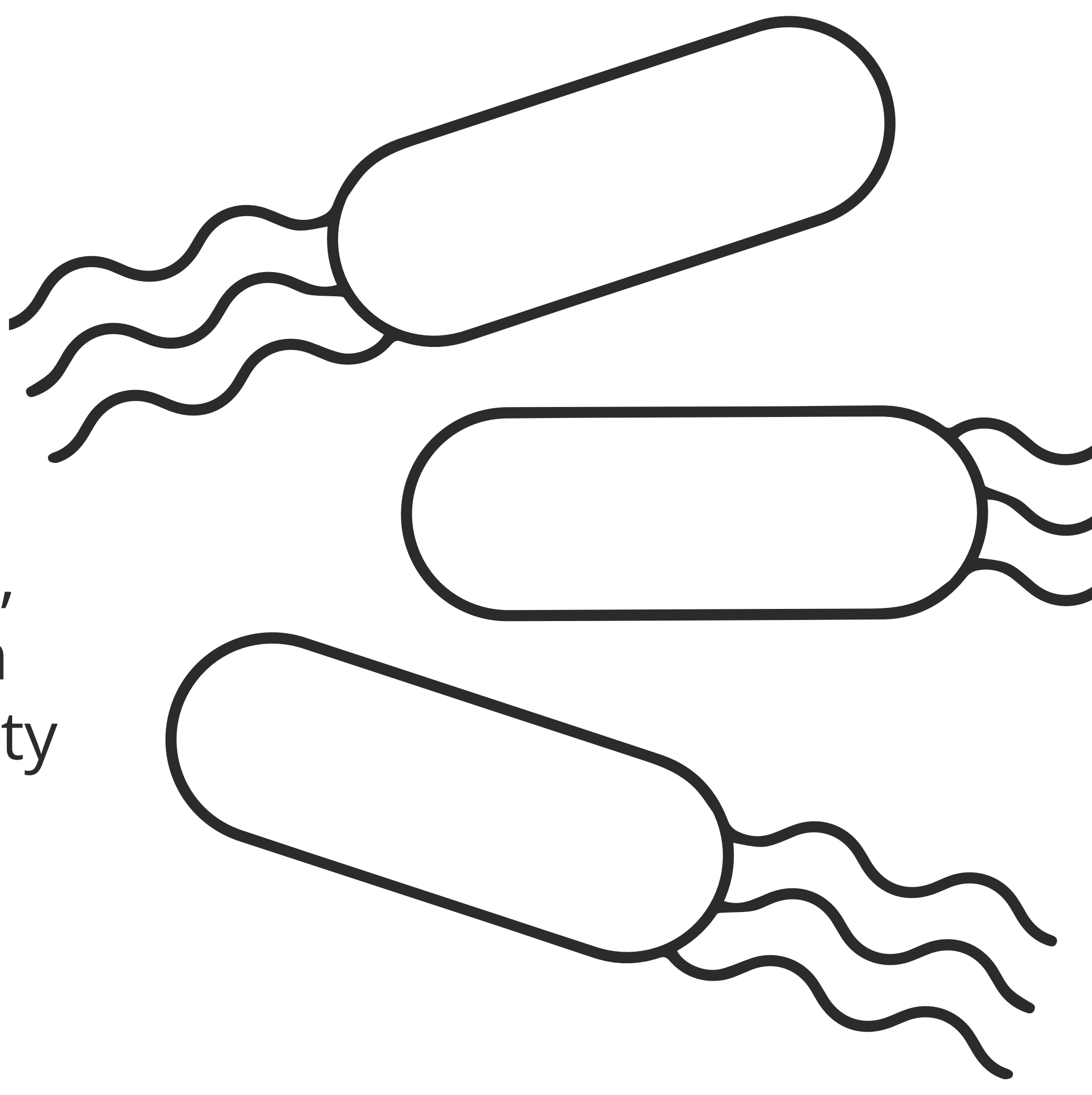
Genomic diversity of *Escherichia coli* from healthy children in rural Gambia

BACKGROUND



***Escherichia coli* is a widespread and versatile colonising bacterium**, and can be categorised across eight different phylogroups. Under appropriate conditions, *E. coli* can lead to diarrhoea, urinary tract infection, neonatal sepsis, bacteraemia, and multi-drug resistant infection in humans. Little is known about its genomic diversity among children living in sub-Saharan Africa, but **such knowledge can help us to better understand bacterial evolution and ecology and their role in infection.**

INVESTIGATING THE ROLE OF *E. COLI* IN INFECTION

In this paper, we studied which distinct strains of *Escherichia coli* live within the gut of healthy children living in the Gambia, West Africa. **Faecal samples were collected from 66 children aged 3-5 years old, and up to 5 colonies of faecal *E. coli* were isolated.**

Genomic Diversity within Hosts:
There are two sources of within-host genomic diversity:

IMMIGRATION/ESTABLISHMENT

OR

WITHIN-HOST EVOLUTION

RESULTS

Immigration events accounted for the majority (76%) of variants, and within-host evolution plays a minor role in the generation of diversity.

Each child carried at least two distinct kinds of *E. coli*, most of them having the potential to cause diarrhoea and armed with genes that can make them withstand treatment with drugs that are usually successful in human infection.

CONCLUSION

Our results show that **most of the distinct *E. coli* strains found in healthy Gambian children were picked up over the course of life** (independent immigration) and very few were the result of changes to *E. coli* already present within the gut (within-host evolution). Additionally, ***E. coli* in these children have certain genes that can potentially contribute to future infections caused by *E. coli* or other bacteria living in the gut of healthy children.**

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