



## EXPERIMENTAL REPORT

EXPERIMENT N° Test-261

INSTRUMENT D22

DATES OF EXPERIMENT 21./22. 11. 1997

TITLE **Time resolved neutron small angle scattering (TR-SANS) of liposomes - feasibility test**

EXPERIMENTAL TEAM (names and affiliation)

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Date of report 15.3.1999 Transient structural changes occur in biological systems in working proteins and at membranes during the development of an electrochemical proton potential (energization), e.g. at liposomes after a pH-jump. In the present work we have tested a novel setup for time resolved neutron scattering (TR-SANS) at the D22 beamline of the ILL and investigated the feasibility limits with protein free lecithine liposomes.

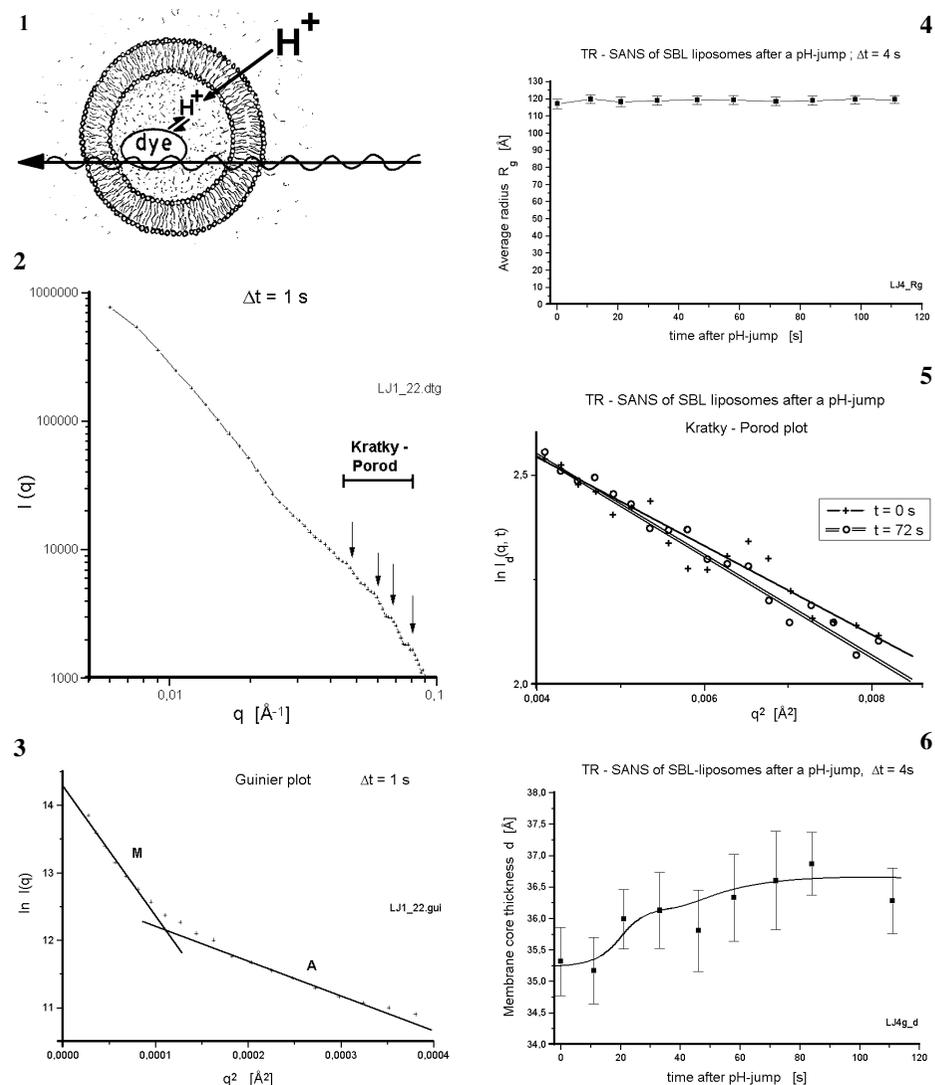
The active sample, liposomes after a pH jump at pH6.4, was formed by rapid mixing ( $< 1$  s) of liposomes (SUV from SBL; 24 g/l, 30 mM Tris-MES pH8, D<sub>2</sub>O) and acid (0,25 M MES in D<sub>2</sub>O) using the TR-SANS setup reported in the experiment TEST-252 (1997) and open flow-through quartz cuvettes (Hellma,  $d = 1$  mm). As depicted in fig.1 the structure was observed during proton flux into the liposomes, i.e. development of the membrane proton potential from  $\Delta\text{pH} = 1.6$  to 0 during 100 s [3]. With a 6x6 mm neutron beam (8 Å), 1mm cell and 1:1 diluted sample (12 g/l) we obtained 82000 cts. Because of the detector count rate limit a 10 mm cell could only be used with neutron attenuators - a challenge for future detector improvements. The scattering in a single 1s frame of a TR-SANS series in fig.2 consists of a Guinier and a Kratky-Porod region ( $q = 0.045$ - $0.088 \text{ \AA}^{-1}$ ), which was disturbed by side maxima from hollow sphere and aggregate scattering (arrows). The evaluation (fig.3) yielded the average radius  $R_g = 121.5 \pm 3.0 \text{ \AA}$  and the maximal radius  $R_g = 237.6 \pm 5.4 \text{ \AA}$  (largest vesicle subpopulation). The TR-analysis (fig.4) showed that no water uptake occurs with SUV after a pH-jump (important for spectroscopic TR-analysis [3]). The Kratky-Porod analysis (fig.5,6) yielded a final membrane core thickness  $d = 36.6 \pm 0.5 \text{ \AA}$ . From these results the average liposome size  $s = 279.8 \pm 6.8 \text{ \AA}$  was calculated as shown earlier [1,2]. As an important result we observed a contraction of the lipid bilayer at high proton potential (fig.6).

1) Nawroth, T.; Conrad, H.; Dose, K. (1989) Physica B 156 & 157, 477-480

2) Nawroth, T.; Dose, K.; Conrad, H.; Koch, H.; Ringsdorf, H. (1989) Physica B 156, 496-8

3) a) Nawroth et al (1998) DGfR German Biophysics Soc. v conference proceedings, 108

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**Figures:** 1) The proton flow into liposomes is followed by TR-SANS and light; 2) A single TR-SANS frame of 1 s; 3) The Guinier region **A** yields the average liposome radius, whereas the maximum radius is obtained by the range **M**; 4) The constant  $R_g$  in TR-SANS indicates that no water uptake occurs after a pH-jump; 5) The Kratky-Porod plot yields at  $t=0$  and 72s different thickness radius  $R_d$  and diameter  $d$ ; 6) Immediately after the pH-jump of 1.6 a contraction of the lipid bilayer is indicated by the decreased membrane core