Maternal gut and breast milk microbiota affect infant gut antibiotic resistome and mobile genetic elements

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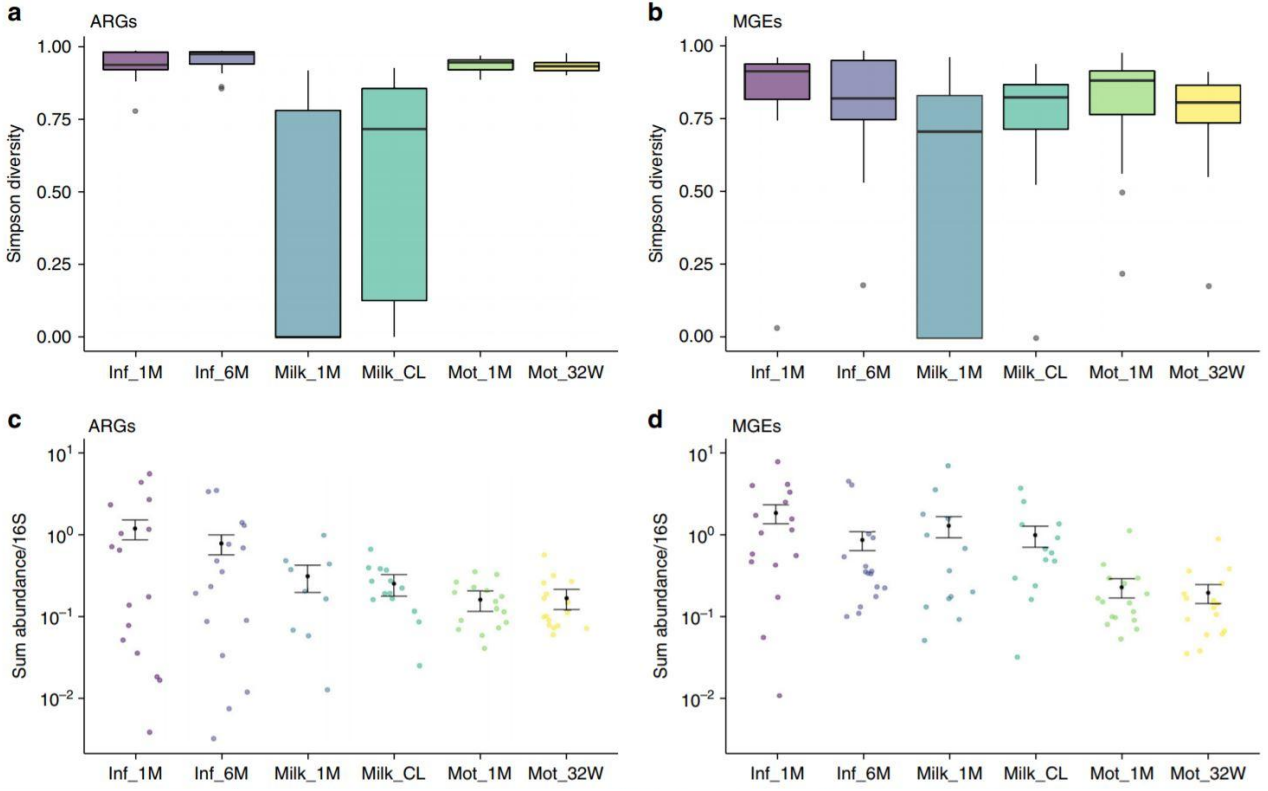
Background / Motivation: Infants have a higher abundance of antibiotic resistance genes (ARGs) compared to adults; however, the source of these ARGs is unknown.

Methods: Metagenomic sequencing of fecal and breast milk samples obtained from 16 mother-infant pairs over an 8 month period (96 samples total).

Results: ARGs and mobile genetic elements (MGEs) in infants are similar to those in their mother's gut and breast milk; early termination of breastfeeding and antibiotic exposure leads to more ARGs in infant.

Conclusions: Infants obtain most ARGs and MGEs directly from their mothers gut and breast milk microbiota, including ARGs resulting from the mother's intrapartum consumption of antibiotics.

Infant gut microbiome has high abundance of ARGs and MGEs

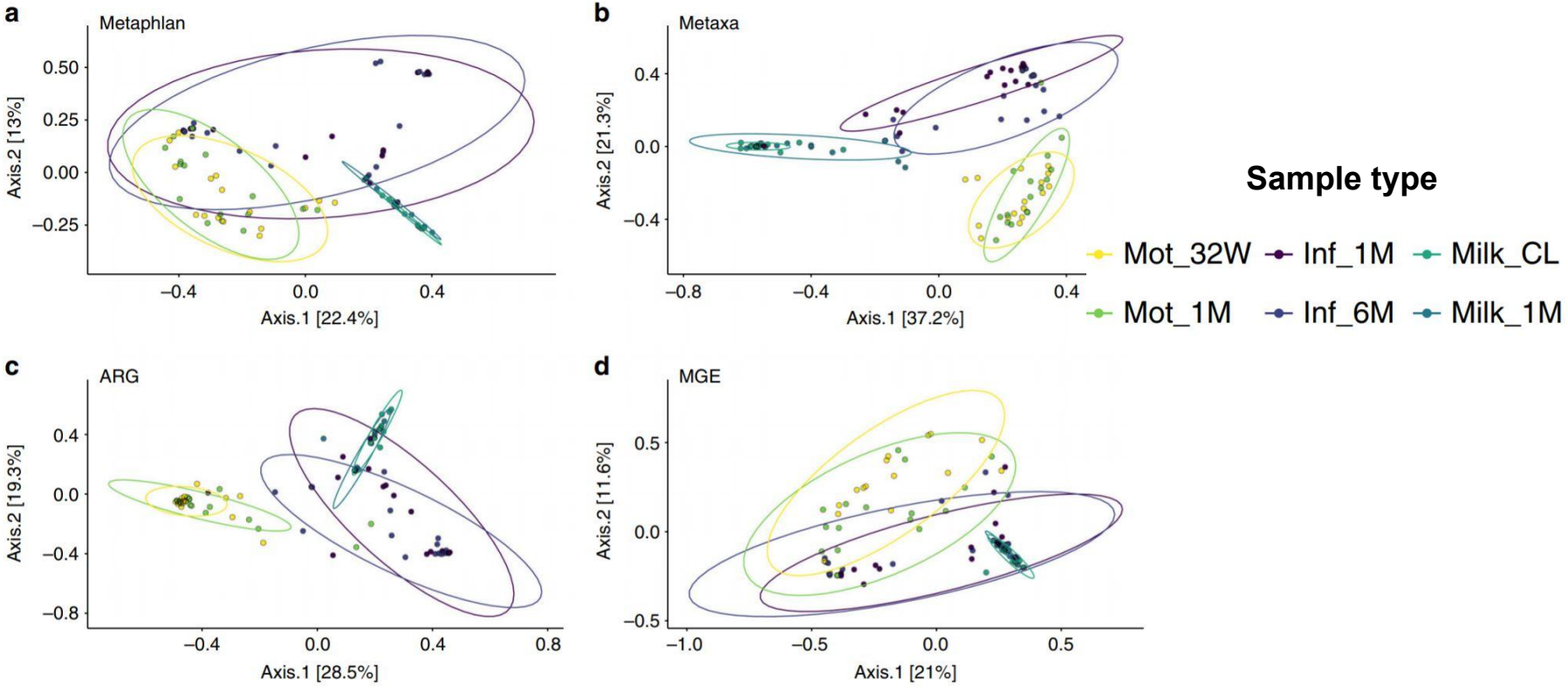


Inf_1M = 1-month-old infants (fecal)
Inf_6M = 6-month-old infants (fecal)

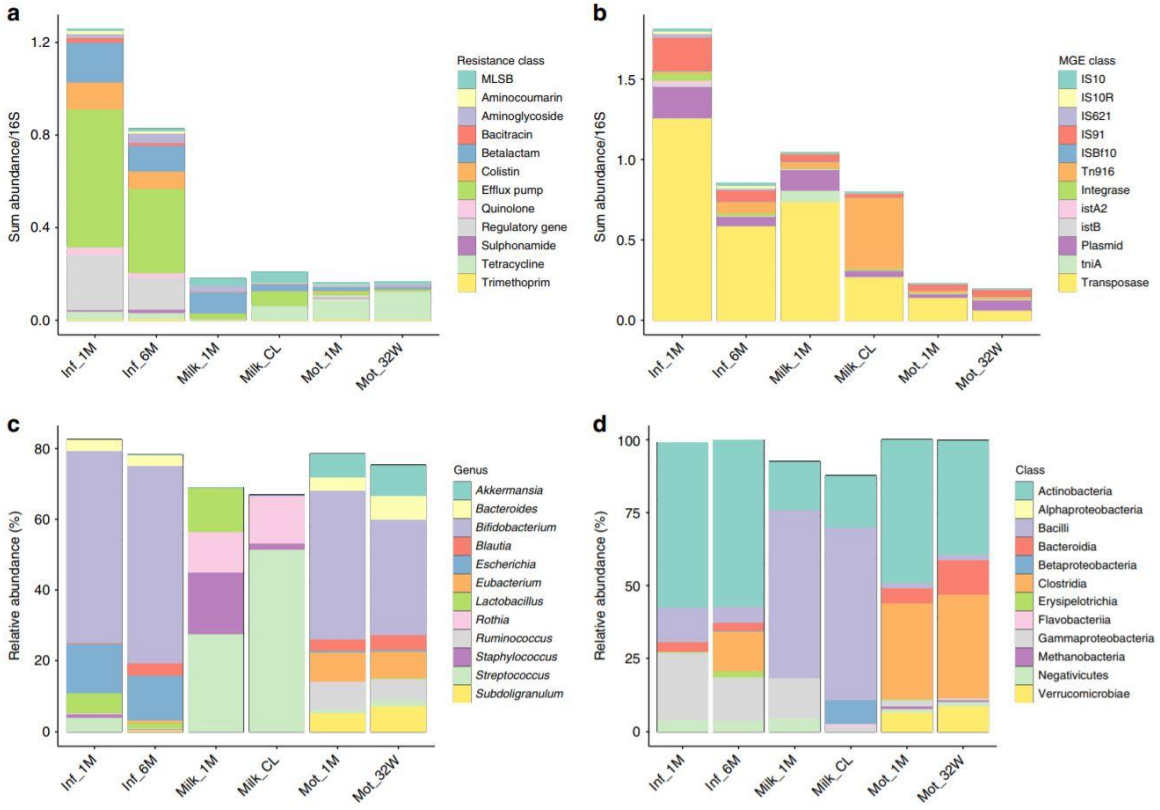
Milk_1M = milk 1 month postpartum
Milk_CL = milk within 7 days of delivery

Mot_32W = mother gestation week 32 (fecal)
Mot_1M= mother 1 month postpartum (fecal)

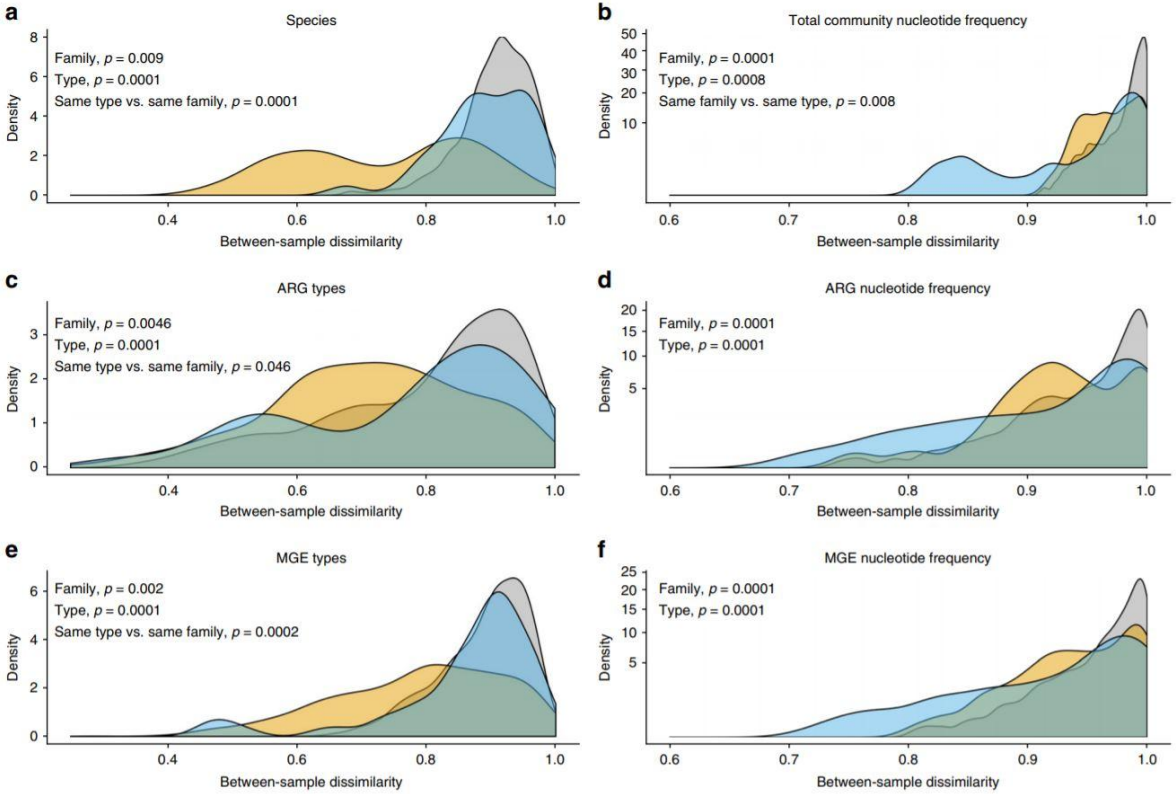
Breast milk microbiome is similar to infant gut microbiome



MGE abundance indicates infants have high-potential for ARG transfer



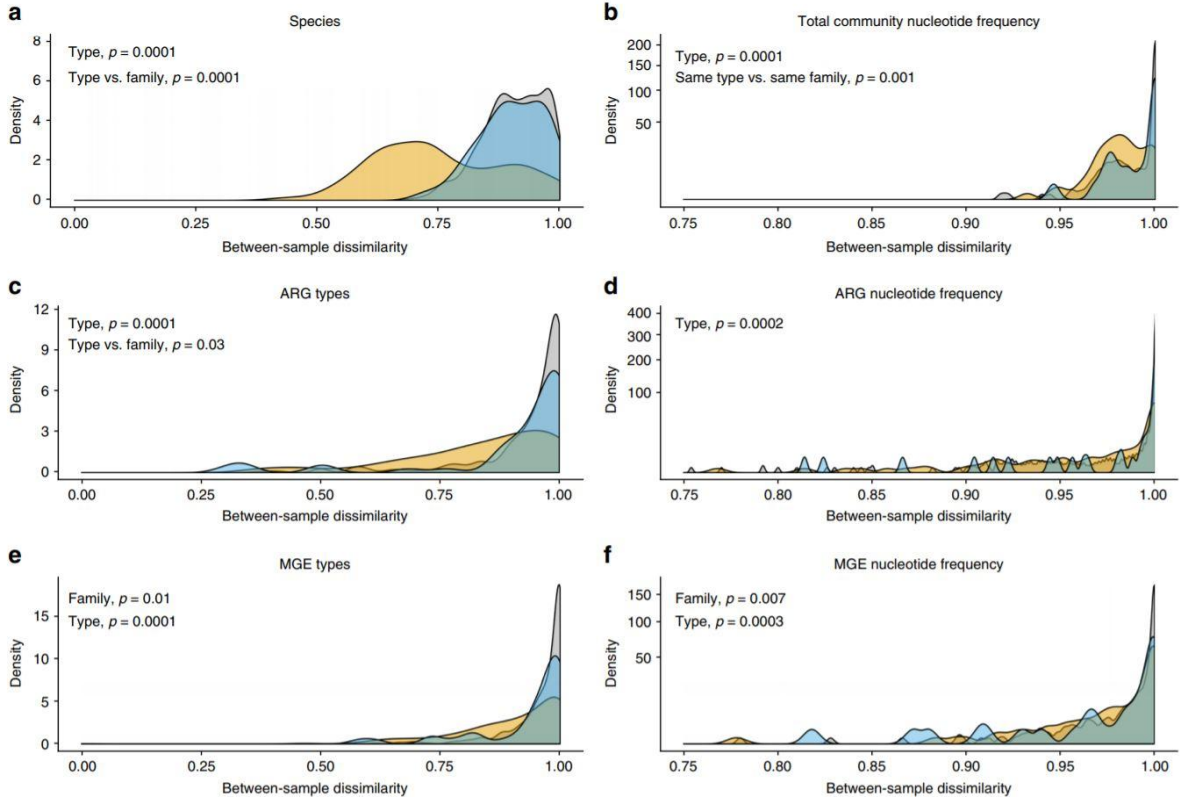
High similarity between ARGs and MGEs in infants' and mothers' gut



Relationship and type

- Unrelated mother and infant
- Unrelated and same type
- Related mother and infant

High similarity between MGEs in infants' gut and mothers' breast milk



Relationship and type

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Early termination of breastfeeding may lead to more ARGs