First rabbit gut microbial gene catalog and metagenomic insights into the resistome : links with antibiotic use

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FIRST RABBIT GUT MICROBIAL GENE CATALOG AND METAGENOMIC INSIGHTS INTO THE RESISTOME : LINKS WITH ANTIBIOTIC USE

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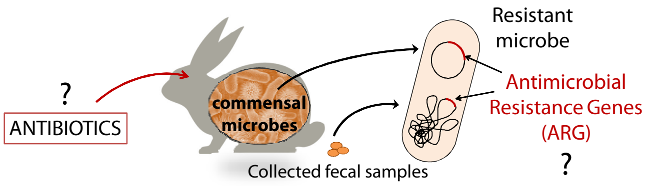
INTRODUCTION

Microbial antibiotic resistance genes emerging in livestock are a major public health concern. It is crucial to consider the prevalence of Antibiotic Resistance Genes (ARG) in commensal microbes which represent the vast majority of the gut microbiota of healthy individuals and can convey ARG between animal and human. ARG can be carried by mobile genetic element and transferred between bacterial species, ending up in human pathogens.

OBJECTIVES

- To generate a first rabbit gut microbial gene catalog.
- To characterize the gut resistome in French meat rabbit farming.



METHODS

Does fecal sampling (Mai-Oct 2014)
DNA extraction (Godon et al., 1997)

→ 30 samples from 30 farms →

HiSeq2500 Illumina sequencing

→ ~ 64M sequences / samples →

Sequences processed with MOCAT (Kultima et al, 2012)
- SOAPdenovo → Assembly
- MetaGeneMark → Geneprediction
- CD-HIT-EST → Redondancy reduction
- Read-mapping → BWA

→ 6,2 M gene catalog →

Annotation and abundance table
- ARG with ResFinder (Zankari et al., 2012)
- ARG prediction with a pairwise comparative modelling approach (PCM)

RESULTS

ANTIBIOTIC USES

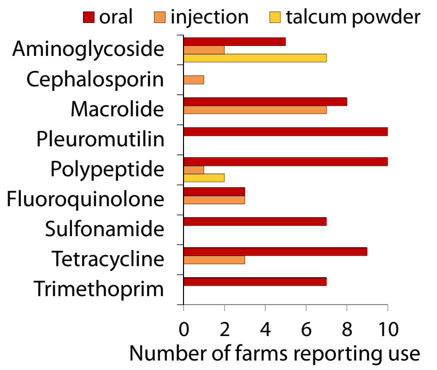


Figure 1 : Number of different antimicrobial molecules used in the rabbit farm panel per class and administration mode.

RESFINDER → 80 ARG DETECTED

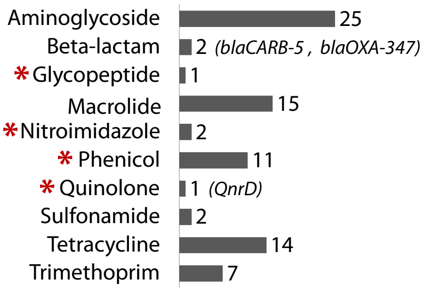


Figure 2 : Number of ARG identified in the gene catalog using ResFinder per antibiotic class. * antibiotics not used

A global link between antibiotic uses and the sum of the relative abundance of all ARG detected.

Table 1 : Antibiotic uses and ARG detected

Farm	# antibiotics used	# detected ResFinder ARG	Sum of ResFinder ARG abundance
02	0	17	5,49E+03
12	0	18	1,06E+04
05	0	23	1,09E+04
32	1	44	1,53E+04
26	0	43	2,22E+04
07	1	20	2,74E+04
33	0	18	3,78E+04
01	0	23	4,58E+04
16	4	18	5,19E+04
18	0	49	5,24E+04
15	4	16	5,71E+04
13	1	22	5,94E+04
27	3	20	6,35E+04
17	3	24	6,51E+04
04	2	21	6,55E+04
24	2	18	6,73E+04
23	4	19	6,85E+04
14	1	61	6,95E+04
30	8	28	7,17E+04
11	4	21	7,53E+04
22	5	62	7,71E+04
03	6	20	7,71E+04
19	4	23	7,78E+04
25	5	24	8,11E+04
31	8	34	8,38E+04
10	5	49	8,74E+04
28[a]	0	68	9,04E+04
08[b]	1	50	9,13E+04
21	6	68	1,07E+05
20	7	77	1,94E+05

🟥 Oral exposure to antibiotics

🟧 Non oral exposure to antibiotics

[a] oral exposure to antibiotics until end-2013

[b] oral exposure to antibiotics until end-2012

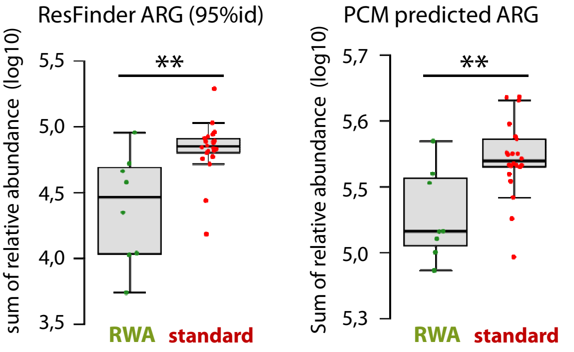
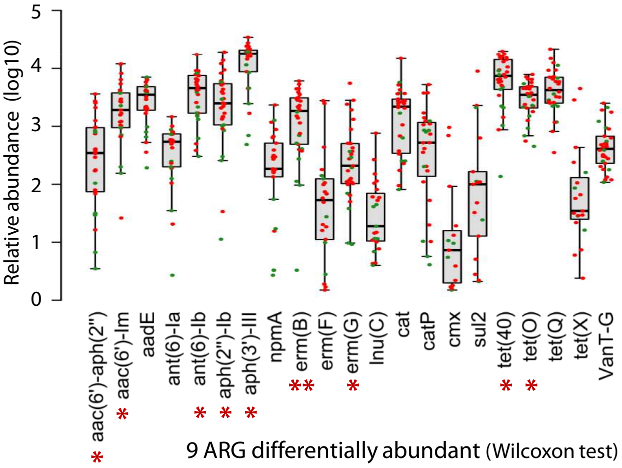


Figure 3 : Sum of relative abundances of all ARG in Raised Without Antibiotic (RWA) farms and in standard farm using antibiotics.

Figure 4 : ResFinder ARG relative abundance ➡
- RWA farms
- standard farms



9 ARG differentially abundant (Wilcoxon test)

CONCLUSION

- First rabbit gut microbial gene catalog : 80 antibiotic resistance genes (ARG Resfinder) and 8235 ARG candidates (pairwise comparative modelling approach).
- Decreasing the antibiotic use decreases the global abundance of antibiotic resistance genes.
- Some antibiotic resistance genes persist in antibiotic farms reducing their antibiotic use : an active strategy is needed (see poster 328B)

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