



Role of the metacommunity in the colonization of rabbit's intestinal tract to fight against antibiotic-resistant bacteria

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Role of the metacommunity in the colonization of rabbit's intestinal tract to fight against antibiotic-resistant bacteria

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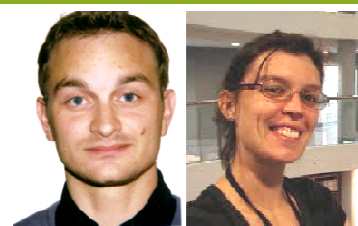
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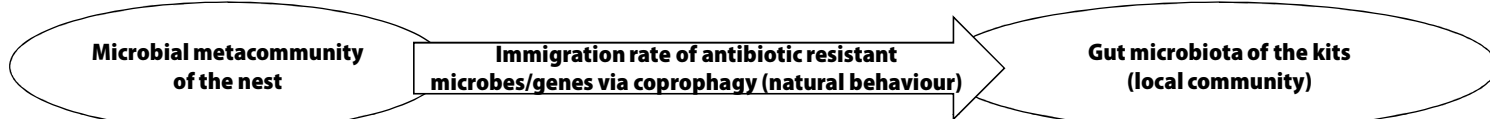
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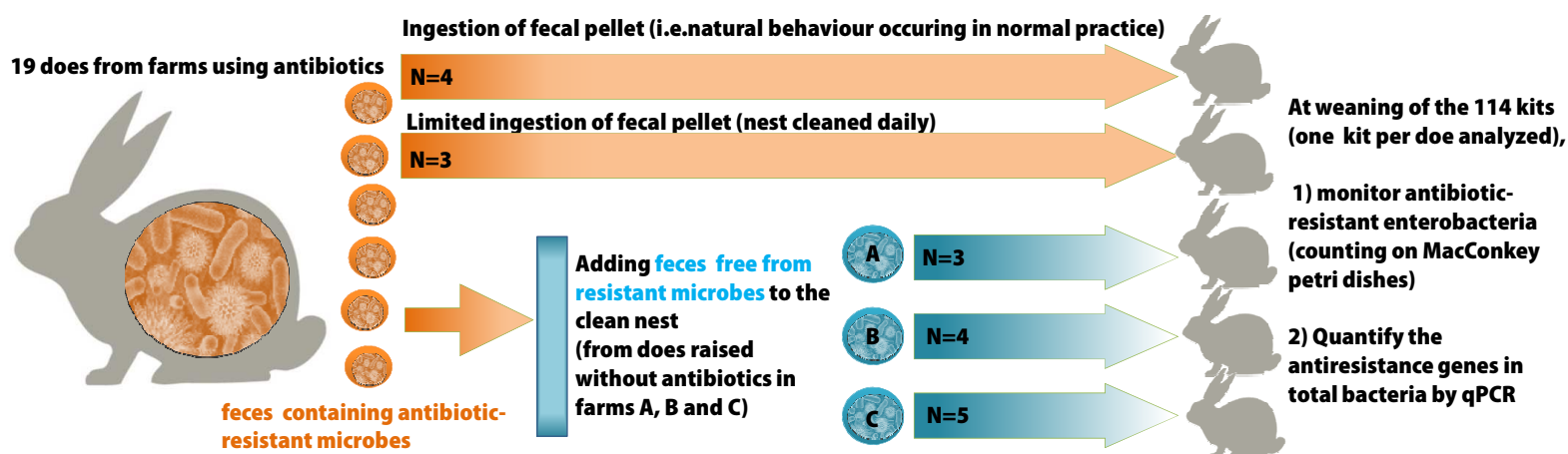


Introduction and objective

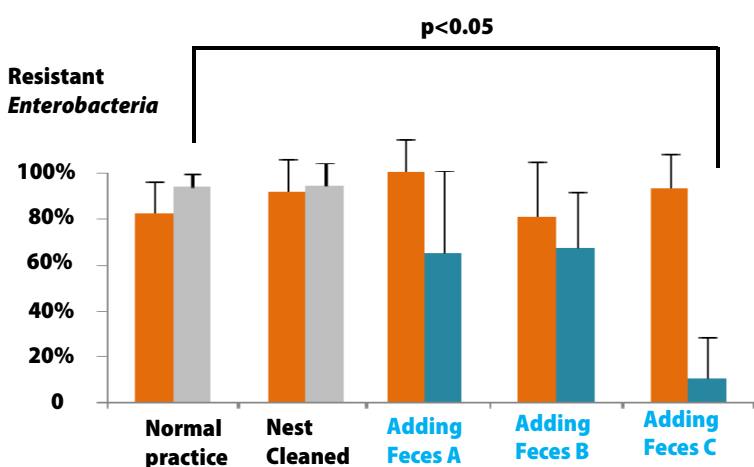
- The (ab) use of antibiotics in farming may favour antibiotic resistant microbes, which may poses a risk to public health.
- Since these microbes may persist even if antibiotics become infrequent, an active strategy is required to limit their diffusion across the farm.
- Competitive exclusion with foreign microbes added to the nest may limit the transmission of persistant resistant microbes to the kits.



Methods and Experimental design

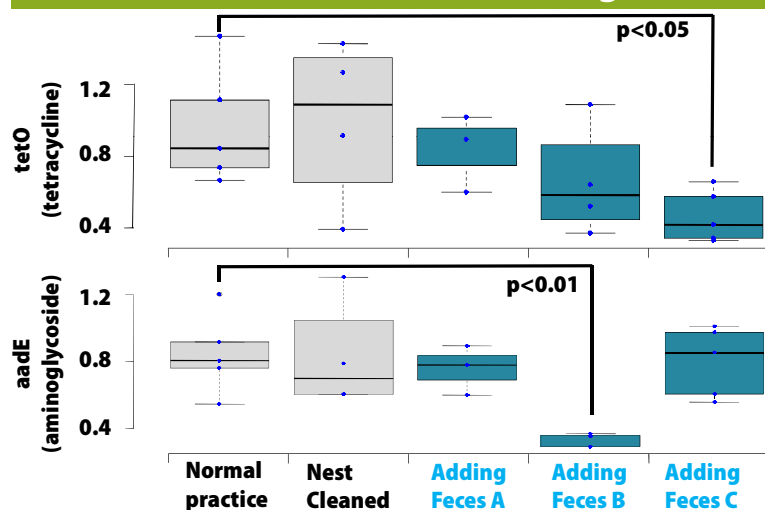


1) Cultivable *Enterobacteria*



Enterobacteria resistant to tetracycline (10 colonies per animal). The proportion of tetracycline resistant *Enterobacteria* in lactating does (orange bars) is stable and similar in each group. Adding chosen fecal pellets to the nest (blue bars) limits the transmission of resistant microbes.

2) Total antibiotic resistance genes



Relative abundance of the microbial antibiotic resistance genes *aphA3* (TOP) and *tetO* (BOTTOM) in the caecal content of the kits at weaning (normalized by the SSU). Adding Feces C decreased 6 out of the 20 antibiotic resistance genes that were quantified (vs 2 for Feces B). The does had similar levels of antibiotic resistance genes in each group (data not shown).

Conclusions

- Changing the metacommunity of the nest changes the microbes colonizing the gut of the kits.
- The exclusion mechanism is not neutral and depends on the microbiota: Feces C seemed more efficient than Feces B.
- Some antibiotic resistance genes remained unaffected : the fecal community used for the competitive exclusion could be improved.