Silaffin 1A₁: Insights to the Processes of Tailored Silica Precipitation

Fanny Kozak^{1,2}, Fabian Daus³, Dörte Brandis^{1,2}, Armin Geyer³, Christian W. F. Becker¹, Dennis Kurzbach¹

¹Institute of Biological Chemistry, Faculty of Chemistry, University of Vienna, Währingerstraße 38, 1090 Vienna, Austria. ²University of Vienna, Doctoral School of Chemistry (DoSChem), Währingerstraße 42, 1090 Vienna, Austria ³Faculty of Chemistry, Philipps-Universität Marburg 35032, Marburg, Germany

E-Mail: fanny.kozak@univie.ac.at, Find us at: www.Kurzbach-group.univie.ac.at

1) Introduction

The variety and intricate beauty of diatom algaes' typical silica shells inherently demands to pose the question of how these organisms are capable of shaping silica from the intrinsically low silicic acid concentration in seawater. Further than the urge to understand biomineralization on a deeper level, the ability to develop tailored silica particles allows for new approaches to drug delivery and provides a further step in rational materials design. Peptide Silaffin 1A₁, isolated from marine diatom species Cylindrotheca fusiformis, is one of the molecules enabling controlled silica precipitation in the presence of positively charged ions.[1] Still, the mechanism leading to controlled silica precipitation under mild conditions is scarcely understood.

2) Diatoms

Their intricate silica shells served as inspiration for designing mimetic peptides and sparked further interest

A) Synthetic Silafin1A₁ (_{syn}Sil1A₁) HO Ö H_2N_{\sim} ΗŃ. NH A) Long Chain Polyamines (LCPA) HŃ

C) ¹H-³¹P Correlation Spectra

4.0

4.5

3.5

pHyl¹²

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ΌH

3) Synthetic Silafin1A₁

Synthetic Silafin1A₁ (synSil1A₁) differs from its natural scaffold by the homogeneous length of polyamine post-translational the modifications. Still, to yield homogeneously sized particles, adding long-chain polyamides LCPA) is necessary. Structures are shown in Figure A). This facilitates supramolecular assembly necessary for precipitation event. Depending on the the conditions chosen, influence is taken on the morphology of the precipitate [2]. This process is closely related to similar biomineralization processes, which are debated to not follow the classical scheme of nucleation, But rather to form prenucleation species, which are subject to growth until sizes susceptible for solid formed [3] formation are (Fig.B)

biomineralisation unraveling Shown: Mastogloia processes. binotata (Grun.) [4,]

40

E) ³¹P Relaxation Rates

svnSil1A1:LCPA (10:1)

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X

30 R_2/s^{-1} pSer14 pSer oser

4) ¹H-³¹P CPMG Pulsesequence

To allow for residue resolution, we detected the post-translational phosphorylations by a specifically designed pulse sequence. Therefore, we traced ¹H-³¹P T_2 relaxation rates in different conditions. Pulse sequence, as well as extracted relaxation rates (E& F) and ¹H ³¹P correlation spectrum, can be seen in Figure C+D. The sequence contains an additional CPMG train during the magnetization transfer as devised by Luy and Marino [5] for enhanced sensitivity (L4) combined with a traditional Carr-Purcell-Meiboom-Gill sequence for T_2 determination.





D) ¹H-³¹P CPMG Pulsesequence



F) ¹H- ³¹P Relaxation Rates 40 svnSil1A₁:LCPA (1:1) 30 s-1 R_2 10

5) ¹H-³¹P CPMG

nser

Figure E and F show the changes LCPA additive depending on concentration. Upon adding different concentrations of LCPA, we observe an increase in R2 rates with increasing LCPA availability. This points towards decreasing mobility and indicates, combined with DOSY-data (not shown) supramolecular assemblies varying in structure, depending on additive presence.



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