Contribution ID: **61** Type: **Poster**

Functional characterization of TgREMIND, an enigmatic F-BAR containing protein involved in vesicular trafficking in Toxoplasma gondii

Toxoplasma gondii, the causative agent of toxoplasmosis, is an obligate intracellular parasite. The ability of this parasite to infect host cells depends on its capacity to release unique factors from special organelles called rhoptries, micronemes, and dense granules. The biogenesis of these organelles relies on vesicular trafficking events whose molecular bases are poorly known. In eukaryotic cells, key players of vesicular trafficking are BAR-containing proteins with a capacity to bind and sense/induce curvature of membrane and to recruit protein partners; however, whether BAR-containing proteins play pivotal roles in *T. gondii* is unknown. Here we characterize a BAR-containing protein called TgREMIND involved in the delivery of rhoptries and dense granule proteins into their destination compartments, and its absence leads to the inability of the parasite to be infectious. Bioinformatics analyses suggest that TgREMIND has a putative F-BAR domain and a domain, referred to as X-REMIND, whose fold and function are unknown. Using circular dichroism and flotation assays, we determined that TgREMIND contains a functional F-BAR domain that binds membranes that are both curved and enriched with phosphoinositide (e.g., PI(4,5)P2), possibly via particular basic residues. Moreover, we found by electron microscopy that this F-BAR domain can induce membrane tubulation. In parallel, we found that the X-REMIND domain is well-folded, and obtained experimental data supporting AlphaFold predictions. We found that this domain neither binds nor remodels membranes. Yet, obtained preliminary data suggests that it might regulate the membrane remodeling capacity of the full-length TgREMIND. Overall our data provide the first clues on the function of BAR-containing protein from the Apicomplexan phylum.

Session

Interaction lipids/polymers/membrane proteins

Primary authors: Mrs AL-QATABI, Noha (Institut de Pharmacologie Moléculaire et Cellulaire, CNRS, Université Côte d'Azur); Mr HOUNGUE, Rodrigue (Institute for Integrative Biology of the Cell (I2BC), CNRS UMR 9198, CEA, Université Paris Sud, Université Paris-Saclay); Mr NDAO, Omar (Institute for Integrative Biology of the Cell (I2BC), CNRS UMR 9198, CEA, Université Paris Sud, Université Paris-Saclay); Mrs GHOUIL, Rania (Institute for Integrative Biology of the Cell (I2BC), CNRS UMR 9198, CEA, Université Paris Sud, Université Paris-Saclay); Mrs PAGNOTTA, Sophie (Centre Commun de Microscopie Appliquée Université de Nice-Sophia Antipolis); Mrs ZINN-JUSTIN, Sophie (Institute for Integrative Biology of the Cell (I2BC), CNRS UMR 9198, CEA, Université Paris Sud, Université Paris-Saclay); Mr TOMAVO, Stanislas (Institute for Integrative Biology of the Cell (I2BC), CNRS UMR 9198, CEA, Université Paris Sud, Université Paris-Saclay); Mr DRIN, Guillaume (Institut de Pharmacologie Moléculaire et Cellulaire, CNRS)

Presenter: Mrs AL-QATABI, Noha (Institut de Pharmacologie Moléculaire et Cellulaire, CNRS, Université Côte d'Azur)

Session Classification: Clip Session