



# The Badger's Transcriptome and Tuberculosis Infection

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## Introduction



Bovine tuberculosis (bTB) is a serious disease caused by *Mycobacterium bovis*.

The disease is known by its economic impact on the cattle industry both globally and in the UK. bTB infection costs an estimated \$3 billion to global agriculture annually. Control of the disease in cattle can be particularly challenging when wildlife becomes part of the epidemiological.

**European Badger (*Meles meles*)** Can acquire bTB infection and act like a reservoir for the mycobacterium. It spreads the disease due to what is believed to be an usual tolerance to the infection (a maintenance host). To Understand the uniqueness of the badger's immune system we performed a transcriptome analysis which is crucial for interpreting the functional elements of the genome and uncovering the molecular components of cells and tissues, and also for understanding the physiological and pathological development.

## Methods

**Badger blood:** Samples obtained from Peripheral blood healthy badgers lived in a Controlled environment (UK)

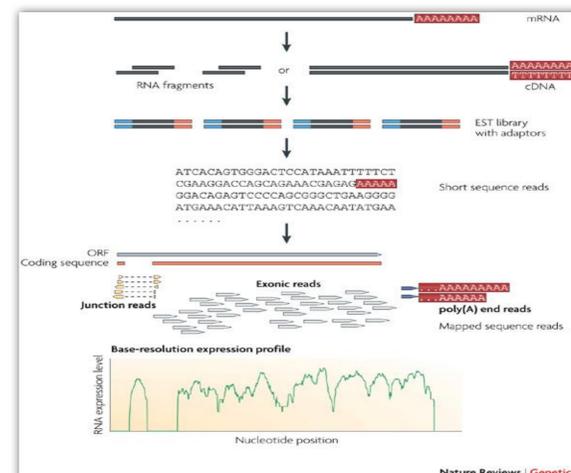
**Transcriptome assembly:** RNA is extracted and RNA Sequencing, annotation by BGI (China)

**Total number of readings 238296 short sequence**

Databases used for annotation :

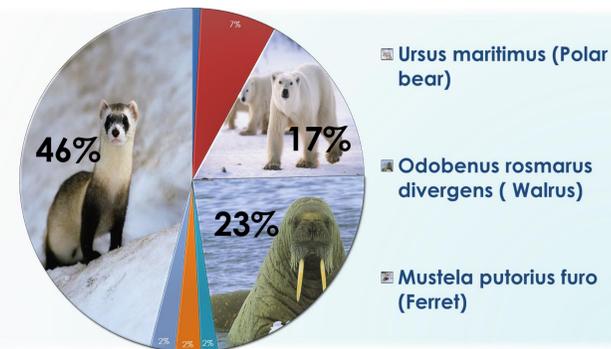
Nucleotide Database, Non-redundant, Kyoto Encyclopedia of Genes and Genomes (KEGG), Swiss-Prot, COG and Gene Ontology (GO)

## Transcriptome assembly

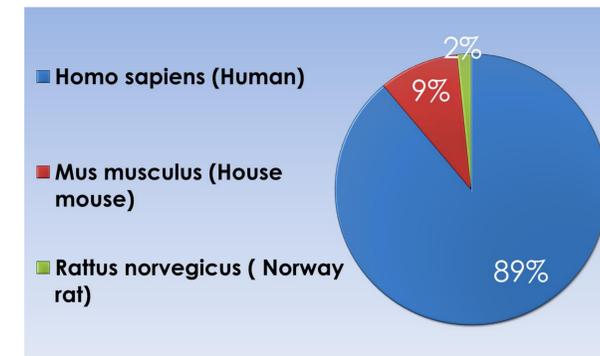


## Results

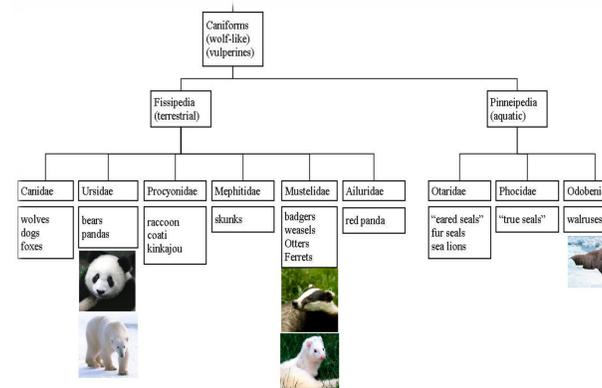
The evolutionary relatedness of the badger's immunoglobulin to the available mammals in NCBI database (Non-redundant database annotation)



Functional similarity of the annotated badger's immunity genes to those of well-known mammals (Swiss-Prot database)



Frequently repeated mammals with similar immune genes in the databases



## Preliminary Conclusions

### TB pathway related readings

Preliminary analysis

There are 183 immunity genes involved in the bTB pathway and 1881 readings extracted from the transcriptome annotation that match some of those genes.

No matching readings found for 18 genes ( However, there are readings of the encoding genes for their receptors)

### Future Work

- Evolution of Badger's immune system to resist the infection in comparison to other mammals available on database
- Possible genes of interest for further analysis (e.g. PCR amplification)

### Thanks to

1. Prof. David Hornby
2. Dr. Roy Chaudhuri
3. Prof. Richard Pleass

### References

1. MACHUGH *et al.*, (2009). *Transbound Emerg Dis*, 56, 204-14.
2. WANG, *et al.*, (2009). *Nat Rev Genet*, 10, 57-63.
3. WARD, *et al.*, (2010). *Preventive Veterinary Medicine*, 93, 2-10.

### Acknowledgement

