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MDPI cancers

Comprehensive Sociodemographic, Clinical and Molecular Profiling of Breast Cancer in Morocco: Insights from 833 Patients at the Mohammed VI Cancer Center

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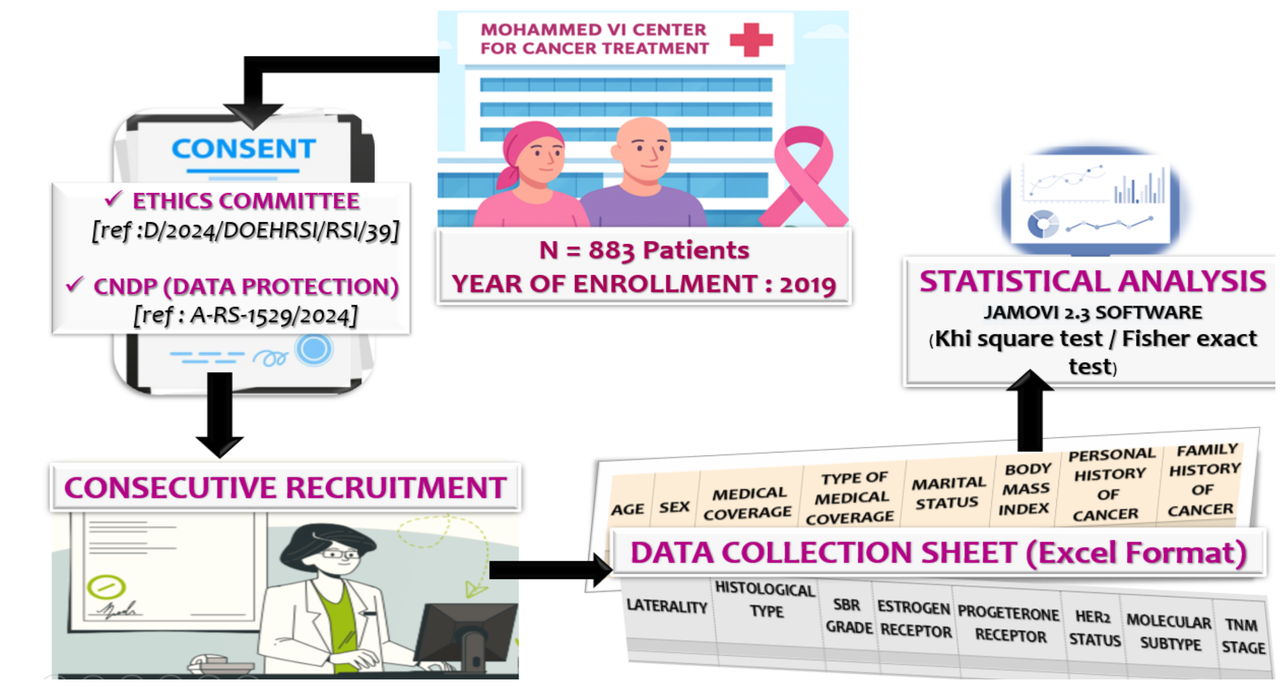
BACKGROUND AND RATIONALE

Breast cancer (BC) is the most leading cause of cancer in women worldwide and is responsible for over 2 million new cases and 666,000 deaths per year. In Morocco, it is the main cancer cause in women, representing about 39%, and it is still the second major cause of death because of its heterogeneity and the extreme variation of molecular subtypes-related prognoses. Numerous regional studies (Casablanca, Rabat, Fez, Tangier, Kenitra, Souss-Massa) have analyzed the epidemiological profile of breast cancer—sociodemographic, clinical, and anatomopathological characteristics, genetic polymorphisms, access to care and psychosocial impact—in order to guide national policies. However, these studies often suffer from limitations (small sample sizes, focus on specific subpopulations, frequent exclusion of relapses, metastases, or patients treated outside the center) and heterogeneous geographical and social coverage, which reduces their national scope. In addition, important parameters are rarely described in detail in the Moroccan literature—notably the laterality of lesions, body mass index (BMI) and personal history of cancer. The molecular profile, meanwhile, remains largely unexplored at the national level, with the few studies available often being fragmentary, limited to partial associations and conducted on exclusive populations. To address these gaps, we propose a comprehensive and inclusive approach based on data from all patients with histologically confirmed BC registered in 2019 at the Mohammed VI Cancer Treatment Center, chosen for its particularly large patient population, which guarantees the representativeness of the results, integrating all profiles (age, initial/metastatic/relapse stage, unilateral/bilateral/multifocal, public or private treatment pathway, lack of coverage) in order to provide representative and generalizable data. It thus aims to fill the current gaps by providing a comprehensive overview of BC molecular subtypes and their clinical-pathological and demographic correlations. Most importantly, the current studies do not provide sufficient mechanistic insights to fully understand the heterogeneity that has been observed and they frequently depend on entirely speculative interpretations. Our integrative approach bases observations on validated biological mechanisms (genomic instability, cellular plasticity, ferroptosis resistance, immune escape), offering a coherent and biologically sound explanation for the heterogeneity of Moroccan BC.

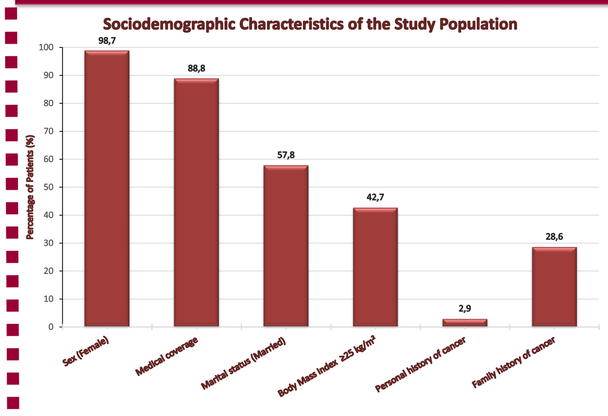
METHODOLOGY

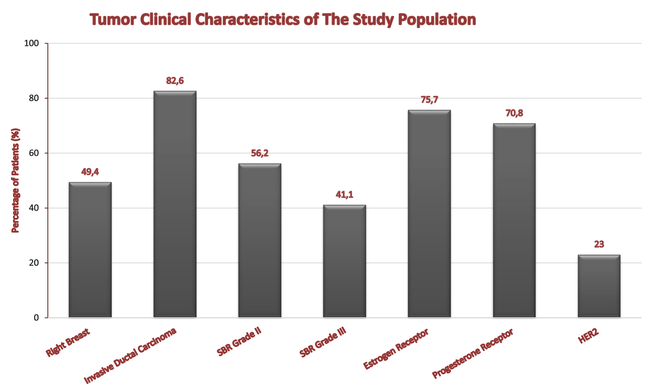


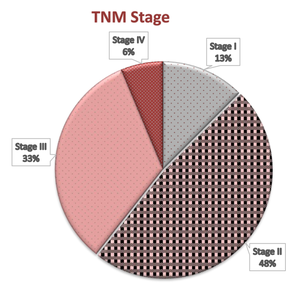
OBJECTIVE

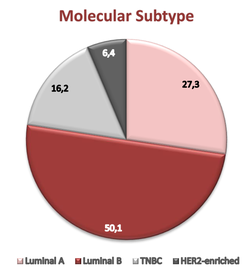
In the context of expanding our epidemiological and molecular understanding of BC, this study has been designed as a retrospective study, with the following: aims:
1- To describe the demographic, clinical, and histopathological profile of BC patients in Morocco;
2- To Analyze the associations between BC molecular subtypes and patients' socio-demographic and clinical features in Morocco, along with mechanistic explanations based on confirmed biological processes.

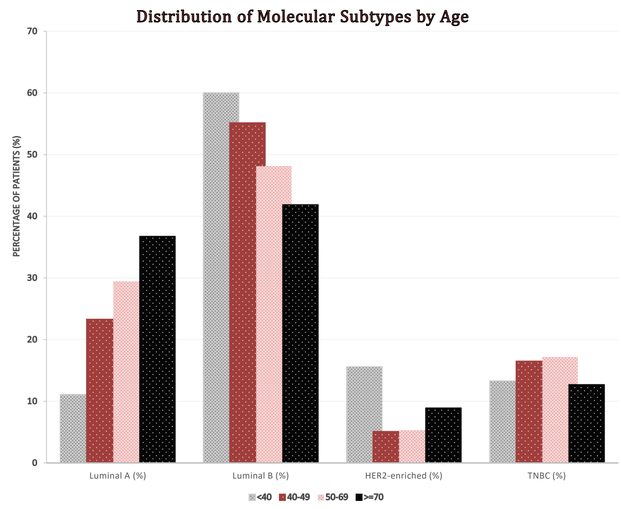
RESULTS

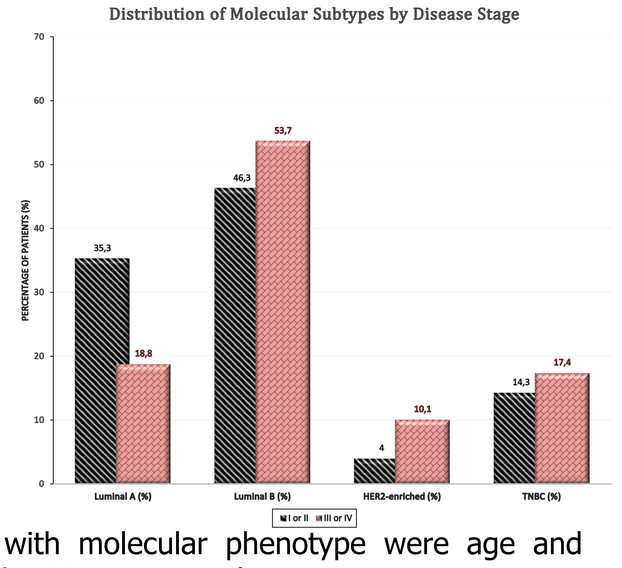








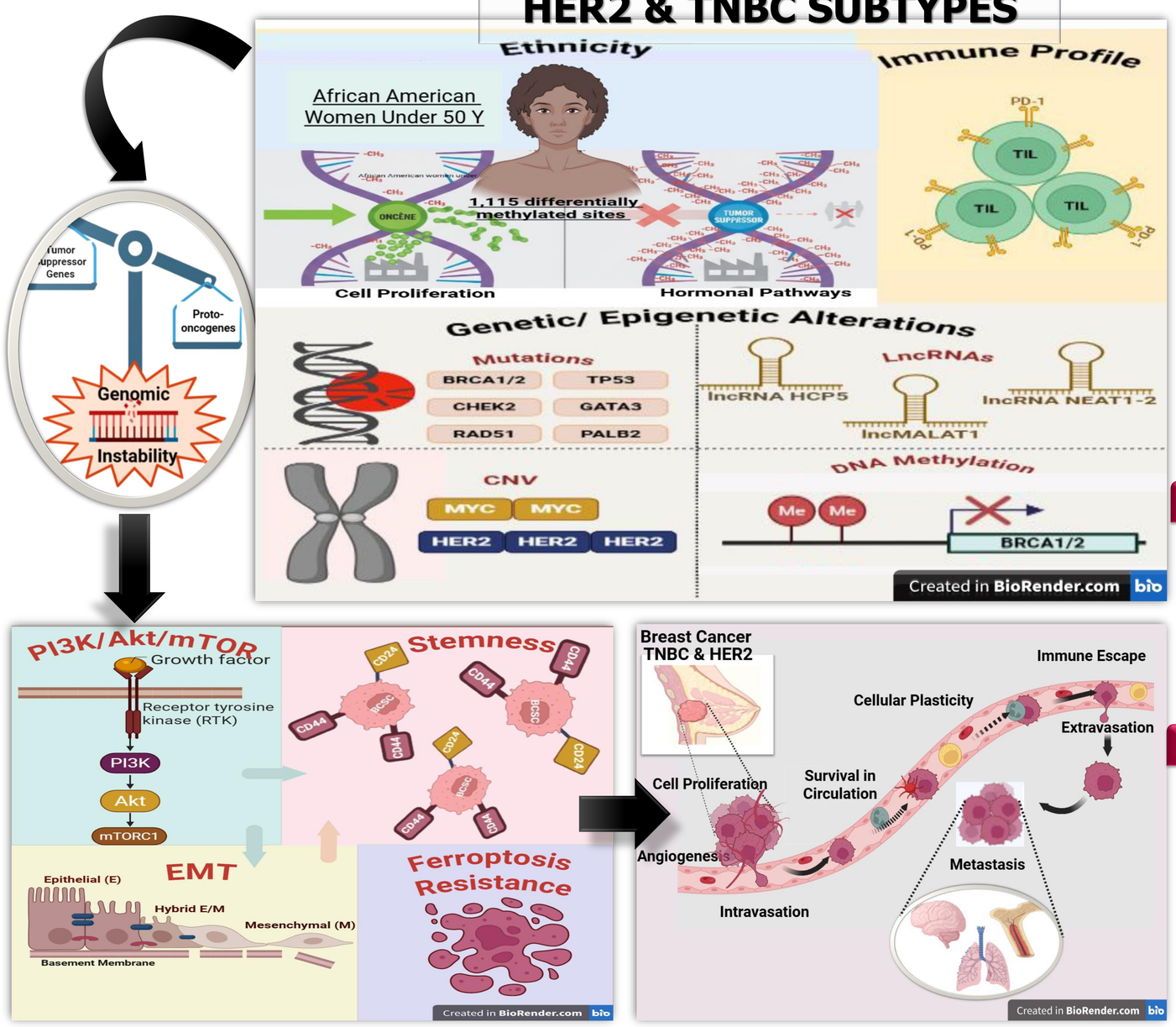


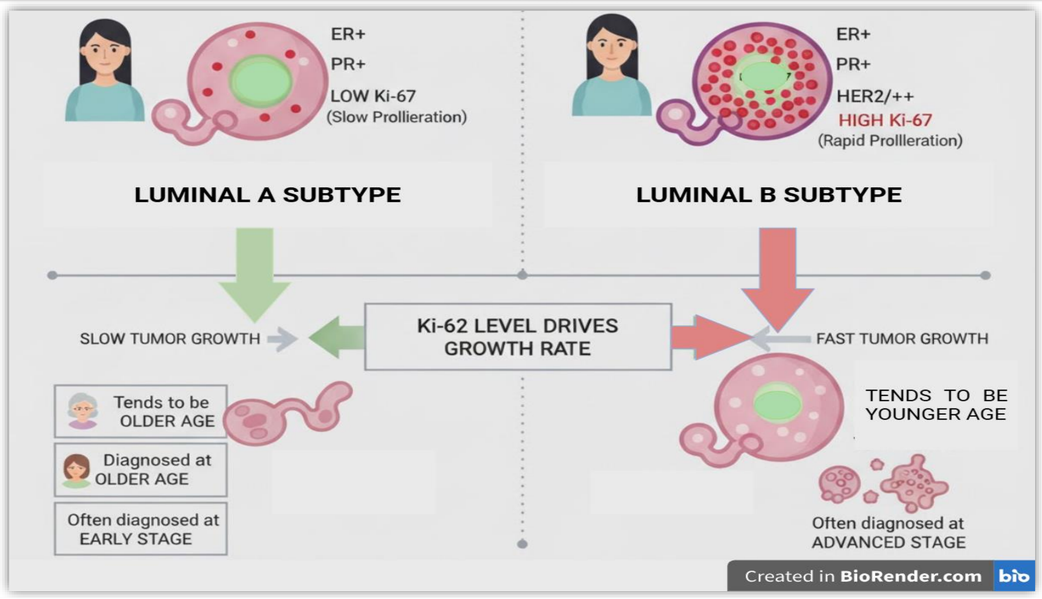


The characteristics found to be associated with molecular phenotype were age and stage, with degrees of significance of 0.02 and 0.001 respectively.
The Luminal A subtype increases with age and is more common in early stages, while Luminal B, HER2-enriched, and TNBC are more common in younger patients and in advanced stages (III/IV).

PHYSIOPATHOLOGICAL INTERPRETATION: MOLECULAR PROFILE DISTRIBUTION BY AGE AND STAGE

HER2 & TNBC SUBTYPES





CONCLUSION AND IMPACT

The study consolidates prior findings that had only been partially and poorly combined from different sources. They emphasize the significance of using age, stage, and molecular profile in a hierarchy to determine the personalized therapeutic strategies most appropriate for the patients. In addition, these results emphasize the necessity to strengthen targeted screening and to extensively dissect genetic profiles and intra-tumor heterogeneity, especially for the highly aggressive variants of the disease.

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