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TITLE: Genome-wide association analysis on breastfeeding duration

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ABSTRACT: Breastfeeding duration (BFD) is heritable. The first twin study on breastfeeding (Colodro-Conde et al., 2013) showed heritabilities of 49% for the initiation of breastfeeding in the first child, 44% for BFD in the first child and 54% for the average BFD to all children. The heritability was of 53% for the average BFD in a replication study with an Australian twin sample (Colodro-Conde, et al., 2015). Using an extended twin-family design, Merjonen et al. (2015) showed a heritability estimate of 70% for the initiation of breastfeeding in Dutch women.

A published genome-wide scan on BFD found no genetic variants reaching genome-wide significance (Colodro-Conde et al., 2015), although the sample was underpowered (N=1521). The aim of this project is to identify novel genes that influence breastfeeding duration in the first child by carrying out large scale genomewide association study (GWAS) meta-analyses and to explore genetic correlations with related traits (e.g. breast cancer).

We will present results of the GWAS conducted in the QIMR samples, with N~8,000 women and replication in the ASLPAC (UK, N = 3,338) and DBNC (Denmark, N = 2,766) cohorts.

Colodro-Conde, L., et al (2013). Heritability of initiation and duration of breastfeeding behavior. *Twin Research and Human Genetics*, 16.

Colodro-Conde, L., et al (2015). A Twin Study of Breastfeeding With a Preliminary

Genome-Wide Association Scan. *Twin Research and Human Genetics*, 18.
Merjonen, P., et al Does Breastfeeding Behavior Run in Families? Evidence From Twins,
Their Sisters and Their Mothers in the Netherlands. *Twin Research and Human Genetics*,
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