From Pathogenic Variant to Action: Genetic Risk Identification and Preventive Oncology in Brazil's Public Health System

Elisângela de Paula Silveira-Lacerda[1], Paula Francinete Faustino Silva[1], Késsila Macedo Veiga[1], Bruno Eduardo Feitosa do Nascimento[1], Igor Marques Cesário Calassa[1], Amanda Santos Limongi[3], Kleber Junior Rodrigues Monteiro[3], Rasivel dos Reis Santos Junior[3], Sérgio Alberto Cunha Vencio[3], Rosemar Macedo Sousa Rahal[2]

[1]Human Genetics Center, Institute of Biological Sciences, Federal University of Goiás, Goiânia, Brazil. [2]CORA, Clinical Hospital, Federal University of Goiás, Goiânia, Brazil. [3]State Health Department of Goiás, Brazil.

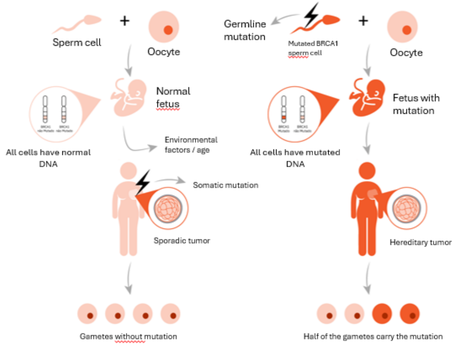
Abstract

Background: Approximately 10% of breast and ovarian cancer cases are hereditary, and identifying germline pathogenic variants is essential for implementing preventive strategies in precision oncology. In Goiás, Brazil, the public health system (SUS) has incorporated genetic risk screening and management, enabling population-level access to genomic medicine. **Objective:** This study aimed to evaluate the frequency of germline pathogenic variants in patients at risk for hereditary breast and ovarian cancer, and to track these variants among their relatives for early diagnosis and prevention. **Methods:** This study evaluated 305 patients who met the 2025 NCCN criteria for hereditary breast and ovarian cancer syndromes, along with 155 relatives. After genetic counseling and informed consent, blood samples were analyzed using next-generation sequencing with the Oncomine™ BRCA Expanded Panel. **Results:** Among the index patients, 14% carried germline pathogenic variants, primarily in BRCA1 (50%) and TP53 (21%). Cascade testing was performed in 30 families, revealing that 38.46% of tested relatives carried the familial variant. All individuals who tested positive were evaluated by a medical geneticist and referred for surveillance and risk-reducing interventions according to the 2025 NCCN guidelines. **Conclusion**: The project established a structured and replicable workflow for hereditary cancer risk management within the SUS, integrating genetic counseling, testing, cascade screening, and clinical follow-up. Incorporating genetic risk management into routine public healthcare enabled early diagnosis and effective prevention, particularly in underserved populations. This initiative demonstrates that comprehensive genomic care and precision prevention can be sustainably implemented in a public system.

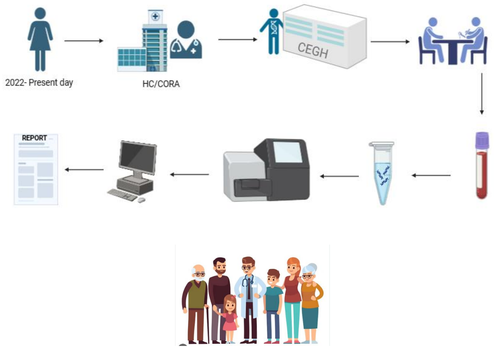
Introduction

Approximately 10% of breast and ovarian cancer cases are hereditary. Identifying germline pathogenic variants and acting on this information through preventive strategies is a key pillar of precision oncology. In Brazil, the public health system (SUS) in Goiás has incorporated genetic risk screening and management, setting a precedent for accessible, population-level genomic medicine. This study aimed to evaluate the frequency of germline pathogenic variants in patients at risk for hereditary breast and ovarian cancer, and to track these variants among their relatives for early diagnosis and prevention.

Figure 1. Comparative diagram between sporadic and hereditary tumors. On the left, the somatic mutation is acquired and not inherited. On the right, the germline mutation (e.g., BRCA1) is present from conception and can be transmitted to offspring.

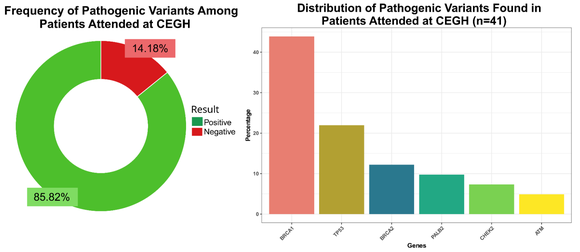


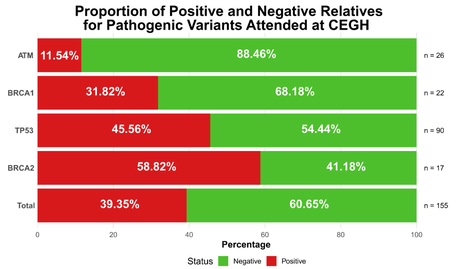
Methods and Materials

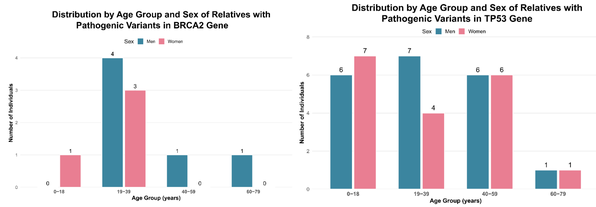


Results

Among the 305 index patients, 14% (38/268) had pathogenic germline variants. The distribution was: BRCA1 (50%, 19/38), TP53 (21%, 8/38), PALB2 (10.5%, 4/38), CHEK2 (2.9%), BRCA2 (5.3%), and ATM (5.3%). Further familial testing was conducted in 30 families. Among eight families with the TP53 c.1010G>A variant, 36 of 99 tested relatives (36.4%) were positive. In two BRCA2-positive families, 9 of 18 relatives (50%) carried the same variant. Altogether, 45 of 117 relatives (38.46%) tested positive for the familial variant.Crucially, all relatives with positive results were evaluated by a medical geneticist and referred for cancer surveillance and risk-reducing strategies according to NCCN 2025 guidelines.







Discussion

This included MRI, mammography, and risk-reducing surgery when indicated, ensuring translation from geneticfinding to clinical action.The project established a structured, replicable workflow for managing hereditary cancer risk in families. This includes genetic counseling, testing, cascade screening, and follow-up within the public healthcare system. By integrating genetic riskmanagement into routine SUS care, the program enables early-stage diagnosis and reduces cancer-related mortality, particularly in underserved populations.This initiative demonstrates that comprehensive genomic care and precision prevention are feasible within a public system and scalable to other regions. It highlights how transforming a genetic finding into preventive action can generate real-world impact bridging the gap between variant and value.

Conclusions

The implementation of hereditary cancer genetic screening within the SUS of Goiás proved feasible, effective, and clinically impactful. Identifying pathogenic variants and performing cascade testing allowed for early detection of at-risk individuals and ensured timely referral for specialized surveillance and preventive measures. This model is scalable to other regions and highlights the importance of translating genetic findings into actionable clinical strategies to reduce cancer-related mortality and advance precision oncology within public healthcare systems.

Contact

Elisângela de P.S. Lacerda
Federal University of Goiás (UFG)
Email: elacerda@ufg.br
Website:
Phone: +55 62 992933121

References

1. Richards S, et al. Standards and guidelines for the interpretation of sequence variants. Genet Med. 2015;17(5):405-424. doi:10.1038/gim.2015.30.
2. gnomAD – Genome Aggregation Database. Disponível em: https://gnomad.broadinstitute.org
3. ABraOM – Arquivo Brasileiro Online de Mutações. Disponível em: http://abraom.ib.usp.br
4. ClinVar – NCBI. National Center for Biotechnology Information. Disponível em: https://www.ncbi.nlm.nih.gov/clinvar/
5. Franklin by Genoox. Disponível em: https://franklin.genoox.com/clinical-db/home
6. Varsome. The Human Genomics Community. Disponível em: https://varsome.com/NCCN – National Comprehensive Cancer Network. Genetic/Familial High-Risk Assessment: Breast, Ovarian, and Pancreatic. Version 2025.

This presentation is the intellectual property of the author/presenter. Contact them at <<your email address>> for permission to reprint and/or distribute.

© Poster Template by Genigraphics® 1.800.790.4001 www.genigraphics.com