

# Researchers discover energy supply for protein secretion

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In order to interact with the environment, bacteria secrete a whole arsenal of proteins. Researchers have now found how one of the transportation systems used for this purpose – the type VI secretion system – works for the single-celled organism *Agrobacterium tumefaciens*. They have identified the relevant transport proteins and their energy suppliers.

With colleagues at the Academia Sinica in Taiwan, RUB biologist Prof. Dr. Franz Narberhaus describes the findings in the *Journal of Biological Chemistry*. "The proteins involved also occur in other secretion apparatuses" explains Narberhaus from the Department of Microbial Biology. "Therefore, the results contribute to the general understanding of the system."

Bacteria use secreted proteins to make nutrients available, to fend off competitors and to infect human, animal or plant host cells.

"*Agrobacterium tumefaciens* is a fascinating bacterium. It can genetically modify plants and stimulate tumour formation", says Narberhaus. Five bacterial secretion systems have been known for a long time. The type VI system was only discovered a few years ago. Among other things, it transports the protein Hcp through two membranes into the environment – for what purpose is, as yet, unclear. The question of how the export of Hcp is driven was also unanswered. This is precisely what the German-Taiwanese team has now revealed.

Narberhaus and his colleagues have shown that two proteins in the cell

membrane of the [bacteria](#), called TssL and TssM, are responsible for the export of Hcp. The molecule ATP, a cellular energy store, serves as fuel for the transport process. The membrane protein TssM binds the energy supplier ATP, thereby changing its own structure and splitting the ATP. The energy thus released allows the associated membrane [protein](#) TssL to bind its cargo (Hcp) so that a tripartite complex of TssM, TssL and Hcp is formed. Hcp only passes from the bacterial cell into the environment when this complex forms.

"Large membrane proteins such as TssM are difficult to study biochemically. Our colleagues in Taiwan have done a great job" Prof. Narberhaus explains. "It will now be particularly interesting to explore the biological significance of the system." The analyses of ATP splitting, also called hydrolysis, were established in Prof. Narberhaus's laboratory by the doctoral student Lay-Sun Ma during a research visit. "Because of the participation in the Collaborative Research Centre SFB 642 'GTP- and ATP-dependent membrane processes', we are able to offer ideal conditions for working with ATP-dependent proteins" the RUB-biologist explains. This is the second time that the DAAD has funded the cooperation between the laboratories of Franz Narberhaus and Erh-Min Lai. The successful cooperation is also to continue in the future. "It is bound to last for many years", the Bochum researcher is convinced. The next exchange of doctoral students is planned for autumn.

**More information:** L.-S. Ma, F. Narberhaus, E.-M. Lai (2012): IcmF family protein TssM exhibits ATPase activity and energizes type VI secretion, *Journal of Biological Chemistry*, [doi: 10.1074/jbc.M111.301630](https://doi.org/10.1074/jbc.M111.301630)

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