

Computational Biology Approaches in Deciphering the Therapeutic Drugs for Cancer from White Pear Family Species

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Abstract:

Cancer is the second lead cause of death accounting for 9.6 million deaths with 20 million new cancer cases as reported by WHO. According to IARC-Global Cancer Observatory statistics for 2022-23, the deadliest cancer in INDIA with the highest recorded death cases are Breast cancer in Women and Prostate Cancer in Men. Breast cancer is the most common cancer in Indian women, with over 200,000 new cases diagnosed annually. Prostate cancer ranks as a leading cancer in Indian men, recording over 34,000 annual incidences. Both diseases share a critical challenge in India: late-stage diagnosis (Stages III and IV) due to limited nationwide screening. The molecular mechanisms underlying these cancer progression have led to the development of a vast number of potential anticancer drugs. Radiation, chemotherapy, and immunotherapy are the alternative methods for cancer treatment. In chemotherapy, one of the most widely used drugs, including gemcitabine, 5-fluorouracil, capecitabine, and methotrexate are used as therapeutic agents. However, the use of chemically synthesized drugs has not significantly improved the overall survival rate over the past few decades due to the inefficiency of timely diagnosis, quality treatment, systemic toxicity, multidrug resistance, heterogeneity, and its mechanistic complexity. The current cancer therapies are limited and urge the need for advanced and alternative therapeutics.

WHO recognises that medicinal plants play an important role in treating various ailments, with this we have identified a species from white pear family having anticancer potential for Breast and prostate cancer by Computational Biology approaches in the detection of lead therapeutic drug for these cancers which is studied via various KEGG and Gene Ontology Pathways.