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Small angle neutron diffractometer

Small angle scattering (SAS) is the collective name given to the techniques of small angle neutron (SANS), X-ray (SAXS) and light (SALS, or LS) scattering. In each of these techniques, radiation is *elastically* scattered by a sample and the resulting scattering pattern is analysed to provide information about the size, shape and orientation of the scattering entity in the sample. The nomenclature 'small angle' has stuck to the technique as a result of historical development of the topic. What is being measured in these techniques is the scattered intensity of the radiation from the sample at small *wave vector transfers* (not necessarily at small angles). The elastic scattering wave vector Q is equal to $(4\pi/\lambda)\sin\theta$, where λ is the wavelength of incident radiation and 2θ, the scattering angle. In order to measure scattered intensity in the Q-range of, say 10^{-4} to 10^{-1} Å^{-1}, which is the range of interest in these techniques, one has to reach small scattering angles if λ is of the order of a couple of Å. However, if λ were larger, say $\geq$10 Å, measurements at larger scattering angles can be resorted to. The length scales that can be probed and the information that can be obtained, depend on the Q-range and nature of the radiation employed. For example, LS cannot be used to study optically opaque samples and SAXS cannot be employed to study thick samples. SANS and SAXS probe different length scales compared to LS. Hence these techniques are complementary. The basic theoretical formalisms are, however, similar. The so-called Guinier, Zimm, Kratky and Porod 'laws' can be used to analyse data from any of the three techniques.

SAS is being routinely employed, world over, to study a variety of materials like crystalline alloys, amorphous materials, nanocrystals, interfaces, catalysts, and a variety of soft condensed materials like gels and other porous materials, polymers, liquid crystals, micellar solutions, membranes, biological molecules and assemblies. The variety of interesting information that has been obtained is impressive and interdisciplinary in character. A triennial meeting discusses the developments in this frontier area regularly.

The paper by Aswal and Goyal (**page 947**) deals with design considerations and experimental realization of an instrument that uses cold neutrons of $\lambda \approx 5$ Å from the reactor and a one-dimensional position sensitive detector. The Q-range that is conveniently covered by the instrument is 0.02 to 0.32 Å^{-1}; hence the instrument is useful in probing length scales of 10–1000 Å, the mesoscopic scale.

One may note that the SANS technique has been used at BARC for over a decade based on an instrument that operated at the lower flux CIRUS reactor. Even with that low throughput instrument, a variety of materials like micellar solutions, ferrofluids, co-polymers, etc. have been studied by researchers based in several universities and other research institutions.

With the availability of a comparatively high throughput instrument described here, which can be further augmented by use of a 2-d detector and auxiliary equipment, one may be able to take up studies in superconducting, magnetic and other materials. The magnetic domain structure of materials at low applied magnetic fields gives rise to neutron *refraction* and to *depolarization* of the transmitted neutron beam, and can thereby be studied. At sufficiently high applied fields, the scattering volume is essentially a single magnetic domain. In this case, magnetic SANS arises from small (static) variations, on the scale of a few nanometers to a few hundreds of nanometers, of the orientation of the magnetization vector about the direction of the applied field. The technique is therefore well suited to study spatial variation of the magnetization. In amorphous ferromagnets, *inelastic* SANS is an established technique for determining the spin-wave stiffness constant. With further experiments using this SANS set-up, new and interesting information are anticipated.

K. R. Rao

TB research in India

Modest estimates showed that there were about 200 tuberculosis (TB) patients in India per 100,000 population in 1997. This means that they harbour actively dividing bacilli and can be treated with a few drugs that are known today and may hope to get rid of all the signs of TB infection in due course of time. However, this is the brighter side of the coin! On the flip side, about 30,000 of this 100,000 population are infected with TB with no sign at all and with no knowledge whatsoever that they are carrying one of the dreadful diseases of this century. The bacteria lie dormant in the macrophage of the host body and may not develop into a full blown case in the whole life time of the host and thus will never be detected. But the rate of conversion of the dormant TB to its active form is increasing and is thus becoming major source of concern for the health authorities in many countries. This prompted WHO to declare a global health emergency and an estimated target drug by 2007. Scientists are looking for drugs that would modulate few important biochemical pathways of this bacteria and the main concern is how to attack a persistor. There is a recent success like the discovery of nitroimidazopyrans but, we will wait to see how they handle dormant TB.

Likewise, TB research in India was very active a few decades ago, but reached its dormancy in between and is trying to be active again! The objective in every researcher is obviously to understand first and then utilize a metabolic pathway in Mycobacteria which would be unique and thus can be manipulated to control its growth. Towards this goal, V. Nagaraja and his group are working for sometime on DNA gyrase from *M. tuberculosis* and they think this could be an important drug target to control the growth of Mycobacteria. DNA gyrase is the only enzyme in bacteria which introduced negative supercoils in DNA and it is essential for cell survival. It is a heterotetrameric ($\alpha_2\beta_2$) enzyme with two subunits GyrA and GyrB. Nagaraja and his group have already made some important contributions. They have cloned and sequenced DNA gyrase genes from *M. tuberculosis*. Recently they observed that in Gram-negative eubacteria there lies a stretch of 165 amino acids at the C-terminal end of GyrB which is essential for DNA binding, yet dispensible in *M. tuberculosis*.

In their article (**page 968**), they have carried this work further and looked at the structural heterogeneity of DNA gyrases from Gram-negative and Gram-positive bacteria. Their results presented here indicate that there may be two sub-classes of gyrases in the bacterial kingdom, making them amenable for a drug target. As gyrase negative strains of bacteria are conditional lethal, the screening against potential assay of drugs appears to be an achievable task.

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