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A mass spectrometry driven proteomics approach identifies new protein families involved in regeneration

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Currently, a small panel of organisms such as the mouse, rat or zebrafish is used to answer a wide range of scientific questions. Beside this group of standard models other organisms exist (niche model organisms), that lack genetic background data in terms of sequences and effective methods for genetic manipulations. However, some of these niche models possess remarkable capabilities. One obvious example is regeneration research, where the choice of model organisms is widely restricted by the fact that only very few organisms are able to fully regenerate tissues in vivo. The green newt *Notophthalmus viridescens* is well known for its regenerative capabilities. Although it is able to regenerate nervous system, optic lens, appendages and heart, the lack of sequence information has severely hampered the investigation of the underlying molecular mechanisms (<150 protein sequences are listed at NCBI). Recent high throughput screenings on the transcriptome and proteome level and their bioinformatical combination provided striking new insights into the control of regeneration. We used a de novo assembled transcriptome following massive parallel sequencing for peptide identifications in a LC-MS based proteomics screening on regenerating tissue. The combination of these HT techniques allowed us to identify completely new proteins and protein families involved in regeneration, lacking any counterpart in standard model organisms. Further, a pSILAC based modification of our approach enabled us to quantify the new proteins, resulting in the identification of a new growth factor family member (CCNs) in the regenerating heart.

Biography

Mario Looso has completed his PhD at the Justus Liebig University of Giessen in 2010. He is Head of Bioinformatics and IT Service Facility at the Max Planck Institute for Heart and Lung research, working in the interdisciplinary field of proteomics, genomics and transcriptomics. He developed methods to combine parallel sequencing followed by the novo assemblies and LC-MS based proteomics approaches. This approach was used to characterize proteomes of niche models.

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