## Mapping of EFO terms from the GWAS catalog data to multiple ontologies at the Rat Genome Database

<u>Stan Laulederkind,</u> GT Hayman, SJ Wang, ML Kaldunski, M Vedi, M Tutaj, L Lamers, J de Pons, MR Dwinell, AE Kwitek

Department of Physiology, Medical College of Wisconsin, Milwaukee, Wisconsin.

The laboratory rat, *Rattus norvegicus*, is an important model of human health and disease, and experimental findings in the rat have relevance to human physiology and disease. The Rat Genome Database (RGD, *https://rgd.mcw.edu*) is a model organism database that provides access to a wide variety of curated rat data including disease associations, phenotypes, pathways, molecular functions, biological processes, cellular components, and chemical interactions for genes, quantitative trait loci, and strains. A major role of a model organism database is to provide data from laboratory animals in comparison to human data.

To be able to compare data between rat and human it is necessary to use common vocabularies. When data from different sources use different vocabularies, there must be some standard way to compare the data. To bridge gaps in data description from different sources, the biocurators at the Rat Genome Database (RGD) have mapped a human GWAS-specific subset of terms (The NHGRI-EBI Catalog of human genome-wide association studies/GWAS Catalog Data) (https://www.ebi.ac.uk/gwas/) from EFO (Experimental Factor Ontology) to multiple ontologies used at RGD. RGD has also made available the ontological mappings via an SSSOM file from the RGD download page.