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Powerhouses in the cell dismantled Flemish technology at VIB / Ghent University creates revolution in protein research

Ghent - All of life is founded on the interactions of millions of proteins. These are the building blocks for cells and form the molecular mechanisms of life. The problem is that proteins are extremely difficult to study, particularly because there are so many of them and they appear in all sizes and weights. Now, Kris Gevaert from VIB/Ghent University and colleagues from the universities of Freiburg and Bochum have achieved a breakthrough in protein research. Using yeast, they have succeeded in making virtually the complete inventory of all the proteins in the mitochondria, the energy producers found in every cell. Their research findings are being published in *Cell*, the most prestigious professional journal in the life sciences field.

During their research, the scientists encountered the Icp55 enzyme, which fulfills an important role in the stabilization of the proteins in the mitochondria. Until now, it was unclear just how the cell accomplished this. Icp55 turns out to be a molecular pair of scissors that snips off one of the ends of certain proteins, so that these proteins are transformed from an unstable to a stable form.

“This is a crucial step for fundamental research on proteins, the building blocks of life,” says Kris Gevaert, VIB researcher at Ghent University. “It’s the first time that such a precise protein determination of the mitochondria has been achieved. Our breakthrough was made possible by COFRADIC, a technology that enables us to analyze protein mixtures much more sensitively and accurately.”

“We’re now able to detect protein forms that were simply overlooked before,” Kris Gevaert continues. “So we’re receiving requests for scientific collaborations from all over the world.”

COFRADIC is a technology developed by VIB/Ghent University researchers Joël Vandekerckhove and Kris Gevaert. With COFRADIC, the traditional conception of protein identification has been turned upside-down. Instead of first separating the intact proteins, the entire protein mixture is cut into small pieces (peptides) – which are more soluble and much easier to separate in order to conduct further analyses. Applying this approach to the samples provided by the German scientists revealed a new protein (Icp55) – which proved to be key in explaining protein stabilization in mitochondria, a mystery that has been unsolved up to now.

Relevant scientific publication

This research appears in the authoritative journal *Cell* (Global Analysis of the Mitochondrial N-Proteome Identifies a Processing Peptidase Critical for Protein Stability, Vögtle *et al.*)

For more information

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Note for the editor

This research has been done by Kris Gevaert, from the research group ‘functional Proteomics: Development and Applications, VIB Department of Medical Protein Research, UGent’.

<http://www.vib.be/Research/EN/Research+Departments/Department+of+Medical+Protein+Research/Joël+Vandekerckhove+-+Kris+Gevaert/>

Mention both VIB and the university

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