**Key genetic variants associated with variation of milk oligosaccharides from diverse human populations**

Human milk oligosaccharides (HMO), the third most abundant component of human milk, are thought to be important contributors to infant health. Studies have provided evidence that geography, stage of lactation, and Lewis and secretor blood groups are associated with HMO profile. However, little is known about how variation across the genome may influence HMO composition among women in various populations. In this study, we performed genome-wide association analyses of 395 women from 8 countries to identify genetic regions associated with 19 different HMO. Our data support FUT2 as the most significantly associated ($P < 4.23\text{-}9$ to $P < 4.5\text{-}70$) gene with seven HMO and provide evidence of balancing selection for FUT2. Although polymorphisms in FUT3 were also associated with variation in lacto-N-fucopentaose II and difucosyllacto-N-tetrose, we found little evidence of selection on FUT3. To our knowledge, this is the first report of the use of genome-wide association analyses on HMO.