

BACTERIA IN HUMAN MILK: DO THEY REALLY MAKE A DIFFERENCE?

AUGUST

3

WESTERN PACIFIC REGION

12:00 AM EDT (AUGUST 2)

6:00 AM CEST

12:00 PM AWST



Speaker: Professor Mark Nicol

Clinical microbiologist and Professor of Microbiology in the School of Biomedical Sciences at the University of Western Australia. Holds an honorary appointment at the University of Cape Town.

We studied the human milk (HM) metabolome and microbiome in women participating in a South African birth cohort, the Drakenstein Child Health Study. A subset of women (45/519, 8.7%) had low HM lactose (>2SD below mean). Low lactose was associated with shorter exclusive breastfeeding duration (28 vs 55 days) and poor infant growth during exclusive breastfeeding. Metabolomic profiling of low-lactose HM revealed an increase in metabolites associated with microbial carbohydrate metabolism. 16S rRNA amplicon sequencing showed that HM samples with low lactose had significantly higher median relative abundance of *Staphylococcus* species compared with normal lactose HM (19% vs 5%) and increased bacterial load. Further, *S. aureus* was isolated from 73% of HM samples with low lactose compared with 20% of samples with normal milk lactose. Growth of *S. aureus* in vitro was inhibited by typical concentrations of lactose found in HM. Low lactose in HM may be permissive for the growth of *S. aureus* and contribute to poorer lactational outcomes.



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