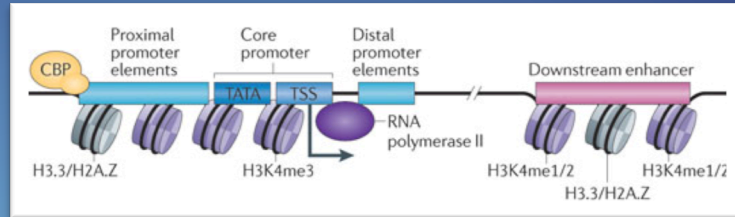


FAANG-Europe



Functional annotation of bovine alveolar macrophages challenged with *Mycobacterium bovis* using chromatin immunoprecipitation sequencing (ChIP-seq)

The aim of the proposed STSM is to functionally annotate bovine alveolar macrophages (bAM) that have been challenged with *Mycobacterium bovis* (*M. bovis*), in comparison to unstimulated control bAM. Specifically, we will characterise two major histone tail modifications, anti-H3K4me3 and anti-H3K27me3, using ChIP-seq 48 hours post infection. These targets have permissive and repressive roles, respectively, in regulation of transcription. Using these methods, we will test the hypothesis that *M. bovis* induces chromatin reconfigurations in infected bAM that are associated with epigenetic regulation of gene expression. This hypothesis was suggested by recently published work from our group that used RNA-seq to profile bAM gene expression up to 48 hours post infection with *M. bovis*. This analysis revealed that a number of key histone modifiers are differentially expressed in infected bAM. The STSM fostered collaborations between University College Dublin and the host institution, the Roslin Institute/University of Edinburgh. Furthermore, the proposed project meshes with a primary goal of the FAANG Consortium to functionally annotate the cattle genome. In addition the project focused on the recommended histone modification targets as outlined by the FAANG Consortium (www.faang.org).

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