

Universidade de São Paulo
Instituto de Física de São Carlos

XIV Semana Integrada do Instituto de
Física de São Carlos

Livro de Resumos da Pós-Graduação

São Carlos
2024

Ficha catalográfica elaborada pelo Serviço de Informação do IFSC

Semana Integrada do Instituto de Física de São Carlos
(13: 21-25 ago.: 2023: São Carlos, SP.)

Livro de resumos da XIII Semana Integrada do Instituto de
Física de São Carlos – Universidade de São Paulo / Organizado
por Adonai Hilário da Silva [et al.]. São Carlos: IFSC, 2023.
358p.

Texto em português.

1.Física. I. Silva, Adonai Hilário da, org. II. Título.

ISSN: 2965-7679

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The role of SEPT7 in *magnaporthe oryzae*: structural insights and functional implications

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Magnaporthe oryzae is a phytopathogen that causes one of the most destructive diseases of cultivated rice in the world. Infections caused by this recalcitrant pathogen leads to the annual destruction of approximately 10– 30% of the rice harvested. Septins are involved in maintaining the appressoria and transpressoria, important cell structures to the process of plant invasion. Understanding septin structure could be of great value in shedding light into this mechanism. Particularly because *Magnaporthe* has two non-canonical septins (Sep7 and Sep8) which may be important for the formation of the massive septin ring which is not seen in other species. Regardless of the extensive physiological information, there is almost no knowledge related to these non-canonical septins. In this study, using a biophysical and structural approach, we characterized an engineering version of the G domain of MoSEPT7 (MoSEPT7 Δ 49). MoSEPT7 Δ 49 was purified as a dimer in solution identified by SEC-MALS, in addition to showing slow activity in GTP hydrolysis. Crystallographic structure revealed that Septin7 has open G-interface showing unique features, such as an unusual helix insertion and some differences in the beta meander region. Some structural resemblances have also been observed between Sep7 of *Magnaporthe* and Sep1 from *Chlamydomonas* (a unique septin in this organism). The implications of this study point towards a deeper comprehension of septin structure and function in *Magnaporthe oryzae* to better understand their cellular roles.(1-3)

Palavras-chave: *Magnaporthe oryzae*; Non-conical; Septins.

Agência de fomento: CAPES (88887.801323/2023-00)

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