Bacterial Pathogens and their Pan-Proteome - From Next-Generation Sequencing to Target Identification

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Bovine respiratory disease (BRD), also known as shipping fever, causes an immense economic loss to the cattle industry. The cause of BRD is multi-factorial. Known factors are viruses, bacteria, and environmental stress such as transportation of the cattle. The severity of BRD is induced by bacteria of the *Pasteurellaceae*: *Mannheimia haemolytica*, *Pasteurella multocida,* and *Histophilus somni* [Melnikow *et al.*, 2008]. Next-generation sequencing allows the application of the pan-proteome concept for proteome wide drug target identification. A pan-proteome consists of (i) strain-specific proteins, (ii) proteins shared by all given organisms (core proteome), and (iii) proteins shared by only a subset of the organisms [D'Auria *et al.*, 2010]. Four genomes from BRD case isolates were sequenced (2 x *M. haemolytica*, 2 x *P. multocida*). The *H. somni 2336* genome sequence is publicly available. Here we describe the bioinformatic workflow starting from the assembly of the sequence, followed by sequence annotation, and finally the calculation of the pan-proteome. For sequence assembly and functional annotation a fully automated tool was implemented using the software PipelinePilot (Accelrys Inc.). The pan-proteome was calculated on the basis of the five BRD-relevant proteome datasets. It is supposed that BRD-specific virulence factors can be found in the core proteome. Nonetheless, other clusters of orthologous proteins could offer valuable clues to species-specific virulence factors as well. This work analyzes the pan-proteome of BRD-relevant pathogens which enables us to learn more about proteins relevant to BRD.

References:

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