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

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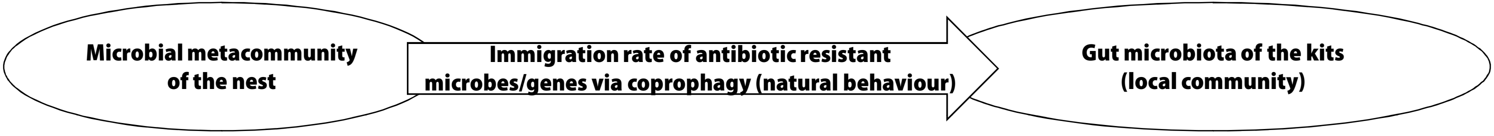
Role of the metacommunity in the colonization of rabbit's intestinal tract to fight against antibiotic-resistant bacteria

Achard C.[1], Gabinaud B.[1], Combes S.[1], Dupouy V.[2], Ramayo-Caldas Y[3], Denis C.[3], Ballester M.[3], Le Floc'h N.[4], Boucher S.[5], Chatellier S.[6], Le Normand B.[6], Bousquet-Melou A.[2], Estellé J.[3], Zemb O.[1]

[1]INRA UMR 1388 GENPHYSE, Toulouse
[2]INRA UMR 1331 TOXALIM, Toulouse
[3]INRA UMR 1313 GABI, Jouy-en-josas
[4]INRA UMR 1348 PEGASE, Rennes
[5]Labovet, Reseau Cristal, Beaupréau et les herbiers
[6]Clinique Veterinaire des Marches de Bretagne
[8]Plateforme Genotoul, Toulouse

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.

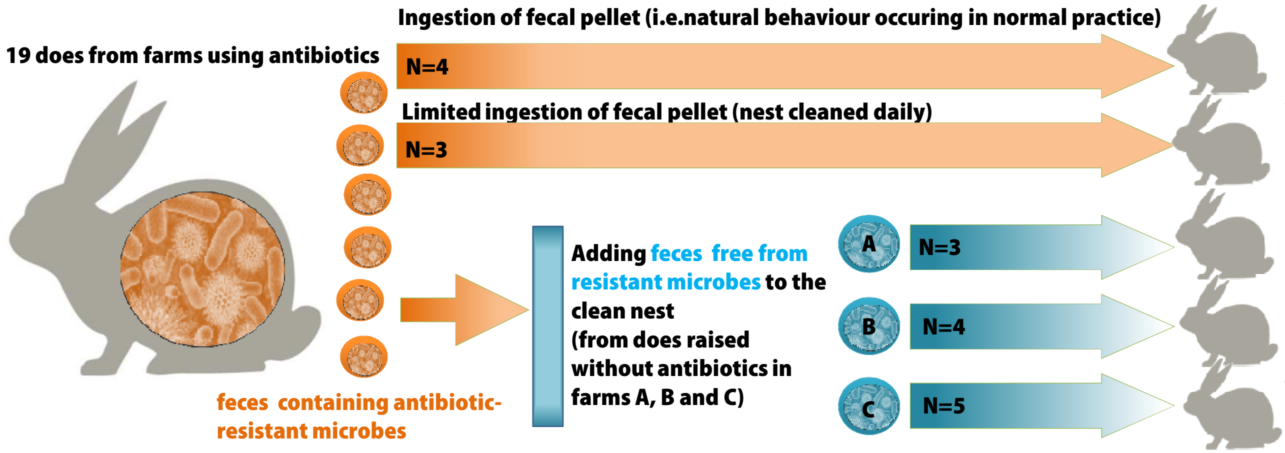


Microbial metacommunity of the nest

Immigration rate of antibiotic resistant microbes/genes via coprophagy (natural behaviour)

Gut microbiota of the kits (local community)

Methods and Experimental design



19 does from farms using antibiotics

feces containing antibiotic-resistant microbes

Ingestion of fecal pellet (i.e.natural behaviour occuring in normal practice)

N=4

Limited ingestion of fecal pellet (nest cleaned daily)

N=3

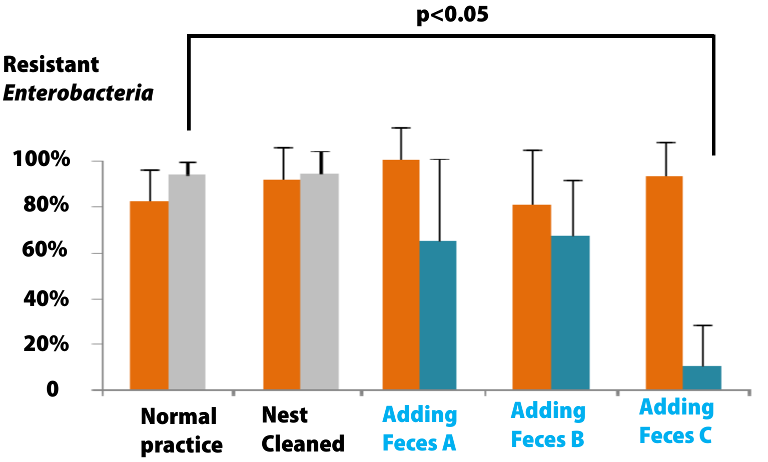
Adding feces free from resistant microbes to the clean nest (from does raised without antibiotics in farms A, B and C)

At weaning of the 114 kits (one kit per doe analyzed),

1) monitor antibiotic-resistant enterobacteria (counting on MacConkey petri dishes)

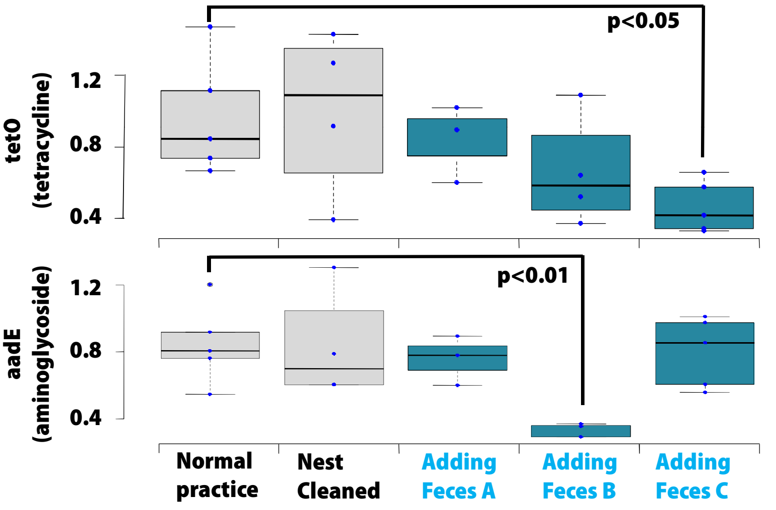
2) Quantify the antiresistance genes in total bacteria by qPCR

1) Cultivable *Enterobacteria*



Enterobacteria resistant to tetracylcine (10 colonies per animal).
The proportion of tetracycline resistant Enterobacteria in lacting 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 mecanism 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.

Centre Toulouse Midi Pyrénées
Chemin de Borde Rouge
CS 52627 • 31326 Castanet-Tolosan cedex
Tél : +33(0) 05 62 28 50 20