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IN SILICO PREDICTION OF ANTICANCER POTENTIAL OF CAMEL GUT MICROBIAL METABOLIC PEPTIDES

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ABSTRACT

Anti-cancer potential of metabolic peptides derived from Camel gut microbial samples was evaluated using computational methods. Genomic data on the microorganisms (Accession number SRR 13205865) was relieved from database of Notational Centre for Biotechnology Information (NCBI). The PATRIC database was used for genome assembly. Metabolic peptides were identified using the Anti SMASH server. The Anti cancer prediction server 2.0 was set at SVM threshold of 0.45 for prediction of Anti-cancer activity of the metabolic peptides. Arylpolyene, Phosphonate and NRPS were identified as metabolic peptides derived from the Camel gut microbial samples. The results indicated that three metabolic peptides (Arylpolyene, Phosphonate and NRPS) identified from Camel gut microbes were predicted to exhibit anti cancer potential using anti CP 2.0 with a score of 0.58 surpassing the 0.45 SVM threshold. Further studies on the therapeutic potential and safety of Camel derived metabolic peptides is recommended.

Keywords: Predicting, Metabolic peptides, Anti-cancer, In silico

INTRODUCTION

Cancer has been identified as one of the leading causes of mortality globally**.** There is therefore, the need to work on novel approaches for the prevention and treatment of cancer. A number of new techniques have been developed for the treatment of cancer, however resistance of cancer cells to drugs posed significant challenge to cancer chemotherapy (Xi *et al*., 2021). Microbial metabolites are reported to influence tumor micro environment resulting in improved tumor treatment outcome. Body immune response and cancer cell behavior are also affected by microbial metabolites (Yuhang *et al*., 2024). The role of microorganisms in regulating response to chemo and immunotherapy have been documented. The initiation and outcome of cancers are influenced by the action of bacterial metabolites in the tumor micro environment. The influence of specific tumor bacterial metabolites on the treatments and outcome of cancer have been documented (Kayla *et al*., 2022). Natural metabolic peptides have been used for the treatment of cancers, these compounds demonstrated more structural diversity compared to synthetic drugs (Patridge *et al*., 2016). Bioactive metabolites derived from bacteria and fungi have demonstrated great potential in the treatment of infections and cancers. These microbes are associated with the synthesis of novel metabolites (Kamur and Kumaresan, 2023). Microbial metabolites from divers sources have demonstrated potent anti-cancer activity (Saturpur *et al*., 2019). Although the anti-inflammatory and antibiotic potential of Camel derived metabolic peptides have been documented (An sari et al., 2024, Mahmood and Essa, 2020), the anticancer potential of metabolic peptides derived from Camel gut microbes have not been explored. The objective of this study is to evaluate the potential of metabolic peptides derived from Camel gut microbes in the treatment of cancer.

MATERIALS AND METHODS

Genomic data on microorganisms isolated from digestive tract of bactrian camel (Camelus bactrianus) was retrieved from data bank of National Centre for Biotechnology Information (NCBI). Genome assembly was done using the database of Bacterial Viral Bioinformatic resource centre (BV-BRC). The SRR run accession and auto assembly method was used for the analysis. The database combines patho system research integration centre , influenza research database and the virus pathogen database (Olson *et al*., 2023). The Anti SMASH bacterial version 4 database was used for the identification of metabolic peptides produced by the gut microbes as described by Blin *et al*., 2023. Contiq.fasta file obtained from BV-BRC was uploaded on antiSMASH for the analysis. The anti-cancer potential of the metabolite was predicted using anti cancer prediction server version 2.0, Fasta format of the peptide sequence was set at support vector machine (SVM) threshold of 0.45 for the analysis. Predicted scores above 0.45 indicate positive anticancer activity. AntiCP 2.0 is a web based server for the prediction of anti cancer peptide as described by Agrawal *et al*., 2021.

RESULTS AND DISCUSSION

The metabolic peptides identified using Anti SMASH server are Arylpolyene, phosphonate and NRPS as shown in table 1.

Table 1: Metabolic Peptides Derived from Camel Gut Microbes Identified using Anti SMASH Server

Metabolic Peptides	Accession No of Gut Microbe	Amino Acid Sequence
Arylpolyene	SRR13205865	LTLSSIFGIGGLSVTVSAAC
Phosphonate	SRR13205865	IIAANEGGAMGIAAGHYLAT
NRPS	SRR13205842	GLDVKTSEILRKPAIRAWIN

The predicted anti-cancer potential of the metabolic peptides is presented in table 2. The support vector machine threshold was set at 0.45. Anti-cancer score of 0.58 which is above the threshold indicated positive anti-cancer activity for all the peptides.

Table 2: Predicting Anti Cancer Potencial of Metabolic Peptides Derived from Camel Gut Microbes using Anti CP 2.0

Metabolites	Peptides	Score	Prediction
Arylpolyene	LTLSSIFGIGGLSVTVSAAC	0.58	Anti CP
Phosphonate	IIAANEGGAMGIAAGHYLAT	0.58	Anti CP
NRPS	GLDVKTSEILRKPAIRAWIN	0.58	Anti CP

Support Vector Machine (SVM) Threshold – 0.45

Discussion

The predicted anticancer score of 0.58 which is above the SVM threshold of 0.45 indicated positive anticancer activity in all the peptides evaluated. The ability of Arylpolyene to inhibit cell membrane proliferation, scavenge free radicals and induce apoptosis have been documented (Dong *et al*., 2024). Phosphonates are reported to exhibit anticancer potential by inhibiting essential enzymes, inducing apoptosis and destroying cell cycle progression (Mohammadi *et al*., 2019). Diverse biological activities and anticancer potential of NRPS make it attractive candidate for drug development (Jepri *et al*., 2022). Pardoxin, a fish mucus derived anticancer peptide disrupt cell proliferation and induce apoptosis in cancer cell lines (Chen et al., 2021).

The low specificity of traditional cancer drugs and development of multi drug resistance to chemotherapy by tumors, necessitate the need for novel anti cancer agents with high specificity and low toxicity. Anticancer peptides have demonstrated efficacy with low risk of drug resistance and low toxicity against mammalian cells (Lath *et al*., 2023). The abundance of anions on the surface of cancer cells enhance electrostatic interaction between anticancer peptides and cancer cells surfaces. Anions are more abundant on the inner surface of normal cells, thereby increasing the specificity of anticancer peptides for cancer cells (Chiangong *et al*., 2020). The high concentration of cholesterol on membrane of normal cell compared to cancer cells reduces membrane fluidity which prevent entry of cationic peptides into membranes of normal cells.

Bioactive compounds derived from microbial metabolites have been used extensively for therapeutic purposes (Eleena *et al*., 2024). Secondary metabolites have demonstrated high potential for therapeutic applications against microbial infections (Berdy,2005). Molecular diversity of microorganisms results in a variety of functions of their metabolic products (Zainab *et al*., 2021). Advances in biotechnology facilitated the approval of microbial derived metabolites for therapeutic purposes. Significant anti-cancer activity of microbial metabolites has been reported by Xinhai *et al*., 2023. The anti cancer activity of the metabolites may be attributed to their immune modulatory effects as reported by Xinhai *et al*., 2023.

CONCLUSION

Arylpolyene, phosphonate and NRPS have been identified as metabolic peptides derived from camel gut microbes. The predicted positive anticancer potential of the metabolic peptides supports further experimental validation as potential therapeutic agents.

The demonstrated anti-cancer activity of the evaluated metabolic peptides provide an opportunity for further validation and use of microbial derived metabolites in the chemotherapy of cancer.

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