Medical Xpress

TGAC reveals novel insights into the induction of autophagy in leading science publication

August 5 2014, by Hayley London

Tamás Korcsmáros, TGAC-IFR Computational Biology Fellow, in collaboration with the NetBiol group, releases new study on the bioinformatics analysis of the possibilities of autophagy induction in 40 unicellular parasitic species that could help to identify novel therapeutic targets, especially for patients with colon cancer or inflammatory bowel disease (IBD), published in *Nature*'s *Scientific Reports*.

Autophagy is a highly conserved self-degradation process of eukaryotic cells, and has found to be important in various cellular processes including stress-response, protein metabolism, differentiation and ageing. Autophagy can be found in essentially all eukaryotic species examined so far. In the gut, autophagy provides a powerful means of removing intracellular pathogens, and the malfunction of autophagy is related to inflammatory bowel disease (IBD) and cancer progression. A better understanding of the effect of particular bacterial species on the regulation of human intestinal autophagy could help to identify prognosis markers for IBD and colon cancer.

Autophagy is also essential in many unicellular parasites, such as Taxoplasma, Trypanosoma and Plasmodium, and found important in their life-cycle transitions. However, how autophagy is induced in these parasites remained largely unrevealed. This newly published study provides a better understanding of autophagy in unicellular parasites that could help to therapeutically target these parasites without effecting human autophagy.

The study examines the full genome sequence of 40 unicellular protist parasites. Surprisingly, the research presented no gene that would code for any component of the Atg1/ULK1-like autophagy inducing complex, generally known to be essential in autophagy regulation in eukaryotes. Therefore, in these parasites, autophagy is induced independently of an Atg1-like protein kinase system. The results are in agreement with previous large-scale data showing that some ATG genes in these organisms exhibit differential expression patterns; suggesting that autophagy in these protists is induced mainly at the post-transcriptional level. Understanding Atg1-independent autophagy induction mechanisms in these parasites may lead to novel pharmacological interventions, not affecting human Atg1/ULK1-dependent autophagy.

Tamas, commented: "We're very happy that this bioinformatics study is

published in such a key journal. With a detailed sequence analysis we showed that potential Atg1/ULK1 orthologs presented in many previous studies are not true counterparts of the functional autophagy inducers known in humans and many other eukaryotes. I hope our study will facilitate future experiments to understand how these dangerous parasites regulate autophagy and how we could medically use this information to overcome infectious diseases. I am particularly proud that this is my first paper since I moved to TGAC, this study is a specific example why detailed and biologically precise analysis is vital to our research, the expert knowledge and methodology at the Institute will help with the data analysis of many more genomes."

The scientific paper, titled: "Starvation-response may not involve Atg1-dependent autophagy induction in non-unikont parasites" by Tamás Korcsmáros and NetBiol Group is published in *Nature*, *Scientific Reports*.

More information: "Starvation-response may not involve Atg1-dependent autophagy induction in non-unikont parasites." László Földvári-Nagy, Eszter Ari, Péter Csermely, Tamás Korcsmáros & Tibor Vellai. *Scientific Reports* 4, Article number: 5829 DOI: 10.1038/srep05829. Received 08 April 2014 Accepted 04 July 2014 Published 25 July 2014

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