ROMA TRE
UNIVERSITÀ DEGLI STUDI

Dipartimento di Scienze

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CELL MEMBRANES: NANOMECHANICS AND DYNAMICS

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Martedì 7 Giugno 2022 ore 15:00 – Piattaforma TEAMS
(short-link: https://bit.ly/3NOwF7Y)

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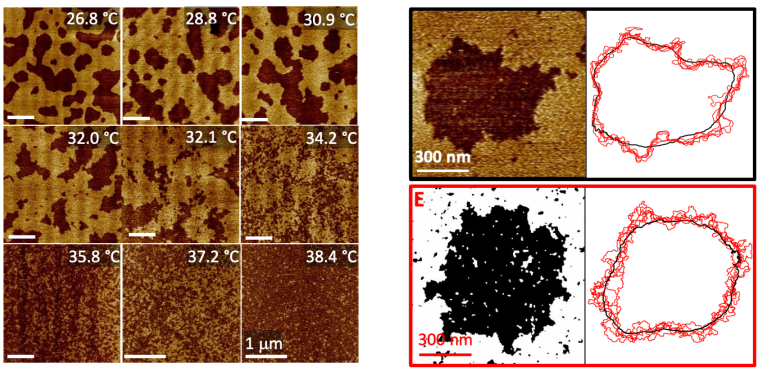
The lateral organization of lipids in biomembranes is fundamental to many cellular processes, and the dominant theory of so-called "lipid rafts" is still one of micro-domains of two liquid phases co-existing at equilibrium. However, it is widely recognised that the lipid phase separation occurring in live cells must be at the nanoscale. There is a body of experimental data that suggests nanodomains exist, but there is no direct evidence, and for this reason there is no characterisation of their properties. To add to the confusion, there are also multiple theories that account for nanodomains, but again there is no definitive solution. One compelling theory is that lipid rafts are actually a manifestation of critical fluctuations in the single phase close to a critical point in the phase diagram. Here we present recent Fast Scan and High Speed Atomic Force Microscopy data of the critical phase behaviour of a model cell membrane. With scanning rates of several seconds per frame, up to 50 frames per second, the nanometre motion of fluid-fluid domain boundaries can be clearly observed, and this is quantitatively analysed using the capillary wave approximation to extract line tensions. As temperature is increased the line tension between phases drops from pico-Newtons down to femto-Newtons approaching the critical temperature. Analysis of the domain structure and line tensions gives a static exponent of 1, indicating the system is well described by the 2D Ising Model, more commonly found in the study of magnetic domain in metallic thin films. Above T_C the domain structure breaks down into highly dynamic fluctuations as the phase switches between ordered and disordered states, resulting result in domains of 5-100 nm with lifetimes of seconds to almost 1 minute. Analysis of the domains vs time reveals a dynamic exponent of 2.0, increasing to 2.4 at higher temperature, indicating that dissipation of the fluctuating structure occurs via 2D hydrodynamic motion within the bilayer, and not via coupling to the bulk fluid as recent theory has suggested. For direct comparison with our results we perform Monte-Carlo 2D Ising model simulations. In this talk I will also discuss the measurement of the mechanics of membranes and how this can be used to determine headgroup hydrogen bonding, and recent work on the interaction of peptides and venom with model membranes.



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