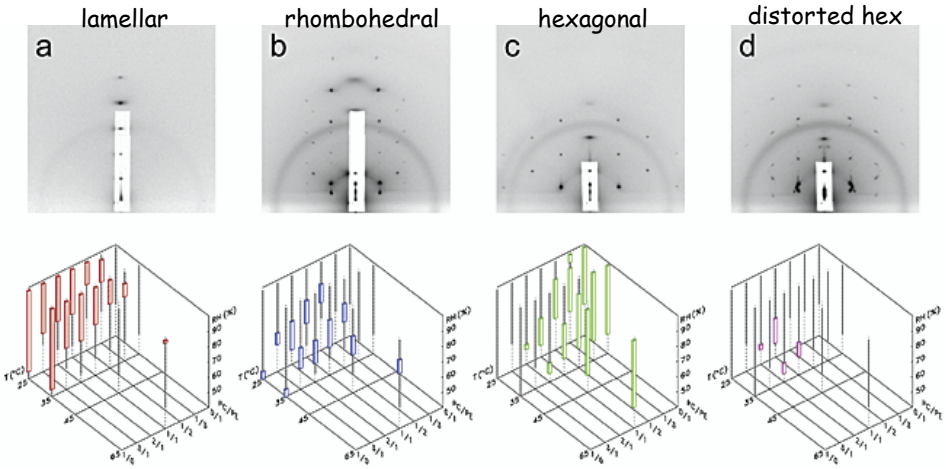
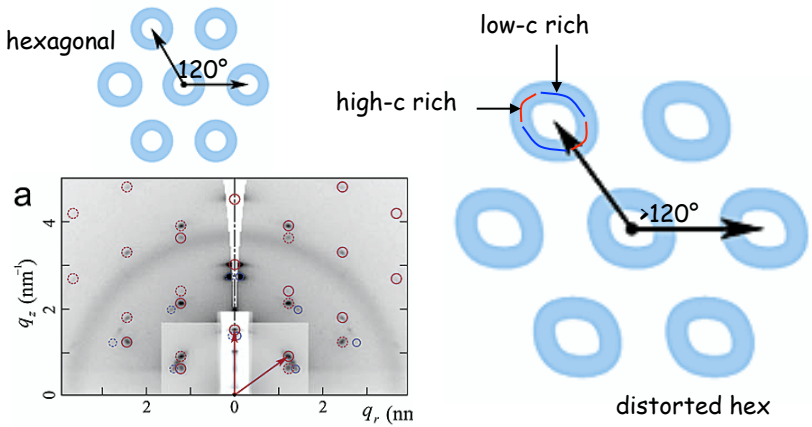
Membrane structures as a function of spontaneous curvature

Motivation: The elastic energy due to membrane bending and external mechanical forces exerted by proteins are likely contributing factors that control of membrane fusion living organisms. In model membranes, the same mechanism determines the overall membrane structure. Systematically variation of membrane spontaneous curvature (c), by mixing two lipids of well known and distinct spontaneous curvatures, therefore is expected to form a variety of membrane structures.



Key result 1: Increasing the spontaneous curvature of the lipid membrane increasingly favors the formation of non-lamellar structures, as is incrasing temperature (higher chain volume and therefore higher spontaneous curvature) and decreasing the hydration of the sample (higher membrane-membrane repulsion).



Key result 2: A new membrane structure was observed at low sample hydration and intermediate lipid mixing ratios. The diffraction pattern suggests that this structure consist of lipid tubes, similar to the hexagonal structure. However, the stacking of the tubes is no longer hexagonal, hinting that the tubes are not circular, likely because the two types of lipids are not distributed uniformly along the tube. This hypothesis was later confirmed by other experiments utilizing Br-labeled lipids.

Conclusion and significance: These results are a good demonstration of that the competition between bending energy and potential energy due to membrane-membrane interactions drives the formation of different membrane structures. The presence of the distorted hexagonal structure suggests that, under mechanical stress, different lipid species in the lipid membrane may demix (phase-separate) to lower the overall elastic energy. This may be an important mechanism utilized in biological membranes, which usually contain multiple species of lipids.

New Phases of Phospholipids and Implications to the Membrane Fusion Problem L. Yang et.al. BIOCHEMISTRY 2003