

Introduction

Databases are essential to store, annotate and provide the scientific community with all the information gathered by different omics studies, so that it can be used to understand the physio-pathological mechanisms underlying sheep diseases, as well as to develop new and improved diagnostic, prognostic and therapeutic strategies.

OvisOme database

OvisOme is a database that integrates the information produced by proteomics and studies that identify and quantify specific proteins in diseases of *Ovis aries*.

When compared to other proteomics databases, the OvisOme stores and displays more information than other databases not specific for sheep, such as UniProt.

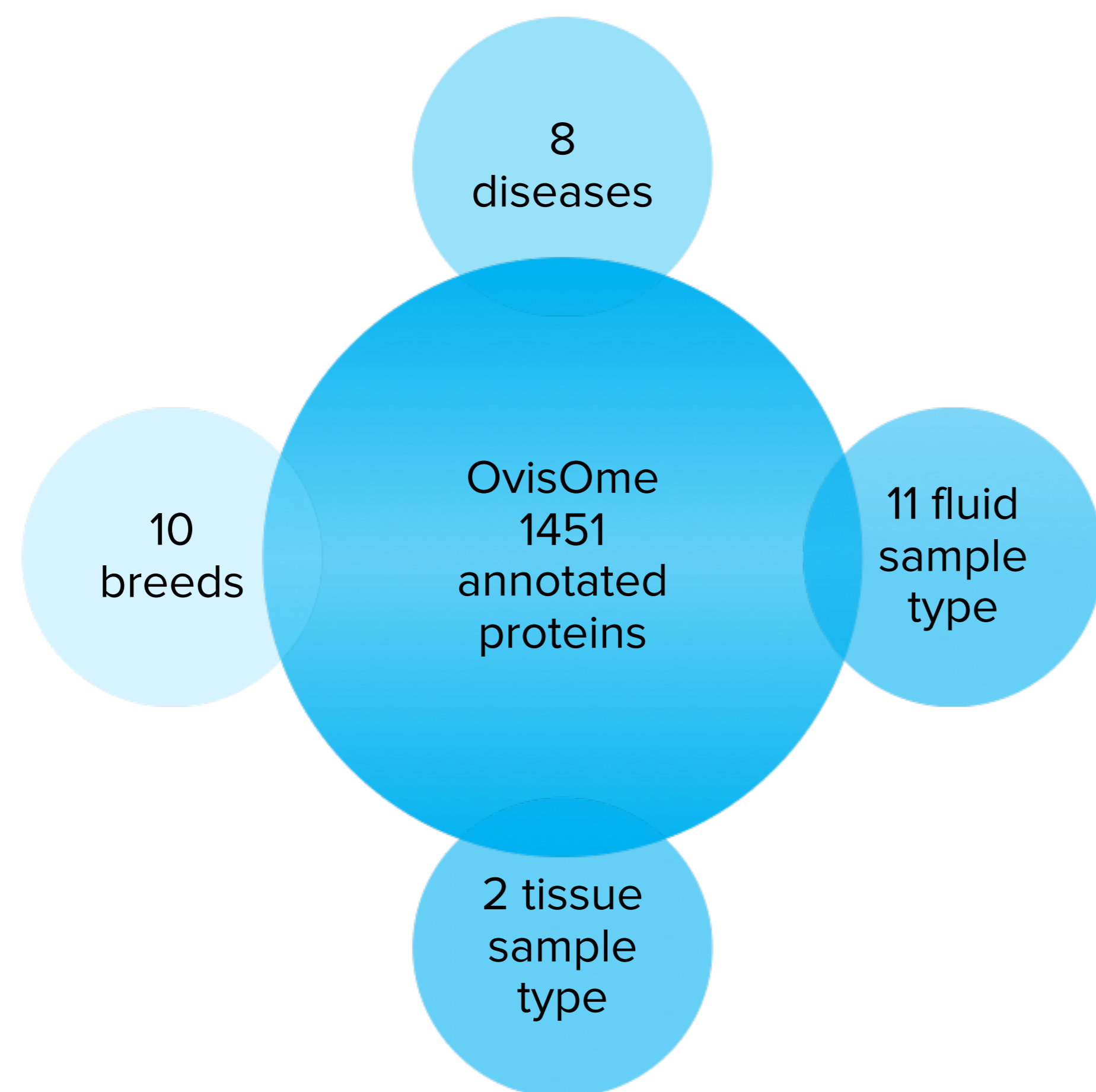
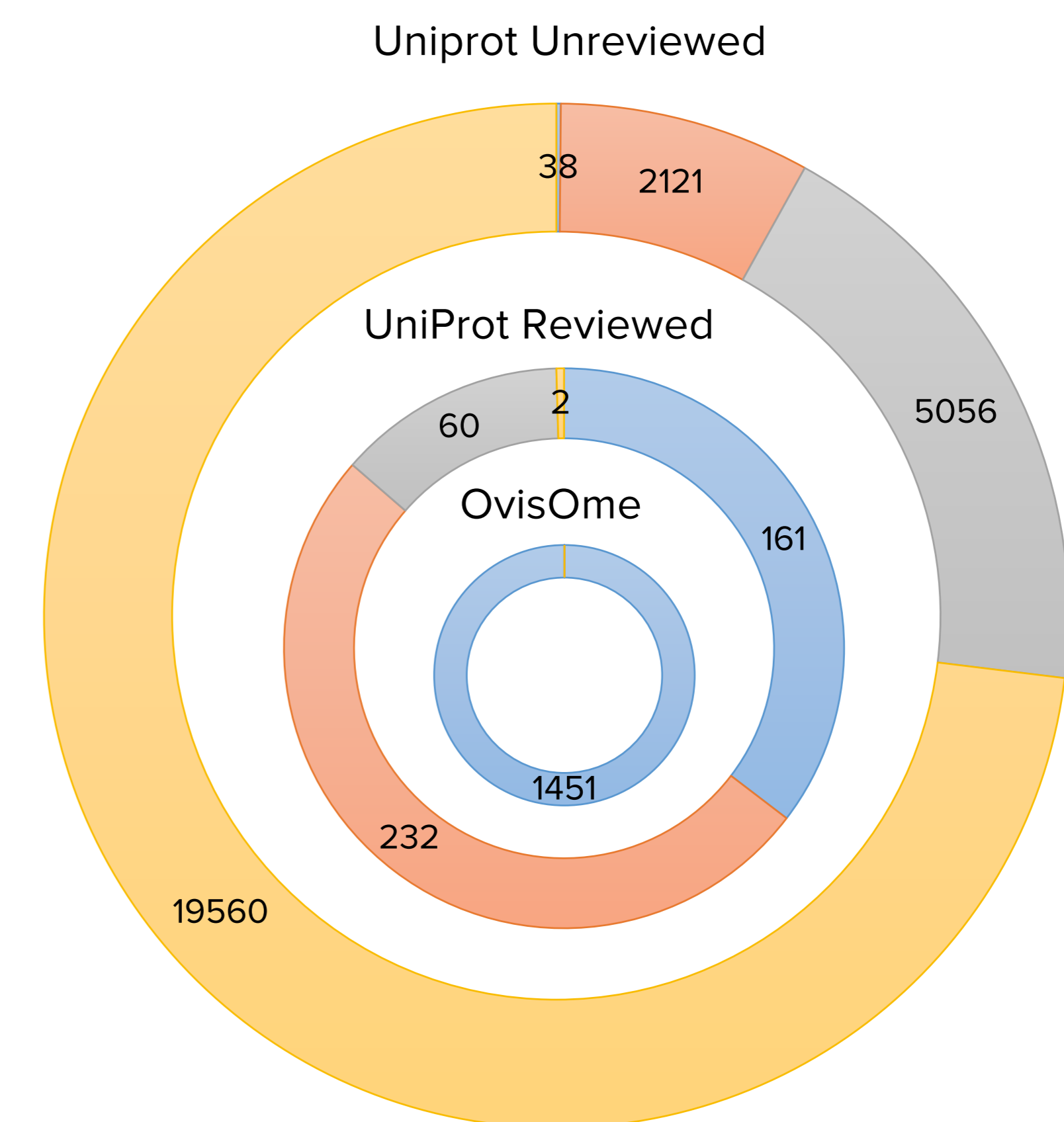


Figure 1: The number of proteins on the OvisOme database according to their distribution by diseases, breeds and type of biological samples.



■ Evidence at protein level ■ Evidence at transcript level ■ Inferred from homology ■ Predicted

Figure 2: Comparison of the protein number and type of evidence for the *Ovis aries* proteome, deposited in the OvisOme and UniProt databases.

OvisOme application

The annotation of the sheep and microbial proteins present in some of the infections allows us to establish the infection mechanisms underlying the sheep's disease.

In this process we were able to identify proteins important in the infection process namely in sheep mastitis.

Main Mastitis Results

- From the common proteins, the most important annotation refers to milk properties such as coagulation and calcium phosphate content.
- From the exclusive proteins in *S. uberis* processes such as “negative regulation of defense response”, “establishment of protein localization to plasma membrane” and “regulation of filopodium assembly” are enriched and all relate to infection response.
- From the exclusive proteins in *M. agalactiae* infection several histones are present which may be related to the Neutrophil extracellular traps (NETs) known to be part of the anti bacterial defense. Additionally RAB7A is also an important target for *Mycobacterium* to interfere with host defenses.
- From the exclusive proteins in *S. chromogenes*, processes such as “regulation of peptide secretion” may also alter immune response.

Mastitis etiologic agents

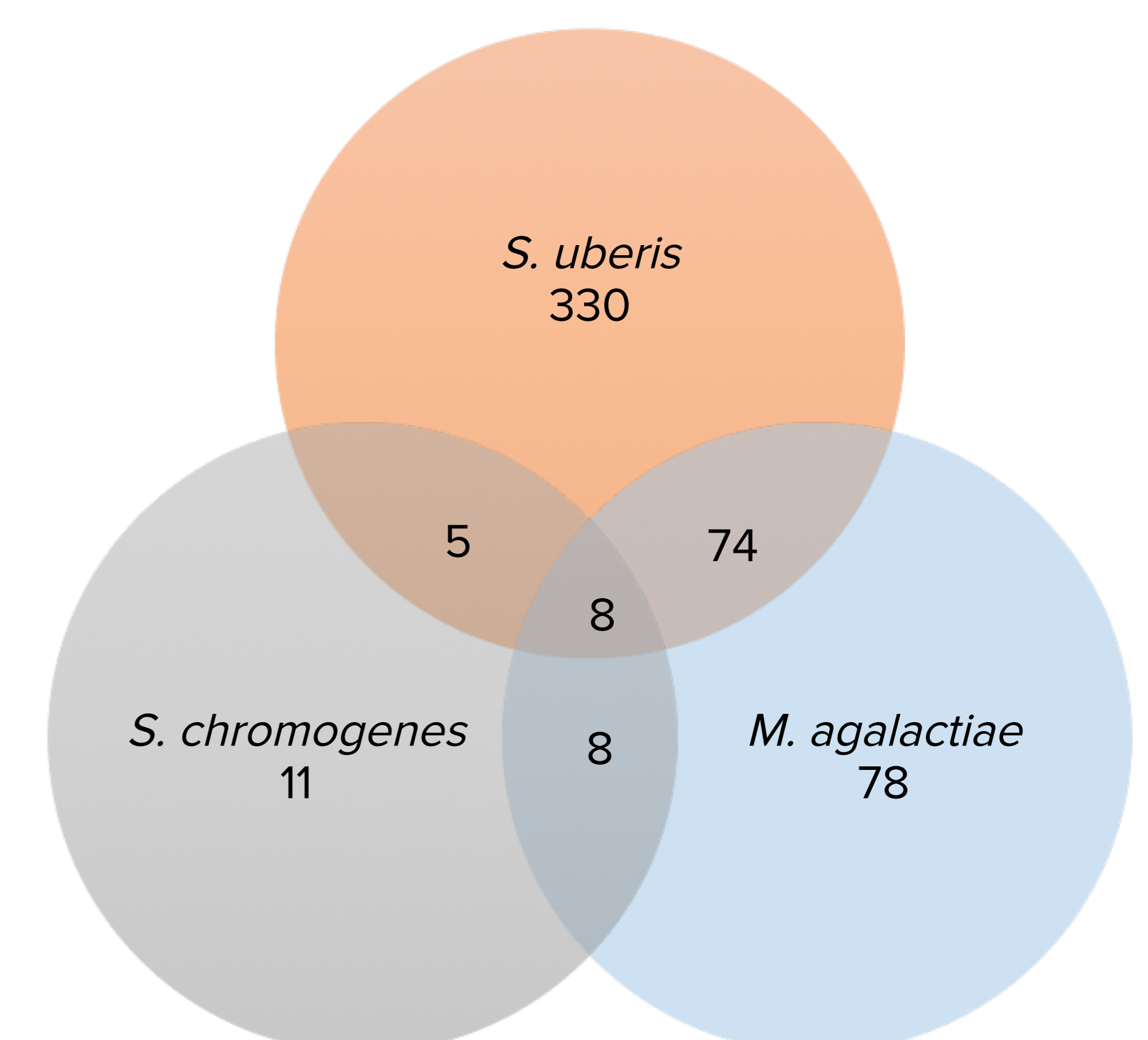


Figure 3: From the 514 proteins annotated on OvisOme database as altered by the mastitis infection with different etiologic agents (*Streptococcus uberis*, *Mycoplasma agalactiae* or *Staphylococcus chromogenes*), 8 are common to all microorganisms but the majority are exclusive.

Table 1: Distribution of the *Ovis aries* proteome by disease and the number of proteins with regulation data and number of biomarker suggested.

Disease	Total number of proteins	Number of quantified proteins	Biomarker proposed
Mastitis	514	198↑, 316↓	7
Fasciolosis	9	6↑, 1↓	9
John Disease	2	1↑, 1↓	2
Kidney Injury	2	2↑	0
Muscle Hypertrophy	17	0	0
Nematode infection	20	0	0
Rhino-trachea-bronchitis	31	3↑, 2↓	0
Scrapie	1	0	1

Conclusion

The analysis of the information in the database is expected to lead to new and improved knowledge of the disease mechanisms and therefore to better diagnostics and therapeutic interventions.

References

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