

Abstract

ABSTRACT

Cervical cancer is a serious global health concern in Tamil Nadu, India. It significantly affects rural women due to their fewer facilities and lesser knowledge regarding healthcare. The study was designed to examine cervical cancer's socio-demographic, clinical, and genetic aspects, thereby identifying existing knowledge gaps, enhancing clinical perception, and determining molecular targets for precision medicine. The socio-demographic assessment revealed poor awareness of the symptoms, preventive measures, and immunization, the most severe deficit in rural areas. Clinical profile analysis of cervical cancer patients from Sri Ramakrishna Hospital, Coimbatore, Tamil Nadu, revealed that middle-aged rural women were the most affected and squamous cell carcinoma is the predominant subtype. The advanced stage of diagnosis was typical, with the prevalent symptoms being abdominal pain and post-menopausal bleeding. It also proved that cisplatin combination therapy is effective enough to change survival results. Considering the dominance of squamous cell cervical cancer, we have tried to profile the mutational patterns from biopsy samples using whole exome sequencing. Genomic analysis of 37 detrimental mutations found in critical genes and confirmation of novel variants in genes like POM121C, PRICKLE1, and GLIS3 by Sanger sequencing revealed bioinformatic dysregulated pathways like Hippo and TGF-beta signaling pathways, highlighting the molecular complexity of the disease and potential targets for precision treatment. Despite the limitations of having insufficient biopsy samples, the study calls for immediate improvement in public awareness, early detection strategies, and genomic-based therapy tailored to individual needs. These results offer crucial insight into the clinical and molecular landscape of cervical cancer and pave the way for precision medicine approaches to reduce mortality rates among affected populations.