

**Research title**

**Omic approaches for understanding, detecting and controlling dairy ruminant mastitis**

**Approcci omici per la comprensione, la rilevazione e il controllo delle mastiti dei ruminanti**

**Tutor**

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**State of the art and aims of the project**

Despite numerous efforts for preventing and controlling intramammary infections, mastitis is still responsible for major economic losses in dairy animal productions, and the issue is further enhanced by the constant increase of antibiotic resistance traits and the current pressure on antibiotic reduction. This project will apply omic technologies to investigate the interactions among microorganisms themselves and with the ruminant host to gain a better understanding of their role in favoring or contrasting mastitis. Specific topics will include investigating the impact of farming practices, such as feeding waste milk to calves, on the gut microbiota and on the selection and maintenance of antimicrobial resistance gene pools, evaluating the use of microbial products as alternatives to antibiotics for preventing intramammary infections, and applying proteomic and proteogenomic approaches to the identification and characterization of beneficial and pathogenic bacteria. Traditional bacteriological, immunological and molecular methods will be combined with innovative proteomic, proteogenomic and bioinformatic methods.

**Recent publications of the tutor in the field**

1. Cremonesi, P., Ceccarani, C., Curone, G., Severgnini, M., Pollera, C., Bronzo, V., Riva, F., Addis, M.F., Filipe, J., Amadori, M., Trevisi, E., Vigo, D., Moroni, P., Castiglioni, B. 2018. Milk microbiome diversity and bacterial group prevalence in a comparison between healthy Holstein Friesian and Rendena cows. *PLoS ONE* 13, e0205054.
2. Addis M.F.\*, Tanca A., Uzzau S., Oikonomou G., Bicalho R.C., Moroni P. 2016. The bovine milk microbiota: insights and perspectives from –omics studies. *Molecular BioSystems* 12:2359-2372.
3. Tanca A., Palomba A., Pisanu S., Deligios M., Fraumene C., Manghina V., Pagnozzi D., Addis M.F.\*, Uzzau S. 2014. A straightforward and efficient analytical pipeline for metaproteome characterization. *Microbiome*. 10;2(1):49.
4. Tanca, A., Biossa, G., Pagnozzi, D., Addis, M.F.\*, Uzzau, S. 2013. Comparison of detergent-based sample preparation workflows for LTQ-Orbitrap analysis of the *Escherichia coli* proteome. *Proteomics* 13:2597-2607.
5. Addis, M.F.\*, Pisanu, S., Ghisaura, S., Pagnozzi, D., Marogna, G., Tanca, A., Biossa, G., Cacciotto, C., Alberti, A., Pittau, M., Roggio, T., Uzzau, S. 2011. Proteomics and pathway analysis of the milk fat globule in sheep naturally infected by *Mycoplasma agalactiae*: insights into the in vivo response of the mammary epithelium to bacterial infection. *Infection and Immunity* 79(9):3833-3845.