Systematic Analysis to Identify Prognostic Biomarkers, Potential Target, and Natural Inhibitors for Cervical Cancer

Saravanan Priyadharshini* and Sanjeev Kumar Singh
Structural Bioinformatics and CADD Lab, Department of Bioinformatics, Alagappa University, Karaikudi
*(Email: *spdrks3@gmail.com, skysanjeev@gmail.com)*

Abstract

Cervical cancer is the fourth most prevalent cancer among women worldwide, majorly caused by the persistent infection of Human papillomavirus (HPV) in the cervix. Besides, the available therapeutics are lacking efficacy, producing side effects and drug resistance. The *in silico* analyses including function and pathway enrichment, PPI network reconstruction, and overall survival rate of the up-regulated genes suggest CDK1, BUB1, BUB1B, KIF11, DLGAP5 as prognostic biomarkers for cervical cancer. CDK1 has been selected as a potential target for cervical cancer and the reconstruction of host-pathogen interaction network has revealed its direct interaction with HPV16 E7 which has already been proven by experimental studies. Following this, we have simulated the interaction between CDK1-HPV16 E7 and identified natural inhibitors targeting this interaction through virtual screening which resulted in the identification of three categories of ligands including (i) ligands targeting CDK1, (ii) ligands targeting HPV16 E7, and (iii) ligands targeting the interface of CDK1-HPV16 E7 complex based on their selectivity towards the binding site of protein-protein complex. The identified ligands exhibited reliable binding affinity and significant interactions with CDK1 and also with HPV16 E7. The identified ligands might possess properties to inhibit cervical cancer and CDK1-HPV16 E7 interaction thus requires further Computational and Experimental investigations.

Keywords: Cervical cancer, PPI network, Biomarker, CDK1-HPV16 E7 interaction, natural inhibitors