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Lamellar liquid crystals are promising systems for topical drug delivery [1]. They are transition states, possessing both the crystalline characteristics of solids and flow properties of liquids [2]. They are composed of oil, surfactant, water, and generally co-surfactant, and they have the advantage of being easily produced, increasing solubility of poorly water-soluble compounds, delivering fragile substances, and controlling release of drugs [3, 4].
In this work, SWAXS analysis of some Lyotropic Liquid Crystal Formulations was carried out to characterize nano aggregations in the structure. In the preparation of the samples, liquid paraffin, non-ionic surfactants (Brij 72 and Brij 721P) and/or ultrapure water have been used. Small and wide angle X-ray scattering (SWAXS) experiments were simultaneously performed with a Kratky compact Hecus (Hecus X-ray systems, Graz, Austria) system equipped with a linear collimation system and X-ray tube Cu target (λ= 1.54 Å).
Various models for the form factor were considered for fitting the SAXS patterns. Lamellar stackings in distorted spherulite forms have been observed in the structures. While the microscopic sizes of these spherulites were measured in the range of 20.33 - 99.15 µm, the range of the lamellar distances occurring inside of the spherulite aggregations was measured as 6.21- 6.47 nm. Briefly, SWAXS analysis has indicated that the polyethylene fibrils themselves were build up bundles of crystalline lamellae separated by layers of disordered material, with a period length of approximately 6 nm such as measured in the previous studies [5, 6].

[1] M. Aytekin, R. N. Gürsoy, S. Hekimoğlu, 35th Annual Meeting and Exposition of the Controlled Release Society (CRS Meeting), New York, USA, (2008). [2] S. Savic Colloid Polym Sci. 283: 439 – 445 (2005). [3] G. Burducea I. Specific structures Rom Rep Phys. 56(1): 66 – 73 (2004). [4] G. Burducea II. Structural polymorphism Rom Rep Phys. 56(1): 87 – 93 (2004). [5] A.Owen, A. Bergmann, Polmer International Vol. 53, No 1. 2004 pp 12-14 (3). [6] Y. Nozue, Y. Shinohara,Y.Ogaawa, Photon Factory Activity Report, 2004,22 Part B 4A

Keywords: SAXS, WAXS, Lamellar Liquid Crystals, LLC

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Small-Angle X-Ray Scattering Analysis of the Ectodomains of VEGFR-3 and the VEGF-C Ligand Complex.

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The Vascular Endothelial Growth Factor receptors (VEGF-Rs) play a significant role in tumor development and tumor angiogenesis and are therefore interesting targets in cancer therapy. Targeting the VEGF-R is of special importance as the feed of the tumor has to be reduced. Receptor tyrosine kinases are activated upon ligand-induced dimerization. Here we show that the monomeric extracellular domain of vascular endothelial growth factor C (VEGF-C) receptor-3 (VEGFR-3) has a flexible structure. Binding of VEGF to membrane-distal immunoglobulin-like domains causes receptor dimerization and promotes further interaction between receptor monomers through the membrane-proximal immunoglobulinlike. By this mechanism, ligand-induced dimerization of VEGFR-2 can be communicated across the membrane, activating the intracellular tyrosine kinase domains.
VEGF-C stimulates lymphangiogenesis and contributes to pathological angiogenesis via VEGFR-3. Here we present the SAXS analysis of VEGF-C bound to the VEGFR-3 h This structure reveals a symmetrical 2:2 complex, in which left-handed twisted receptor domains wrap around the 2-fold axis of VEGF-C. In the VEGFs, receptor specificity is determined by an N-terminal alpha helix and three peptide loops.
Our structure shows that two of these loops in VEGF-C bind toVEGFR-3 subdomains D2 and D3, while one interacts primarily with D3. Additionally, the N-terminal helix of VEGF-C interacts with D2, and the groove separating the two VEGF-C monomers binds to the D2/D3 linker. VEGF-C, unlike VEGF-A, does not bind VEGFR-1. We therefore docked VEGF-A, VEGF-C to VEGFR-1, VEGFR-2. This molecular simulation analysis, together with our structural data, defined VEGFR-3 residues critical for the binding of VEGF-C. Our results provide significant insights into the structural features that the Dimmer Complex of VEGFR3 inducing upon VEGF-C binding in solution.

Keywords: Small angle X-ray scattering (SAXS), VEGF-C, VEGFR3

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Investigation of alternative methods of holding samples for X-ray solution scattering.

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Small Angle X-ray Scattering (SAXS) is a powerful technique used to analyze liquid samples, such as proteins in solution, particles in solution, melts, foams, etc. The availability of bright x-ray sources coupled to state-of-the-art x-ray optics combined with beam conditioning hardware and photon counting detectors allows collection of SAXS data in the home lab without the need to travel to a synchrotron. Home labs typically utilize Cu-Ka radiation which requires evacuation of the beam path and therefore necessitates containment of liquid samples in a "cell" or capillary. While quartz or glass capillaries are the traditional choice, they are not without their limitations, being fragile, non-uniform and producing non-negligible background scattering. Cells have a metal super-structure with two transparent x-ray windows and o-ring seals. Kapton™ and mica are two of the usual choices for the windows. In order to extract structural information of the particles in solution the background scattering from the buffer or solvent and the container should be subtracted properly. It is particularly critical for solution scattering. Ideally, the exact same container at the exact same position should be used for both the background and the sample data collections. This presentation will discuss alternative methods of holding liquid