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Diversity and transfer efficiency of IncHI2 plasmids from Escherichia coli

Resume:

Antibiotic resistance is a major challenge for human and animal health. The spread of resistance genes is mediated in part by plasmids, which are DNA molecules distinct from the bacterial chromosome that can carry resistance genes and be transferred between bacteria. IncHI2 plasmids are of particular interest because of their large size, diverse genetic content, and presence in several bacterial species. They can therefore contribute to the dissemination of multiple antibiotic resistance genes in animals and their environment.

By combining bioinformatic analyses and transfer experiments, my project will provide a better understanding of the diversity of IncHI2 plasmids found in pathogenic Escherichia coli of porcine origin and the factors influencing their transfer.

For my first objective, pathogenic E. coli strains (ETEC and ETEC-STEC) carrying IncHI2 plasmids were identified, and the presence of these plasmids was confirmed through Nanopore sequencing. Bioinformatic analyses were used to characterize their genetic content, including their antibiotic resistance genes. Gene comparisons will help explore their diversity and identify shared or variable features. Conjugation experiments will then be conducted to assess plasmid transfer efficiency. Transfers will be performed both between E. coli strains (intraspecies transfer) and between E. coli and other bacterial species (interspecies transfer). These experiments will allow me to compare transmission to different bacterial hosts.

For my second objective, three suspected genes essential for interspecies transfer will be mutated to assess their contribution to this process. The transfer efficiency of the mutants will be compared with an IncHI2 plasmid without mutations. This approach will help determine whether the genes studied promote transfer different species bacteria.

The results will deepen our understanding of IncHI2 plasmids. Also, the knowledge gained will help clarify their role in the spread of antibiotic resistance in livestock, particularly in pork, and may guide future research aimed at limiting their dissemination.