Maternal Obesity Alters Vertical Transmission of Gut Microbiota and Metabolites in Mexican binomia.

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Vertical transmission of microbiota and metabolites plays a pivotal role in shaping neonatal development. This study investigates how maternal obesity alters the enteromammary axis, disrupting early-life microbial and metabolic inheritance in newborns. In this study, we examined a cohort of 42 Mexican mother-infant dyads, categorized according to maternal pre-pregnancy body mass index (BMI). The microbial communities were analyzed using high-throughput 16S rRNA gene sequencing, while metabolomic profiles were characterized through FT-ICR mass spectrometry. Our sample collection included maternal fecal samples, human milk, and neonatal feces. We employed microbial source tracking methodologies alongside multi-omics integration to evaluate vertical transmission dynamics and inter-compartmental microbial shifts. Obese mothers exhibited gut dysbiosis with reduced microbial diversity and increased pro-inflammatory taxa. Human milk was identified as the primary microbial source for neonatal colonization, its composition significantly influenced by maternal BMI. Neonates born to obese mothers showed elevated levels of inflammation-associated genera (e.g., *Klebsiella*, *Ruminococcus_D*) and reduced abundance of beneficial bacteria (e.g., *Bifidobacterium*). Metabolomic profiles revealed a depletion of health-promoting SCFAs and an accumulation of inflammatory metabolites in both maternal and neonatal compartments. Integration of microbial and metabolite data uncovered BMI-specific signatures that suggest disrupted microbial-metabolic programming in obese binomia. Maternal obesity profoundly reconfigures the enteromammary transmission of microbiota and metabolites, potentially predisposing neonates to long-term health risks. These findings underscore the biological significance of maternal metabolic status on the earliest stages of life and highlight key targets for microbiome-centered intervention strategies. This work was supported by CONACyT 163235 INFR-2011-01 and CONACyT FORDECYT-PRONACES/6669/2020_Programa Presupuestario F003-Ciencia de frontera 2019.