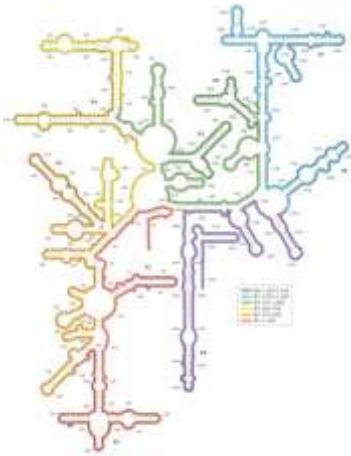


Metagenomics and antibiotic resistance



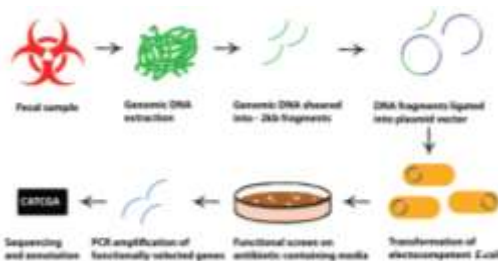
Etienne Ruppé
Genomic Research Laboratory
Hôpitaux Universitaires de Genève



16S rDNA sequencing: diversity, OTUs identification, but not for addressing antibiotic resistance



Shotgun metagenomics: reconstruction of genes through the assembly process, identification of ARDs by sequence homology with known ARDs



Functional metagenomics: identification of ARDs with no assumption on their sequence

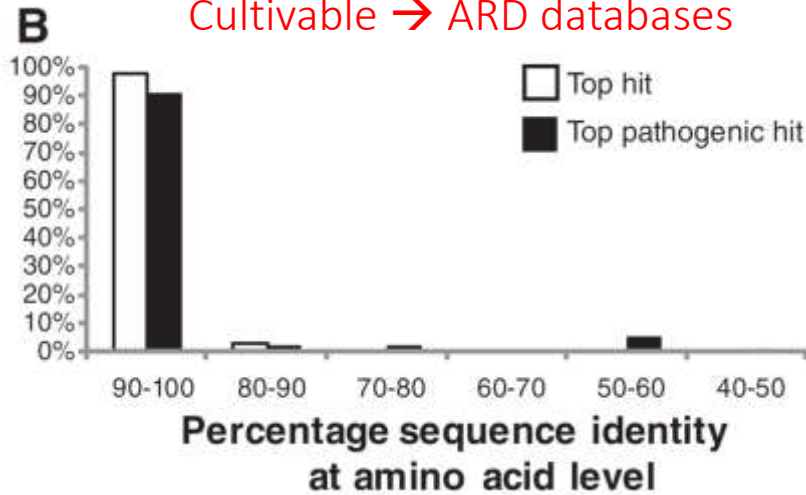
Identifying ARDs in complex environments by shotgun metagenomics is complex

Example of the intestinal microbiota: only ARDs close to known ARDs are found, not those from anaerobic bacteria.

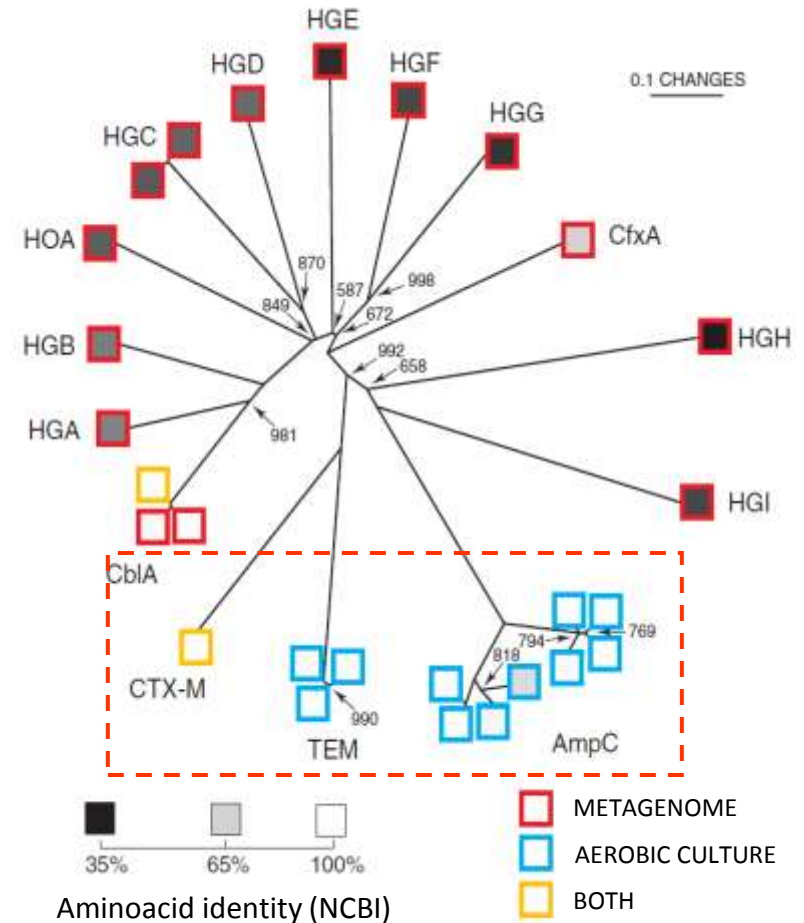
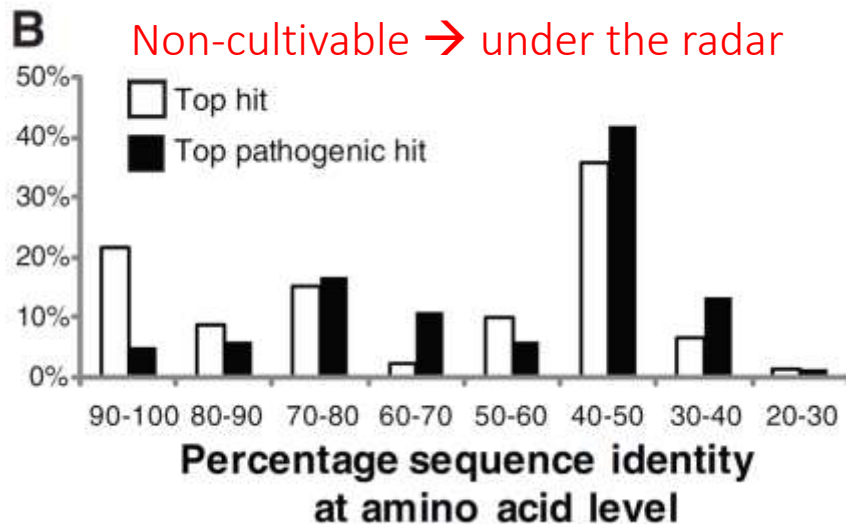
	Forslund, K. et al	Ghosh, TS. Et al	Hu, Y. et al.
Journal	Genome Research	Plos One	Nature Communications
Published in	2013	2013	2013
N individuals	252	257	162
Origin of individuals	American, Danish, Spanish	American, Danish, French, Italian, Japanese, Spanish, Indian, Chinese	Danish, Spanish, Chinese
ARD reference database	ARDB (enriched in-house)	ARDB	ARDB
Search algorithm	Blastn	Blastx	Blastp
N unique ARDs (>95%)	100	157	156
Beta-lactamases	TEM, SHV, AmpC_E. coli, CCRA, CBLA, CFXA, CEPA	TEM, LEN, SHV, OXY, CTX-M, CFXA, CBLA, CEPA, AmpC_E. coli, CMY-2	KPC, ROB, TEM, CTX-M, OXY, PER, SHV, CARB, PSE, LCR, OXA-1, OXA, SME, L1, IMP

Functional metagenomics enables the discovery of new ARDs

Cultivable → ARD databases



Non-cultivable → under the radar



Genomics refer to the analysis of organisms at the genome level.

NGS+bio-informatics now enable a « simple » analysis of genomes (including the plasmids and other mobile genetic elements): « whole genome sequencing »

