crystallization was conducted in 1994 using tube-like vapor diffusion apparatus on a Chinese re-entry satellite. More than 14 different proteins have been tested on the two missions. In comparison with the first mission, much better results were acquired on the second mission. Besides hen egg-white lysozyme, an acidic phospholipase A2 from snake venom and hemoglobin from bareheaded goose have produced good- quality crystals. The positive effects of microgravity on protein crystal growth and even results of protein crystallization in space can be reproducible. As an important factor affecting protein crystal growth, the microgravity may display its role in different degree depending on the protein crystallized and the crystallization conditions used.

Our first attempt to grow protein crystals with the liquid-liquid diffusion method was carried out on the August 1995 flight of the US space shuttle, STS-69. The hardware, MDA Minilab developed by the Instrumentation Technology Associates in US, was employed in this space experiment. Although the experiment was restrained by some conditions, the three proteins which we supplied to use six diffusion cells in a MDA unit, were crystallized on this mission. An important finding of our experiments is that in contrast with the case of vapor diffusion technique, the optimized conditions for growing good protein crystals on Earth may be different remarkably from those to be optimized in space. These differences could be caused by the density-driven convection and will be discussed in this report.

PS16.05.02 MULTI-USER FACILITY FOR PROTEIN CRYSTAL GROWTH IN MICROGRAVITY: RESULTS FROM PCAM AND DCAM. Daniel C. Carter, Pam D. Twigg, Brenda Wright, Joseph X. Ho, Kapp Lim, Jenny Chapman, Teresa Miller, NASA ES76 Laboratory for Structural Biology, Marshall Space Flight Center, Huntsville, Alabama, USA

Two newly developed microgravity multi-user facility-based hardwares for protein crystal growth will be described. Both hardwares feature disposable interfaces for improved logistics and handling. PCAM (Protein Crystallization Apparatus for Microgravity) is a high capacity device which closely approximates a common laboratory vapor diffusion method to grow crystals. DCAM (Diffusion-controlled Crystallization Apparatus for Microgravity) is a unique multi-user dialysis device which offers passive control of the diffusion profiles for each individual experiment. DCAM was specifically designed for long duration microgravity opportunities. The hardware is operated as government facility and access is provided through peer reviewed proposals. Significant improvements in crystal size and perfection obtained from flight experiments conducted over the course of less than a year will be described.