Abstract #729 PCNA IN CERVICAL INTRAEPITHELIAL NEOPLASIA AND CERVICAL CANCER: AN INTERACTION NETWORK ANALYSIS OF DIFFERENTIALLY EXPRESSED GENES

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Introduction/Background The investigation of differentially expressed genes (DEGs) and their interaction could provide valuable insights for the development of markers to optimize cervical intraepithelial neoplasia (CIN) screening and treatment. This study investigated patients with cervical disease to identify gene markers whose dysregulated expression and protein interaction interface were linked with CIN and cervical cancer (CC).

Methodology Literature search of microarray datasets containing cervical epithelial samples was conducted in Gene Expression Omnibus and Pubmed/medline from inception until March 2021. Retrieved DEGs were used to construct two protein-protein interaction (PPI) networks. Module DEGs that overlapped between CIN and CC samples, were ranked based on 11 topological algorithms. The highest-ranked hub gene was retrieved and its correlation with prognosis, tissue expression and tumor purity in patients with CC, was evaluated.

Results Screening of the literature yielded 9 microarray datasets containing cervical epithelial samples was conducted in Gene Expression Omnibus and Pubmed/medline from inception until March 2021. Retrieved DEGs were used to construct two protein-protein interaction (PPI) networks. Module DEGs that overlapped between CIN and CC samples, were ranked based on 11 topological algorithms. The highest-ranked hub gene was retrieved and its correlation with prognosis, tissue expression and tumor purity in patients with CC, was evaluated.

Conclusion Our study identified that cervical PCNA exhibited multi-algorithmic topological significance among DEGs from CIN and CC samples. Overall, PCNA may serve as a potential gene marker of CIN progression. Experimental validation is necessary to examine the screening, diagnostic and prognostic value of PCNA in patients with CIN and CC.

Disclosures n/a