

Saumya Wickramasinghe

CURRICULUM VITAE

Assistant Project Scientist
Dept. of Food Science and Technology, University of California Davis
swickramasinghe@ucdavis.edu

EDUCATION:

INSTITUTION AND LOCATON	DEGREE	YEAR	FIELD OF STUDY
University of California, Davis, CA	PhD	2011	Animal Biology
Oklahoma State University, Stillwater, OK	MS	2006	Animal Science
University of Peradeniya, Sri Lanka	BVSc (D.V.M)	2003	Veterinary Medicine

PROFESSIONAL EXPERIENCE:

2019-2021 April	Visiting Assistant Professor, Dept. of Food Science and Technology, University of California Davis
2013- 2019 Feb	Senior Lecturer Dept. of Basic Veterinary Sciences, University of Peradeniya, Sri Lanka
2016 Sep-2016 Nov	Visiting Assistant Professor, Dept. of Food Science and Technology, University of California Davis, USA
2015 Sep-2015 Nov	Visiting Assistant Professor, Dept. of Food Science and Technology, University of California Davis, USA
2012- 2013	Post-Doctoral Researcher, David Mills lab, Dept. of Viticulture and Enology University of California Davis, USA

RESEARCH EXPERIENCE

- Study on host microbial interaction in the gut using RNAseq gene expression. Designed and conducted RNASeq experiments in mammalian (Caco2 cells, milk somatic cells) and bacterial cells (Bifidobacterium and Lactobacilli). Study on the genetic response of host cells and the bacterial cells to prebiotics such as BMO and HMO
- Analysis of next generation sequencing (RNAseq) data of eukaryotes and prokaryotes using CLC genomic workbench, K base and DSeq
- Metabolic Pathway analysis using Ingenuity, DAVID and Reactome
- Bacterial genetics - Microbial genome assembly and annotation using Kbase, JGI/IGM and CLC genomic workbench
- Growth of anaerobic bacteria in different carbon sources, glycorpofiling and analysis if glycan consumption by bacteria
- Bacterial cloning and gene knockout studies, Gene deletion in E.coli by Red-mediated recombination

- Collaborated with a project that involved General automation lab technology (GALT) that did high throughput culturomics of Bifidobacterium and familiarized with the GALT technology and the downstream
- Expertise on RNA extraction from mammalian and bacterial cells, cDNA and RNA-Seq library preparation, gene expression (Real time PCR, microarray and RNA-Seq), genotyping (KASPAR, sequenome, RFLP), TAG SNP identification and candidate gene based association analysis
- RFLP, ARMS and MLST genotyping to identify variations in bovine genes (casein cluster genes) and characterization of bacterial species
- Establish and maintain a cell culture lab at Dept. of Food Science and Technology, University of California Davis. Work on human intestinal (Caco2, T84) and bovine adipose tissue primary cell culture
- KASP and Sequenome genotyping to study candidate gene based association analysis in beef and dairy cattle
- MicroRNA-Sequencing on human urine samples and data analysis
- Metagenomics studies using 16S sequencing in bacteria (water and hot water springs) and data analysis using QIIME
- Use of mouse model for studies on host–microbe response to prebiotics

PUBLICATIONS:

Wang, H., J. H. Simpson, M. E. Kotra, Y. Zhu, **S. Wickramasinghe**, D. A. Mills and N. H. L. Chiu (2021). "Epitranscriptomic profile of Lactobacillus agilis and its adaptation to growth on inulin." BMC Research Notes 14(1): 154

Wickramarathna, S., Chandrajith, R., Senaratne, A., Paul, V., Dash, P., **Wickramasinghe, S.**, & Biggs, P. (2021). Bacterial influence on the formation of hematite: Implications for Martian dormant life. International Journal of Astrobiology, 1-15. doi:10.1017/S1473550421000124

M Pry, J., W. Jackson, R. Rupasinghe, G. Lishanthe, Z. Badurdeen, T. Abeysekara, R. Chandrajith, W. Smith and **S. Wickramasinghe (2021)**. "A pilot case-control study using a one health approach to evaluate behavioral, environmental, and occupational risk factors for chronic kidney disease of unknown etiology in Sri Lanka." One Health Outlook 3(1): 4.

R.K. Rupasinghe, N. Shanjayan, L.G.S. Lokugalappatti, **S. Wickramasinghe**. 2020. Genetic Variants of β -casein Gene in Indigenous and Exotic Dairy Cattle Breeds in Sri Lanka. Asian Journal of Dairy and Food Research (39):217-220

Boudry, G., M K. Hamilton, M. Chichlowski, **S. Wickramasinghe**, D. Barile, K. M Kalanetra, D. A. Mills and H. E Raybould (2017). Bovine milk oligosaccharides decrease gut permeability and improve inflammation and microbial dysbiosis in diet-induced obese mice. Journal of Dairy Science

Wickramasinghe S, Pacheco SA, Lemay D and Mills D (2015) Bifidobacteria grown on human milk oligosaccharides downregulate the expression of inflammation-related genes in Caco-2 cells. BMC Microbiology 15(1):172

Wickramasinghe S, Cánovas A, Rincón G and Medrano JF (2014) RNA-Sequencing: A tool to explore new frontiers in animal genetics. Livestock Science 166: 206-216

Khaldi N, Vijayakumar V, Dallas DC, Guerrero A, **Wickramasinghe S**, Smilowitz JT, Medrano JF, Lebrilla CB, Shields DC and German JB (2014) Predicting the important enzyme players in human breast milk digestion. *J Agric Food Chemistry* 62(29):7225-32

Wickramasinghe S, Rincon G, Islas-Trejo A and Medrano JF (2012) Transcriptional profiling of bovine milk using RNA sequencing. *BMC Genomics* 13:45

Barboza M, Pinzon J, **Wickramasinghe S**, Froehlich JW, Moeller I, Smilowitz JT, Ruhaak LR, Huang J, Lönnerdal B, German JB, Medrano JF, Weimer BC and Lebrilla CB (2012) Glycosylation of human milk lactoferrin exhibits dynamic changes during early lactation enhancing its role in pathogenic bacteria-host interactions. *Molecular & Cellular Proteomics* 11(6)

Wickramasinghe S, Hua S, Rincon G, Islas-Trejo A, German JB, Lebrilla CB and Medrano JF (2011) Transcriptome Profiling of Bovine Milk Oligosaccharide Metabolism Genes Using RNA-Sequencing. *PLoS ONE* 6(4): e18895

Wickramasinghe S and Medrano JF (2011) Primer on genes encoding enzymes in sialic acid metabolism in mammals. *Biochimie* 93:1641-1646

Wickramasinghe S, Rincon G and Medrano JF (2011) Variants in the pregnancy-associated plasma protein-A2 gene on *Bos taurus* autosome 16 are associated with daughter calving ease and productive life in Holstein cattle. *Journal of Dairy Science* 94:1552-1558

Cánovas A, Rincon G, Islas-Trejo A, **Wickramasinghe S** and Medrano JF (2010) SNP discovery in the bovine milk transcriptome using RNA-Seq technology. *Mammalian Genome* 21:592-598

REVIEW OF DATABASES:

Sialic acid metabolism in Reactome data base (2014)
http://www.reactome.org/PathwayBrowser/#DB=gk_current&FOCUS_SPECIES_ID=48887&FOCUS_PATHWAY_ID=4085001&ID=4085001