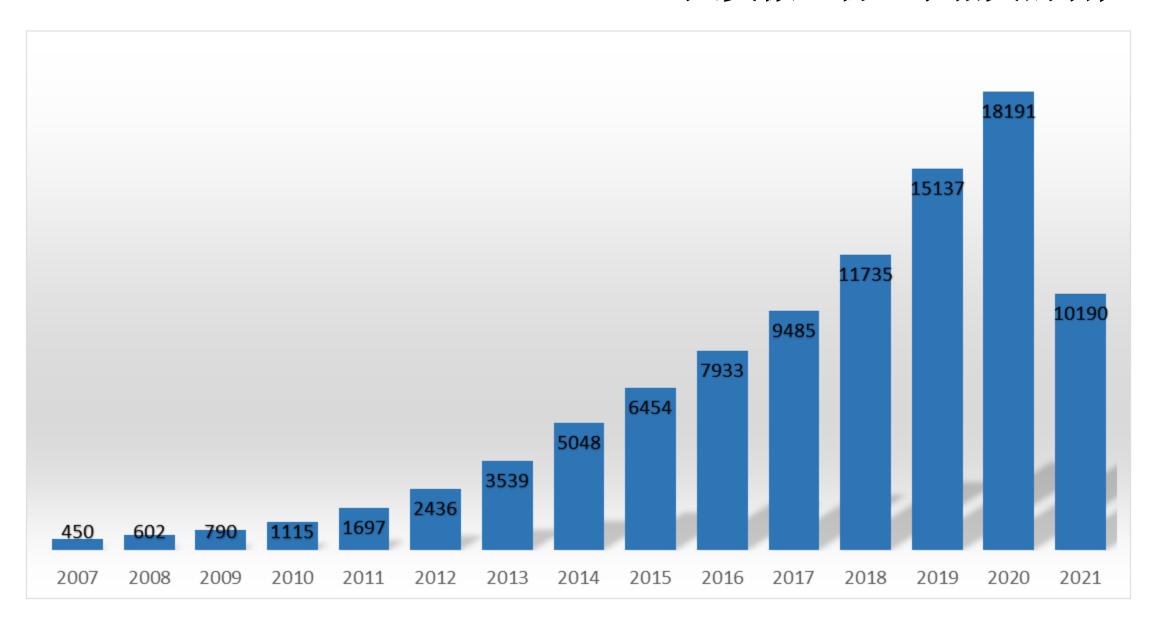
Detecting animal disease and foodborne pathogens in pork supply chain: application of microbiome research

微生物组学在猪肉供应链病原微生物检测中的应用

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Human microbiome studies 人类微生物组学相关的研究



COMMENTARY Open Access

Microbiome definition re-visited: old concepts and new challenges



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Abstract

The field of microbiome research has evolved rapidly over the past few decades and has become a topic of great scientific and public interest. As a result of this rapid growth in interest covering different fields, we are lacking a clear commonly agreed definition of the term "microbiome." Moreover, a consensus on best practices in microbiome research is missing. Recently, a panel of international experts discussed the current gaps in the frame of the European-funded MicrobiomeSupport project. The meeting brought together about 40 leaders from diverse microbiome areas, while more than a hundred experts from all over the world took part in an online survey accompanying the workshop. This article

Table 1 Microbiome definitions

Ecological definitions

Definitions based on ecology describe the microbiome following the concepts derived from the ecology of multicellular organisms. The main issue here is that the theories from the macro-ecology do not always fit the rules in the microbial world.

"A convenient ecological framework in which to examine biocontrol systems is that of the microbiome. This may be defined as a characteristic microbial community occupying a reasonably well-defined habitat which has distinct physio-chemical properties. The term thus not only refers to the microorganisms involved but also encompasses their theatre of activity "[40].

"...This term refers to the entire habitat, including the microorganisms (bacteria, archaea, lower and higher eurkaryotes, and viruses), their genomes (i.e., genes), and the surrounding environmental conditions. This definition is based on that of "biome," the biotic and abiotic factors of given environments. Others in the field limit the definition of microbiome to the collection of genes and genomes of members of a microbiota. It is argued that this is the definition of metagenome, which combined with the environment constitutes the microbiome. The microbiome is characterized by the

Organisms/host-dependent definitions

The host-dependent definitions are based on the microbial interactions with the host. The main gaps here concern the question whether the microbial-host interaction data gained from one host can be transferred to another. The understanding of coevolution and selection in the host-dependent definitions is also underrepresented. "A community of microorganisms (such as bacteria, fungi, and viruses) that inhabit a particular environment and especially the collection of microorganisms living in or on the human body" [43]. "Human Microbiome Project (HMP): [...] The Human Microbiome is the collection of all the microorganisms living in association with the human body. These communities consist of a variety of microorganisms including eukaryotes, archaea, bacteria and viruses" [44].

Genomic/ method-driven definitions

There is a variety of microbiome definitions available that are driven by the methods applied. Mostly, these definitions rely on DNA sequence-based analysis and describe microbiome as a collective genome of microorganisms in a specific environment. The main bottleneck here is that every new available technology will result in a need for a new definition.

"The collective genomes of microorganisms inhabiting a particular environment and especially the human body" [43].

Table 1 Microbiome definitions (Continued)

"Totality of genomes of a microbiota. Often used to describe the entity of microbial traits (=functions) encoded by a microbiota." [48]

Combined definitions

There are some microbiome definitions available that fit several categories with their advantages and disadvantages.

"A microbiome is the ecological community of commensal, symbiotic, and pathogenic microorganisms that literally share our body space" [49].

"The microbiome is the sum of the microbes and their genomic elements in a particular environment" [50].

"The genes and genomes of the microbiota, as well as the products of the microbiota and the host environment" [51]. The microbiome is defined as a characteristic microbial community occupying a reasonable well-defined habitat which has distinct physio-chemical properties. The microbiome not only refers to the microorganisms involved but also encompass their theatre of activity, which results in the formation of specific ecological niches. The microbiome, which forms a dynamic and

The microbiota consists of the assembly of microorganisms belonging to different kingdoms (Prokaryotes [Bacteria, Archaea], Eukaryotes [e.g., Protozoa, Fungi, and Algae]), while "their theatre of activity" includes microbial structures, metabolites, mobile genetic elements (e.g., transposons, phages, and viruses), and relic DNA embedded in the environmental conditions of the habitat.

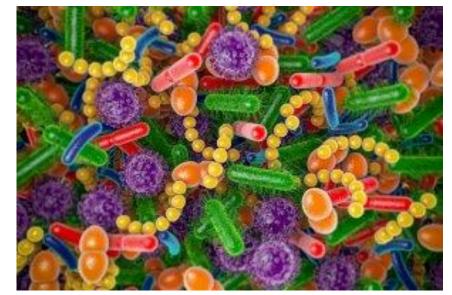
Term Definition

Microbiome Microbiota Metagenomics The gene complement of a microbial community
The microorganisms that inhabit a defined niche
A culture-independent, DNA-sequence-based approach to analysing the
total genetic content of a given niche

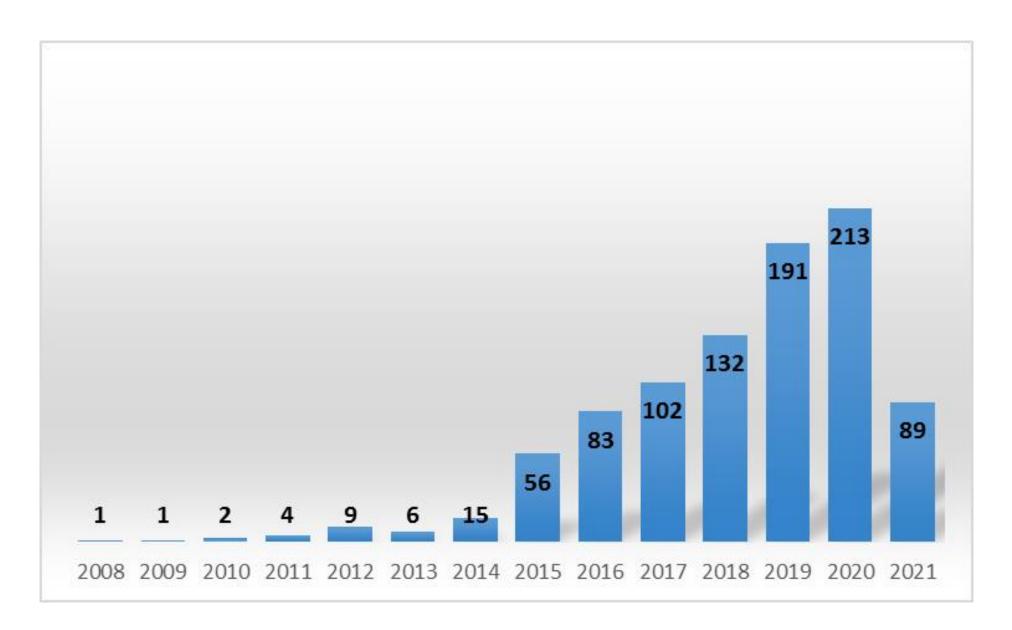
Microbiome, Microbiota, Bacterial communities

Gut microbiome, oral microbiome, skin microbiome

微生物组,菌群,微生物群落,宏基因组



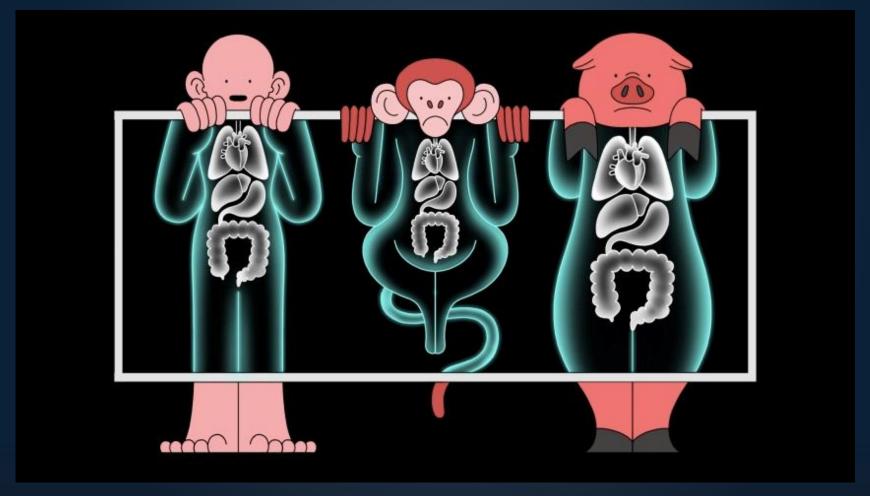
Swine gut microbiome studies 猪肠道微生物组学相关的研究



Why do we care about swine gut microbiome? 为什么研究猪肠道微生物组

Pigs have similar organs as humans (猪跟人器官的相似性)

Size, anatomy and physiology



ttps://www.tochnologyroviou.com/2010/06/12/22001//crispr.pig.organs.arg.hoing.implanted.ip.monkovs.to.cog.if.thourg.safe.for.humans/

Pigs as animal models for human diseases

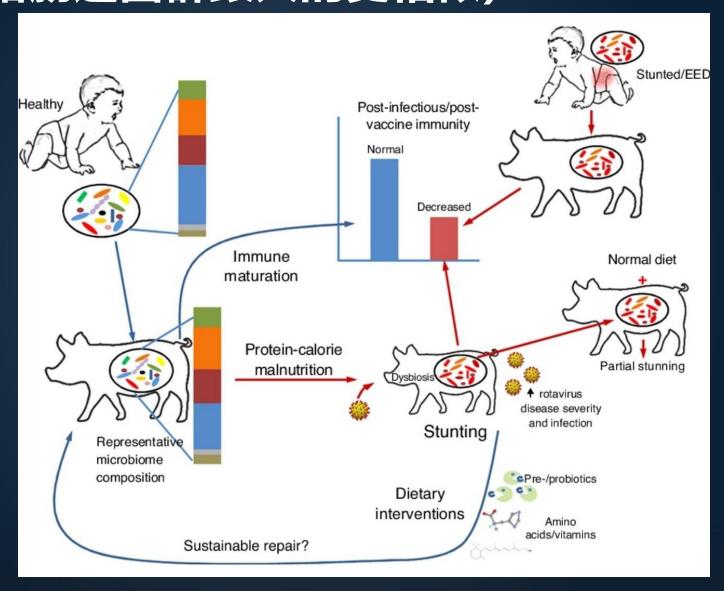
(猪作为人类疾病的动物模型)







Swine gut microbiome is more similar human gut microbiota (猪肠道菌群跟人的更相似)

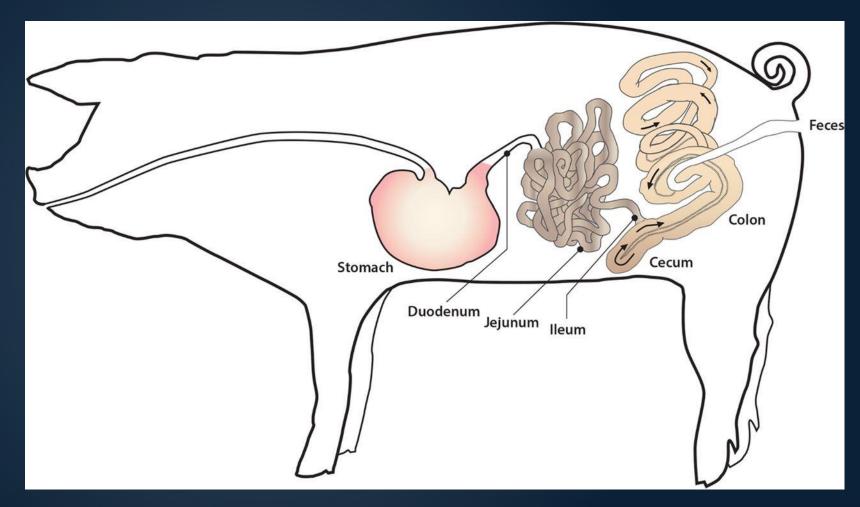


Roles of the swine gut microbiome (猪肠道菌群在营养和健康中的作用)

Animal Health

- Educate the immune system
- Competitive exclusion of pathogens

- Animal Nutrition
- · Digestibility
- Additional energy from nondigestible feed

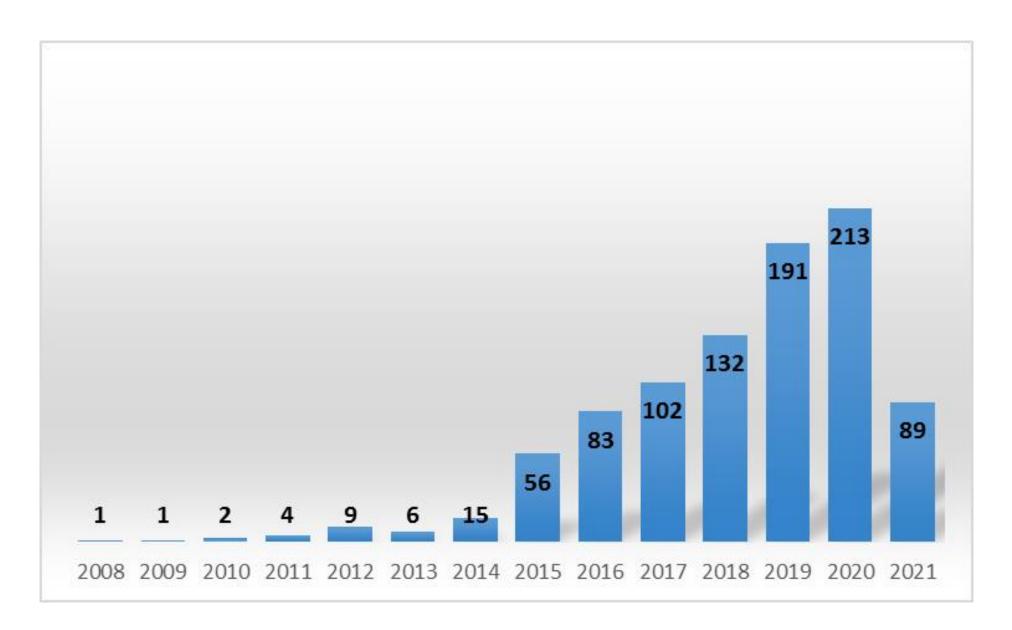


Devin B. Holman et al. mSystems 2017; doi:10.1128/mSystems.00004-17

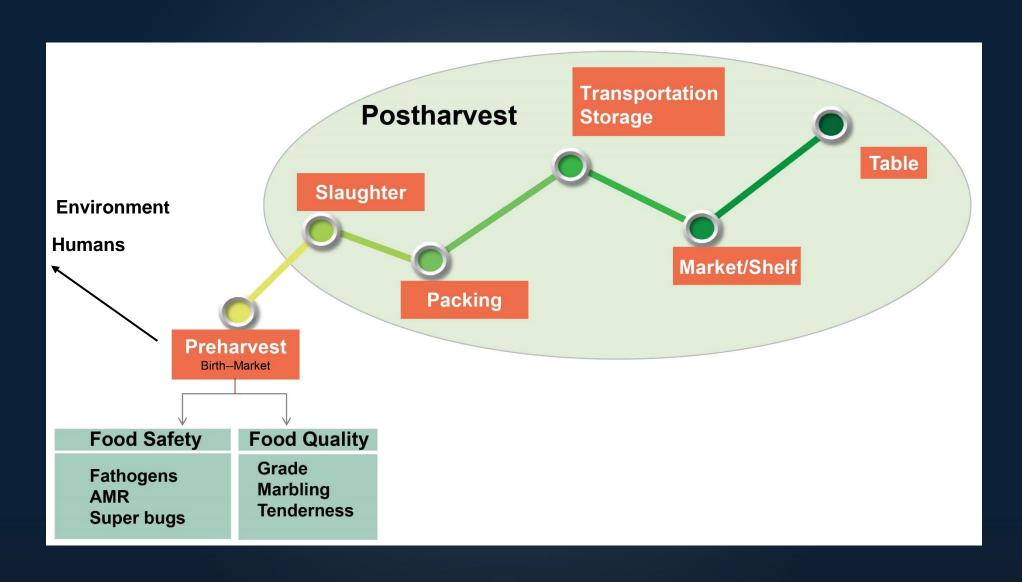




Swine gut microbiome studies 猪肠道微生物组学相关的研究

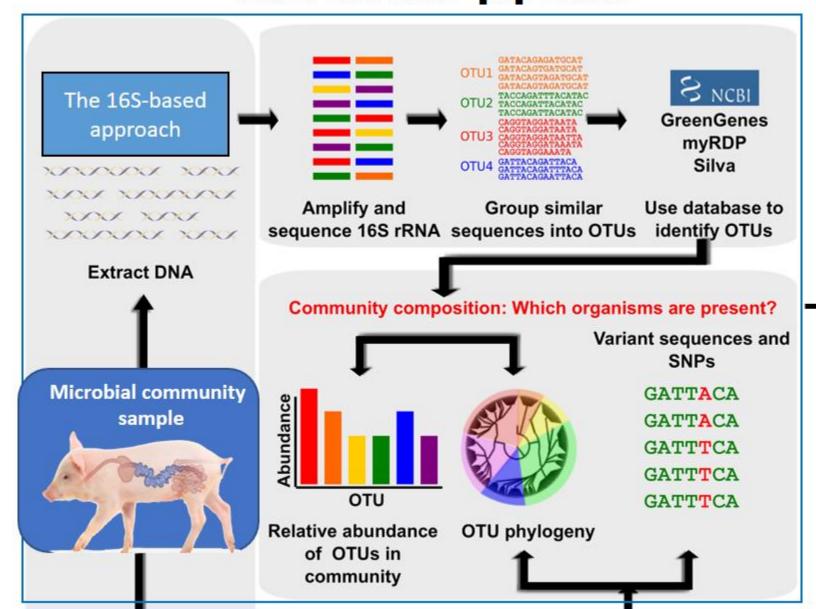


Application of microbiome in food safety (微生物组在食品安全中的应用)



微生物组研究流程

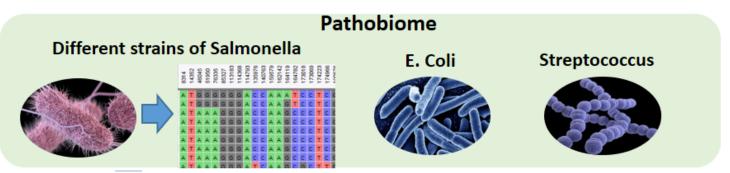
Microbiome pipeline



微生物组在猪肉供应链中的应用

Microbiome pipeline S NCBI GreenGenes myRDP Amplify and Group similar sequence 16S rRNA sequences into OTUs identify OTUs **Extract DNA** Variant sequences and Microbial community GATTACA GATTACA GATTTCA GATTTCA GATTTCA Relative abundance OTU phylogeny community

Microbiome application in pork supply chain









Gut Microbes



ISSN: (Print) (Online) Journal homepage: https://www.tandfonline.com/loi/kgmi20

Life-long dynamics of the swine gut microbiome and their implications in probiotics development and food safety

Ying Li , Xiaofan Wang , Xiu-qi Wang , Junjun Wang & Jiangchao Zhao

To cite this article: Ying Li, Xiaofan Wang, Xiu-qi Wang, Junjun Wang & Jiangchao Zhao (2020) Life-long dynamics of the swine gut microbiome and their implications in probiotics development

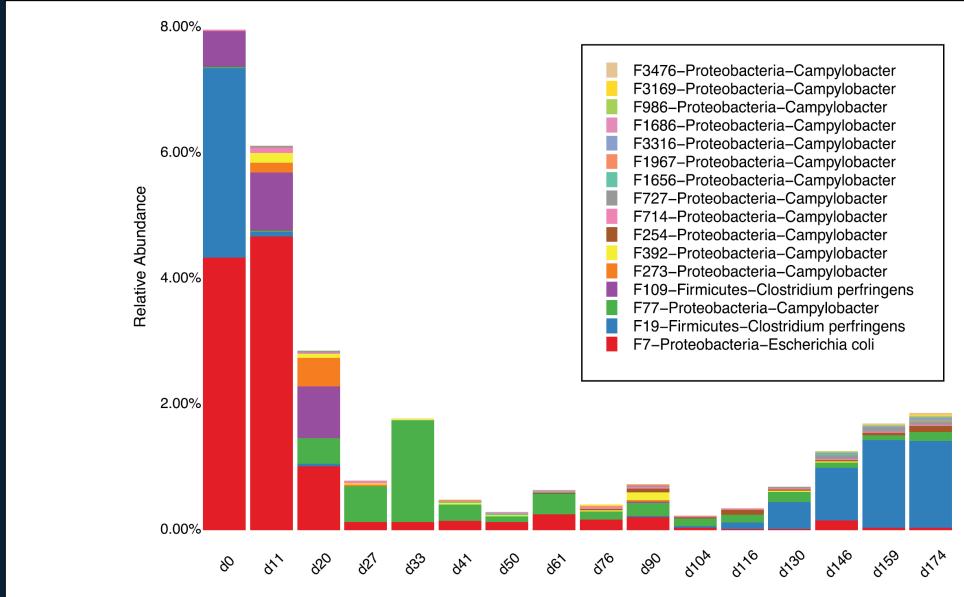
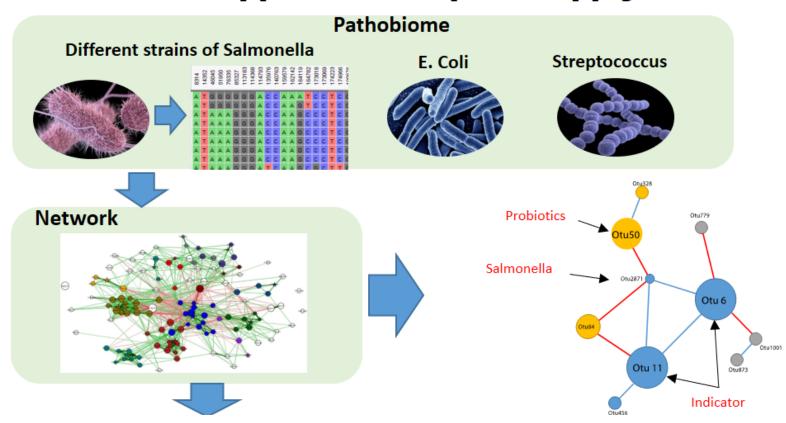


Figure 4. The dynamics of foodborne pathogens (members of *Campylobacter* and *E. coli*) in pigs during the pre-harvest section of the pork supply chain.

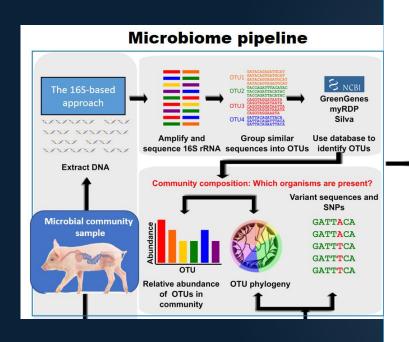
微生物组在猪肉供应链中的应用

Microbiome pipeline S NCBI The 16S-based GreenGenes myRDP Silva Amplify and Group similar Use database to sequence 16S rRNA sequences into OTUs identify OTUs **Extract DNA** Community composition: Which organisms are present? Variant sequences and SNPs Microbial community GATTACA GATTACA GATTTCA GATTTCA GATTTCA community

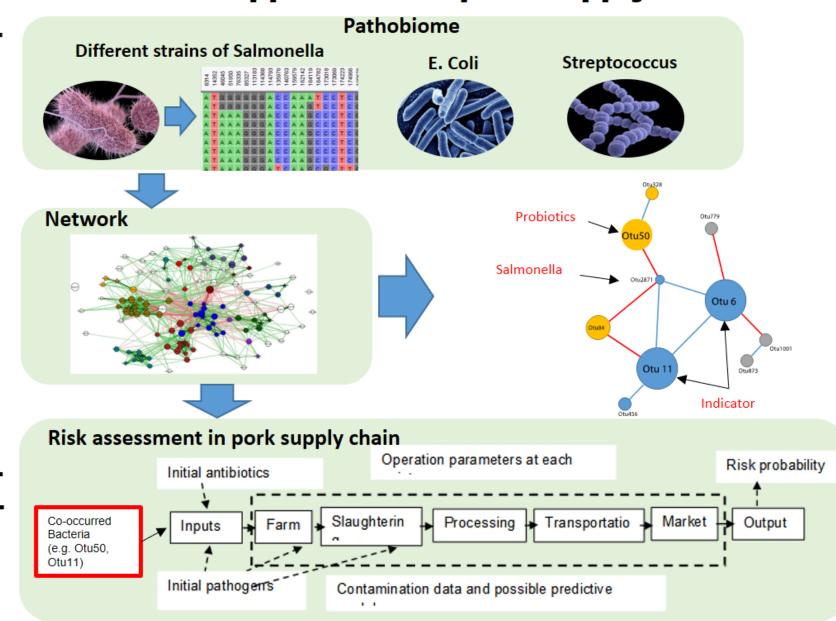
Microbiome application in pork supply chain



微生物组在猪肉供应链中的应用

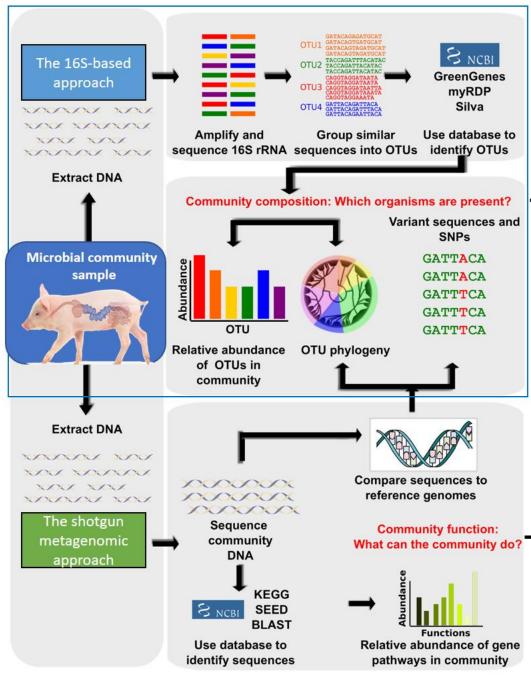


Microbiome application in pork supply chain



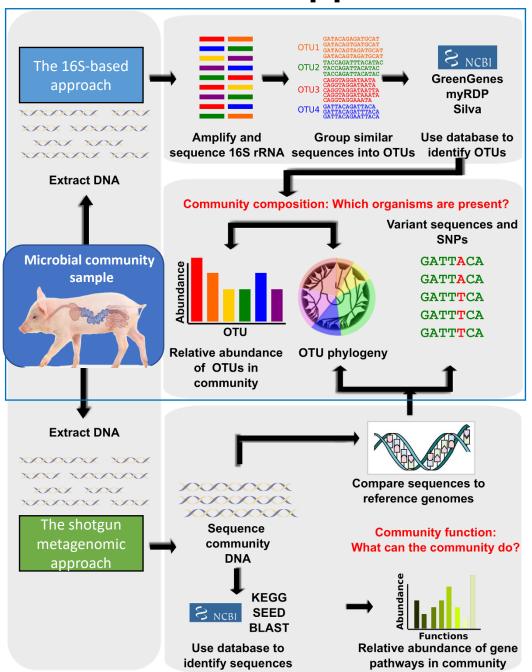
Microbiome pipeline

微生物组

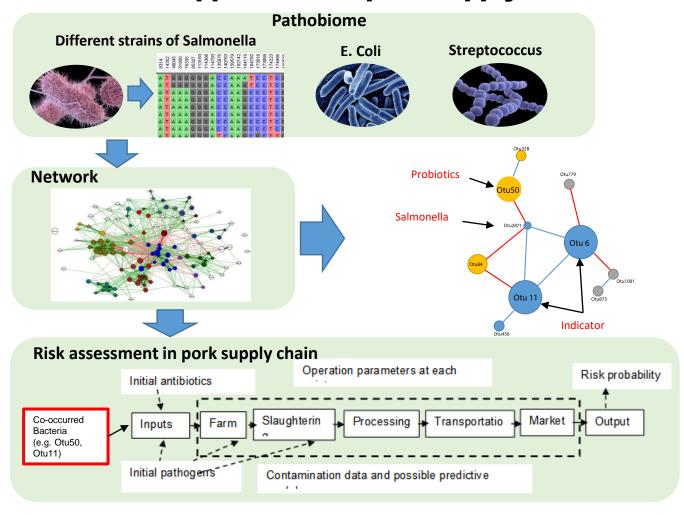


宏基因组

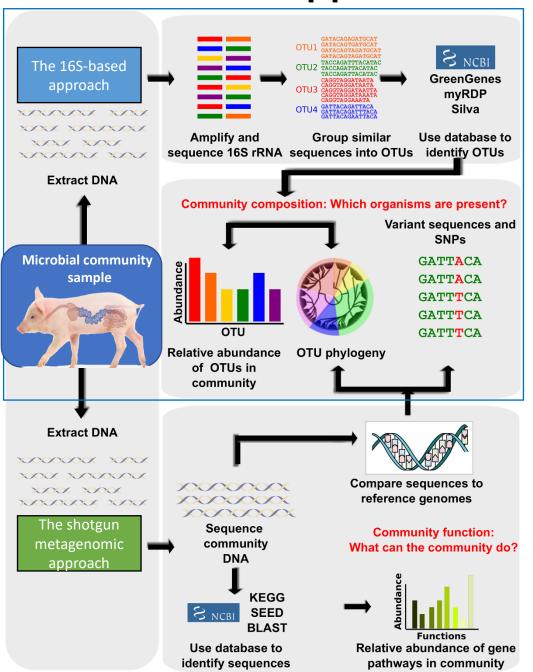
Microbiome pipeline



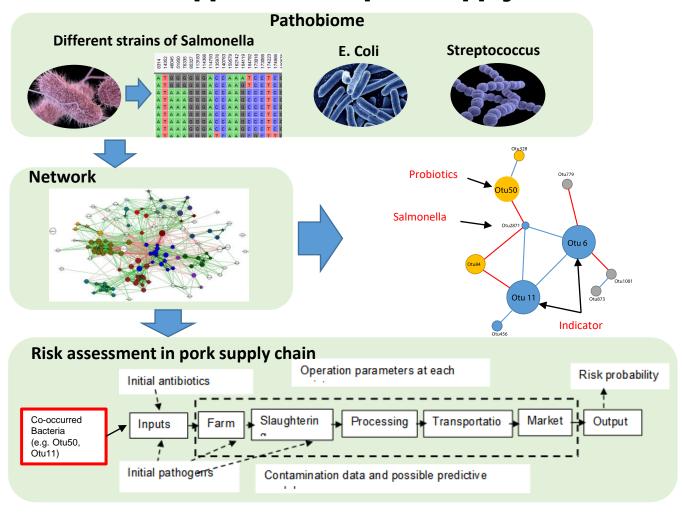
Microbiome application in pork supply chain

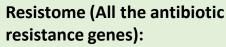


Microbiome pipeline

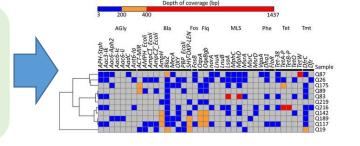


Microbiome application in pork supply chain

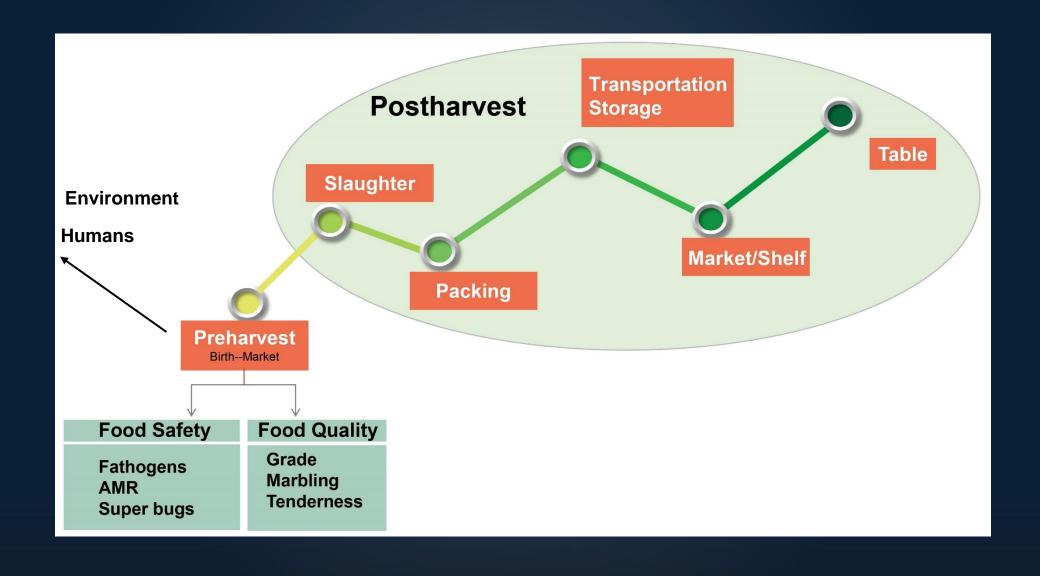




AGly (aminoglycosides),
Bla (\(\theta\)-lactam),
Fos (Fosfomycin),
Flq (fluoroquinolones),
MLS (macrolide-lincosamide- streptogramin)



Application of microbiome in food safety

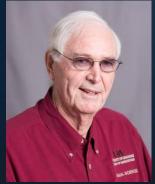


Acknowledgement

Zhao lab members:

Xiaofan Wang, ANSC Postdoc Jianmin Chai, ANSC Postdoc Bin Zuo, ANSC PhD Chris Hansen, CEMB PhD Samantha Howe, ANSC PhD Hunter Usdrowski, ANSC master Taylor McKinney, ANSC master Robert Story, Program Associate





· 小组1- 动物疾病和食源致病菌:检测,分析,微生物和模型

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USDA NIFA (award number: 2018-67015-27479)
Division of Agriculture Animal Health Grant
Department of Animal Science
Kent Nutrition Group
Walmart Foundation



