Press Release, September 25, 2020

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Repairing the photosynthetic enzyme Rubisco

Researchers at the Max Planck Institute of Biochemistry decipher the molecular mechanism of Rubisco activase

Manajit Hayer-Hartl, head of the research group "Chaperonin-assisted Protein Folding", has a long-standing interest in the central enzyme of photosynthesis called Rubisco. Her team has already reported on many of the interacting partners of Rubisco that are required for the folding and assembly of this highly abundant protein. In the current study, they have elucidated how Rubisco activase works. As the name indicates, this enzyme is critical for repairing Rubisco once it has lost its activity. The study was published in *Cell*.

The enzyme Rubisco catalyzes the assimilation of CO_2 from the atmosphere into organic matter. This is the central step in photosynthesis that generates sugar molecules for the production of essentially all biomass. Despite its pivotal role, Rubisco works relatively slowly and is easily inhibited by sugar products. By improving the function of Rubisco Hayer-Hartl hopes to be able to boost the process of photosynthesis. The goal is to address the growing global demand for food and reduce the current greenhouse gas-induced climate change.

The enzyme Rubisco activase, Rca, is present in plants, algae and certain cyanobacteria. Rca is a ring-shaped complex of six subunits with a central pore. How exactly Rca interacts with the inhibited Rubisco and releases the bound sugar from the active site pocket of Rubisco, restoring its CO_2 fixing activity, was unclear until now. With the help of biochemistry, crystallography and cryo-electron microscopy, Hayer-Hartl & colleagues have now succeeded in deciphering the molecular mechanism of a cyanobacterial Rca.

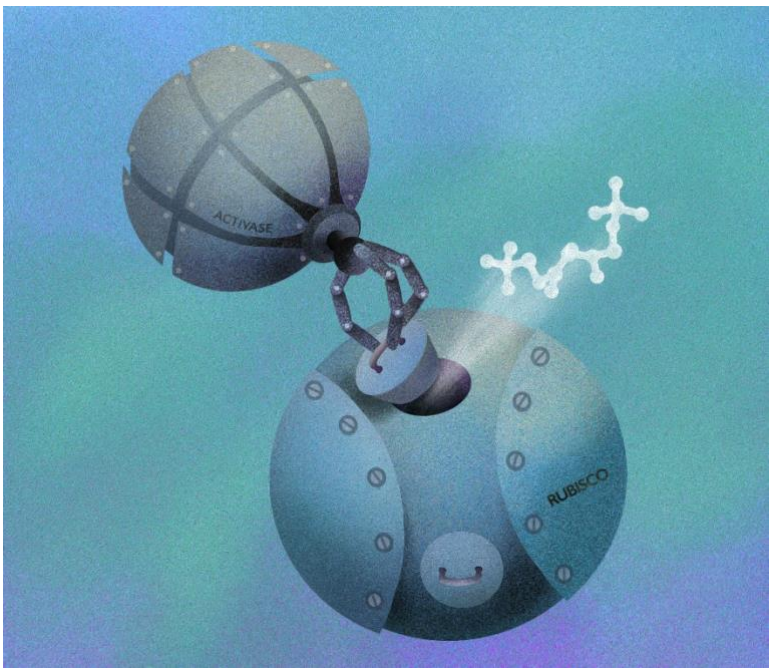
They discovered that the Rca grabs the N-terminal tail of Rubisco and by pulling and pushing actions, using the energy of ATP, opens the active site pocket. This results in the release of the inhibitory sugar molecule. In cyanobacteria Rubisco is packaged into specialized micro-compartments called carboxysomes, in which a high concentration of CO_2 is generated to facilitate the function of Rubisco.

In an earlier study, Hayer-Hartl showed how Rubisco is recruited into carboxysomes via interactions with the SSUL domains of the scaffolding protein CcmM. Interestingly, the researchers now found that Rca is recruited

into carboxysomes using a very similar trick. The Rca hexamer also contains SSUL domains that dock onto Rubisco during carboxysome formation. This makes sure that enough Rca is present inside carboxysomes to perform its essential repair function. Thus, Rca not only functions in Rubisco activation but also mediates its own recruitment into carboxysomes.

Manajit Hayer-Hartl concludes: "Rca is absolutely required for Rubisco to function optimally. Deciphering its mechanism and dual function in cyanobacteria will further help us to make photosynthesis more effective in the future. Hopefully, this will get us closer to our ultimate goal, to increase agricultural productivity".

Original publication:
M. Flecken, H. Wang, L. Popilka, F.U. Hartl, A. Bracher and M. Hayer-Hartl:
“Dual Functions of a Rubisco Activase in Metabolic Repair and Recruitment to Carboxysomes”
Cell, September 2020. https://doi.org/10.1016/j.cell.2020.09.010



Caption: Rubisco activase catalyzes the opening of the active site pocket of Rubisco and facilitates release of the inhibitory sugar.
The image is an artistic interpretation of the mechanism. Artwork: Julia Kuhl
Manajit Hayer-Hartl © MPI of Biochemistry

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About Manajit Hayer-Hartl Manajit

Hayer-Hartl received her Bachelor of Science degree at the University of Stirling, Scotland, UK, where she afterwards gained her PhD. Her interest in structural and cellular biology motivated her to several postdoctoral fellowships at renowned research institutions, among them the Louis Pasteur Institute in Strasbourg, France and the Sloan-Kettering Institute in New York, USA. Hayer-Hartl joined the Max Planck Institute of Biochemistry in 1997 as a group leader in the department "Cellular Biochemistry". Since 2006, she is head of the research group "Chaperonin-assisted Protein Folding". Her research focuses on chaperones and how these molecular machines assist in proper protein folding and assembly. Hayer-Hartl is an elected member of the European Molecular Biology Organization (EMBO) and of the German National Academy of Sciences (Leopoldina). For her research, she has received the Dorothy Crowfoot Hodgkin Award (Protein Society), the Charles F. Kettering Award (ASPB), and the Merck Award (ASBMB).

About the Max Planck Institute of Biochemistry

The Max Planck Institute of Biochemistry (MPIB) belongs to the Max Planck Society, an independent, non-profit research organization dedicated to top level basic research. As one of the largest Institutes of the Max Planck Society, 850 employees from 45 nations work here in the field of life sciences. In currently eight departments and about 25 research groups, the scientists contribute to the newest findings in the areas of biochemistry, cell biology, structural biology, biophysics and molecular science. The MPIB in Munich-Martinsried is part of the local life-science-campus where two Max Planck Institutes, a Helmholtz Center, the Gene-Center, several bio-medical faculties of two Munich universities and several biotech-companies are located in close proximity. https://www.biochem.mpg.de/en

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