
Theses

2016

Towards the identification of metabolite markers of nipple pain and inflammation in human milk

Erin Fee

Follow this and additional works at: <http://researchonline.nd.edu.au/theses>



Part of the [Life Sciences Commons](#), and the [Medicine and Health Sciences Commons](#)

COMMONWEALTH OF AUSTRALIA
Copyright Regulations 1969

WARNING

The material in this communication may be subject to copyright under the Act. Any further copying or communication of this material by you may be the subject of copyright protection under the Act.

Do not remove this notice.

5 Conclusion

Nipple pain is a common problem for breastfeeding mothers in Australia and often persists for several weeks post partum. As a result it is largely responsible for cessation of breastfeeding in early lactation (weeks 1-4), which can adversely affect the developing infant. It is important to establish the effect of nipple pain and trauma on breast health via breast milk composition, which would then enable rapid diagnosis of pathology, timely intervention and appropriate monitoring of treatment.

In this study microbial analysis of the milk of mothers with nipple pain found limited numbers of potentially pathogenic bacteria, therefore participants were unlikely to have subclinical mastitis, which is reflected also in the pain scores and Na^+/K^+ ratios. However, GC-MS analysis identified differences in metabolite composition between the human control and nipple pain groups. A series of amino acids, previously found to be associated with inflammatory conditions, was elevated in nipple pain milk samples, suggesting that indeed metabolomics may potentially identify mothers with nipple pain that might be predisposed to infection. Consequently, if severity of trauma is related to an underlying infection, then profiling the metabolites may lead to identification of differences in the metabolite composition between mothers'.

Future analysis of human milk should employ LC-MS for analysis of the non-polar fraction of the milk to further the understanding of the milk metabolome. Following the optimisation of an untargeted metabolomics approach, a targeted analysis for the identification of bacterial and fungal metabolites will also increase the potential for diagnosis and provide insight into the breast microbiome.

In conclusion, these results provide preliminary support to confirm the concept that milk expressed by mothers presenting with nipple pain contain compositional differences, detected by metabolomics, which may be related to the early stages of the continuum of mastitis. Further study is required on much larger sample sets to determine the efficacy of this technique in the detection of breast infection and the relationship between compositional change and severity of infection.