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| **Personal network inference identifies children at risk of recurrent wheezing** |
| LA Coleman1,2, SK Khoo2,3, K Franks2,3, F Prastanti2,3, J Bizzintino2,3, M Borland4,5, PN Le Souëf1,2, D Hancock2,5#, YV Karpievitch2,3#, A Bosco6#, IA Laing1,3# |
| *1 Medical School (Paediatrics), University of Western Australia, Western Australia, Australia*  *2 Wal-yan Respiratory Centre, Telethon Kids Institute, Western Australia, Australia*  *3 School of Biomedical Sciences, University of Western Australia, Western Australia, Australia*  *4 School of Medicine, University of Western Australia, Western Australia, Australia*  *5 Perth Children’s Hospital, Western Australia, Australia*  *6 College of Medicine, University of Arizona, Arizona, USA*  *#These Authors have joint Senior Authorship and equal contribution.* |
| **Introduction/Aim:** An area of clinical need for the treatment and management of acute wheezing/asthma is identifying children at risk of developing persistent exacerbations, compared to children who will have a few episodes that resolve with age. We hypothesised that clustering individual gene expression networks would identify children with increased risk of recurrent wheezing/asthma.  **Methods:** Children recruited on presentation to a tertiary children’s hospital emergency department with an acute lower respiratory illness were assigned a recurrence phenotype (few, multiple or persistent) using public hospital data on presentations from birth onwards. RNA was extracted from PBMCs and gene expression was quantified using *Affymetrix* Human Gene 2.1 ST micro-arrays. The data were analysed using the *lionessR* package to construct individual gene networks. Genes were grouped into modules using Fuzzy clustering by Local Approximation of MEmbership (FLAME), and networks were quantified using the proportion of genes from each FLAME module present. Children were divided into sub-groups based on shared gene network patterns using the *mclust* package. Time until the next exacerbation was compared between groups using survival curves, as well as phenotypes using contingency tables.  **Results:** We identified three sub-groups of children based on the similarity of their individual network patterns. One of those sub-groups had faster re-presentation to hospital with another exacerbation (recurrence) and increased risk of developing a persistent exacerbation phenotype, mostly likely due to asthma. Robust expression of interferon-associated genes reduced the risk of recurrence and persistence, whereas network patterns related to adaptive immunity and cytotoxic cells were associated with increased risk of recurrent wheeze and persistent exacerbations.  **Conclusion:** Systemic immune profiling in young children with acute wheeze can be used to predict future risk of respiratory exacerbations.  **Grant Support:** Wal-yan Respiratory Centre Inspiration Award, NHMRC, Telethon – Perth Children’s Hospital Research Fund, AstraZeneca  **Key Words:** paediatric, asthma, wheezing, endotypes, transcriptomics |