

SPECIMEN FORMAT FOR THESES OF MONTH

Faculty	:	School of Bio Sciences
Department	:	Biochemistry, Biotechnology and Bioinformatics
Branch/ Area:	:	Biotechnology
Sub Subject Heading:	:	Cancer biology
Candidate's Name	:	Sudha B
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Title of the thesis	:	Genomic and epidemiological profile of cervical cancer patients - identifying risk factors, pathways and novel variants through integrated survey and whole exome sequencing strategies
(i) In Roman Script		GENOMIC AND EPIDEMIOLOGICAL PROFILE OF CERVICAL CANCER PATIENTS - IDENTIFYING RISK FACTORS, PATHWAYS AND NOVEL VARIANTS THROUGH INTEGRATED SURVEY AND WHOLE EXOME SEQUENCING STRATEGIES Genomic and epidemiological profile of cervical cancer patients - identifying risk factors, pathways and novel variants through integrated survey and whole exome sequencing strategies
(ii) In roman Script		
Nomenclature of Degree:	:	PhD
Month & Year of Enrolment:	:	July 2019
Month & Year of Registration:	:	July 2019
Month &Year of Submission:	:	January 2025
Month &Year of Award	:	January 2026
Name of Supervisor	:	Dr S Sumathi
Designation of Supervisor	:	Professor
Centre/department/school in which research was conducted	:	Bioscience
University's Name & Address	:	Avinashilingam Institute for Home Science and Higher Education for Women, Coimbatore – 43.

Abstract within 300 words:

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.

i) Major objectives :

- To assess cervical cancer awareness, knowledge, and prevention behaviors among women via online surveys.
- To investigate cervical cancer patient's socio-demographic profile and causative biological factors through a hospital-based cohort study
- To identify genetic variants by whole exome sequencing and evaluate their pathogenicity and associated pathways in cervical cancer patients samples.
- To validate the identified novel variants using Sanger sequencing

ii) Hypothesis:

- **Null hypothesis:** The combination of knowledge, awareness, socio-demographic factors, biological risk factors, and genetic variants does not significantly predict cervical cancer incidence and progression.
- **Alternate hypothesis:** There is a significant correlation between knowledge, awareness, and prevention behaviours, and a combination of socio-demographic factors, biological risk factors, and specific genetic variants increase the risk of cervical cancer incidence and progression.

iii) Methodology :

To address our objectives, the study was carried out in four phases.

Phase 1, we conducted an online survey to understand awareness, knowledge, and preventive practices related to cervical cancer.

Phase 2, we performed a hospital-based cohort study to analyze socio-demographic details and clinical risk factors in cervical cancer patients.

Based on these findings, in Phase 3, we then carried out whole exome sequencing to identify genetic changes involved in cervical cancer. Phase 4, the novel variants identified were confirmed using Sanger sequencing.

iv) Findings:

Our study revealed awareness gaps and clinical risk factors in cervical cancer and identification of novel genetic variants in *GLIS3*, *POM121C*, and *PRICKLE1* reported for the first time, may serve as biomarkers to guide early detection, risk screening, and personalized treatment for cervical cancer.

Examiners

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