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Domaine de recherche (1 mot, Calibri 11pt) :
Research domain (1 word, Calibri 11pt):
Microbiology

Titre (court, Calibri 11pt) | **Title (short, Calibri 11pt):**

In Silico Analyzing of Conjugative Plasmids in Salmonella relevant to Poultry

Courte description (60 mots, Calibri 11pt) : (indiquer la langue, nous vous recommandons de soumettre dans les deux langues, donc deux vidéos MP4 et deux fichier PDF) | **Short description** (60 words, Calibri 11pt): (indicate language, we recommend submitting in both languages, so two MP4 videos and two PDF files)

This resarch is aim at building up an in-silico workflow to study conjugative plasmids fron poultry Salmonella.

Auteurs : étudiant qui présente [numéro], coauteurs [numéro] | **Authors:** student presenting [number], co-authors [number]

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Résumé (2500 caractères espaces inclus, Calibri 11pt) | **Summary (3000 characters including spaces, Calibri 11pt):**

Objectives: To study conjugative plasmids from poultry-origin Salmonella by in-silico methods for predicting spread of antimicrobial resistance and virulence in Salmonella in poultry.

Methods: We applied PlasmidFinder 2.1 and VRprofile 2 to detect plasmids from Salmonella sequences downloaded from NCBI refseq database, and then applied oriTfinder to determine conjugative plasmids. The antimicrobial resistance genes (ARGs) and virulence factors in plasmids were identified by both VRprofile 2 and oriTfinder, and the phenotype of ARGs was predicted by ResFinder4.1 and phenotype of virulence was predicted by oriTfinder.

Results: We identified 183 plasmid sequence fragments from 309 downloaded sequences, in which 77 (42.08%) plasmid fragments were conjugative, 25 (13.67%) plasmid fragments were mobilizable, and 81 (44.26%) plasmid fragments were non-mobilizable. Among 183 plasmid fragments, 105 fragments were found to carry 58 putative acquired ARGs, in which was classified as 22 gene groups. The most prevalent ARG groups in plasmids are aph group, bla group, sul group and tet group, while the armA, lnu(F), rmt group were the least popular detected ARGs in plasmids; 49 plasmid fragments were detected with virulence factors and 36 different virulent genes were detected in plasmids, in which was classified as 12 gene groups. The most prevalent virulent protein encoded genes in plasmids are ybt group, fae group, and pef group (Fig 3a), while the most unpopular virulent genes were iutA, htpB, and fyuA.

Conclusions: The in-silico workflow we built by the combined use of programs could be reliable to detect conjugative plasmids from sequences, and the genotype and phenotype of antimicrobial resistance and virulence could be predicted by this in-silico workflow.