Abstract IDDF2021-ABS-0113 Figure 6

Conclusions Our data indicate that *H. pylori* infection increases ACVR1 expression, promoting gastric IM via regulating CDX2, which is an essential step in *H. pylori* carcinogenesis.

IDDF2021-ABS-0123 STREPTOMYCES PLURIPOTENS MUSC 135T AS A TREASURE TROVE FOR ANTI-COLON CANCER AND ANTI-MRSA AGENTS

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Background The genus *Streptomyces* is well-known for the production of numerous bioactive compounds with interesting chemical scaffolds. *Streptomyces pluripotens* MUSC 135^T was isolated from a mangrove forest in Malaysia during a screening program for bioactive actinobacteria. The crude

fermentative extract of MUSC 135^T was shown to inhibit the growth of several pathogens, including methicillin-resistant *Staphylococcus aureus* (MRSA). Thus, this study aimed to explore the potentials of *Streptomyces pluripotens* in producing valuable bioactive compounds via fermentation experiments and genome mining to identify the presence of biosynthetic gene clusters (BGCs) for secondary metabolites.

Methods The genome mining analysis was performed by applying the anti-SMASH pipeline to annotate and analyze potential biosynthetic gene clusters of secondary metabolites in *S. pluripotens*. Gas chromatography-mass spectrometry (GC-MS) analysis was performed to detect the presence of bioactive compounds in the methanol extract of the fermentation product of *S. pluripotens*. Anti-colon cancer and anti-MRSA activities of identified bioactive compounds were evaluated.

Results GC-MS analysis detected several bioactive compounds that possess anti-colon cancer cells properties in the methanol extract of the fermentation product of *Streptomyces pluripotens*. For instance, compound (1) exhibits cytotoxic activity towards colorectal cancer HCT116 cell line (IDDF2021-ABS-0123 Figure 1. *Streptomyces pluripotens* MUSC 135^T, a treasure trove for anti-colon cancer and anti-MRSA agents). The result of BCGs prediction revealed 28 putative biosynthetic gene clusters, 8 of them showed high similarity to known gene clusters (>80%). These predicted gene clusters were reported to encode compounds with promising anti-colon

Abstract IDDF2021-ABS-0123 Figure 1

cancer properties, including ectoine, desferrioxamine B/E, and antimycin. Subsequently, one of the predicted genes from the LAPs gene cluster was selected and de novo synthesized for expression study using *Escherichia coli* model. In the anti-MRSA test, the purified protein Protein135 showed a minimum inhibitory concentration (MIC) of $3\mu\text{M}$ against MRSA ATCC 33591 at 24-hour incubation. Intriguingly, Protein135 demonstrated higher growth inhibition than vancomycin, both at sub-MIC of $0.25\mu\text{M}$, against MRSA ATCC 33591.

Conclusions Altogether, these findings highlight the importance of novel strain from the mangrove forest, particularly in searching for beneficial bioactive compounds. In addition, our preliminary study unveils the promising wound healing property of Protein135 in the MRSA infection murine model.

IDDF2021-ABS-0126

EXPLORING THE GUT MICROBIOTA VARIATION IN RESPONSE TO VIBRIO INFECTION

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Background Our gut microbiota is composed of trillions of bacteria residing in the human gastrointestinal system. Any

Abstract IDDF2021-ABS-0126 Figure 1