New research that opens new opportunities for biofuel production, regulation and manipulation of proteins

Authors: Kathy Ramirez Kathryn Cooper Daniel Fernandez Jennifer Campbell Steven Tran

Published Date: 04-06-2019

University of Central Arkansas

School of Economics

Here is an abbreviated summary and discussion of the study published in the journal Nature via the Institute of Electrical and Electronics Engineers (IEEE). While the study focused on metabolism and macro structure within the monosodium urate crystal (MSU) that is induced by biofuels, the results shed light on the mechanical reactions and how they are regulated in individual molecules.

Monosodium urate (urate) is commonly found in the form of soluble salts, purines and, quite interestingly, granules that contain both urate and silicon. SSOs are formed from the breakdown of monosodium urate crystals at the pH and temperature extremes of low carbon dioxide (in an inert world). Another highly soluble salt â€“ resist sulfite â€“ is also the building block of DMIs.

A working atypical case study is that of Shuji Ogawa and Akiko Tanaka, who in 2003 developed a method for creating PEM and GYOs by applying temperature and pressure to trigger the breaks between U2 crystals. As noted in the paper, their work on these topics led to the development of SMARTSO2, a solution containing over 30,000 u and a surprisingly high concentration of nanoparticles. Thus SMARTSO2 has enormous potential for diverse applications including production of viable biofuels and destruction of resistant surfaces, currently made primarily from petroleum (or other non-renewable sources). This new approach allows precise control of the timing and conditions that tend to make crystals develop and structural changes are possible in the crystal.

But, outside the realm of silica crystals. It can also be used to manipulate the crystalline structure, and thereby the microstructure of the proteins with which molecules bind. The issue is not whether the spatial distribution of non-protein molecules is stable or not â€“ it is indeed stable â€“ but whether the structure of proteins is affected in an â€œappropriateâ€ manner. By applying detergent droplets to the germ (shown in the picture) or fingerprint (taken from the black square), the scientists controlled the structure for the crystal binding to a protein during the crystallization. The amount of molecules in a boundary layer is approximately equal to the concentration of partially dissolved molecules, which is why after pricking (to increase the diameter of the boundary layer) the researchers can produce a uniform clot and test the quality of microstructure. In other words, the hydrophobic surface (shown in the green square) is degraded by adhering molecules and by scattering the water causing a defined symmetry-defying shape. By changing the salt concentration in the plasma to a small level (the unit S0 in the figure), the nano-sized hydrophobic network becomes unpalatable to waveguides and can be less than 2 nano-centimeters, which is quite hard to measure. The installation image from Nature is a schematic chart illustrating the effects on crystals.

With the ability to identify the leading effect on the shape of proteins, the researchers were able to analyze how the structure is affected when a polymer bond is damaged and modified. This can offer a mechanism for the transformation of proteins and can also be applied to the control of other proteins, including those used in bio-materials. Here again, an embedded imaging technique enables a measurement of protein structure distribution to maximum accuracy by combining atomic force microscopy with MRC microscope. The information obtained is published in a newly-published Science paper by Mats H. Yamamoto, Daisuke Tamada, Satoshi Sugiyama, and Yury Asakoff (Nanomedicine -a group within the MIT/NASC research network) and was recently awarded a grant from the U.S. Department of Energy.

A Close Up Of A Bird On A Wooden Fence