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Análisis de un panel multigénico y prevalencia de variantes genéticas en pacientes con cáncer de mama hereditario en Córdoba, 2016-2020

Jorge Hernan Hoyos Verbel

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Tutores
Cristiano Trindade
Jorge Andres Rugeles Mindiola

RESUMEN

Introducción: El cáncer de mama es una enfermedad neoplásica que afecta una de cada 8 mujeres (12.5%), siendo esta la patología más frecuente en mujeres en lo que se refiere a cáncer. Sus causas son multifactoriales por lo que confieren un riesgo variable en diferentes poblaciones, dado a condiciones esporádicas, o a una predisposición hereditaria o poligénica. Cerca del 10% de los tumores son hereditarios por mutaciones de línea germinal en genes con un grado de susceptibilidad variable en el desarrollo del cáncer de mama. La identificación de variantes patogénicas por secuenciación de siguiente generación tiene gran utilidad en la toma de decisiones. Por lo que este estudio realizó un análisis descriptivo de variantes genéticas de un panel multigénico realizadas a pacientes con diagnóstico de cáncer de mama, enfocado a evaluar la prevalencia de mutaciones de línea germinal en un instituto oncológico para determinar las variantes encontradas en la población de córdoba.

Objetivo: Determinar la prevalencia de las variantes genéticas del panel multigénico y caracterizar las variables clínico-epidemiológicas de pacientes con diagnóstico de cáncer de mama hereditario en la clínica IMAT-Oncomedica de Montería durante el periodo del 2016-2020.

Métodos: Mediante los resultados de un panel multigénico realizado a 452 pacientes con cáncer de mama no seleccionada por edad o historia familiar, que han acudido al instituto oncológica IMAT-Oncomedica, se hizo un análisis estadístico de la prevalencia de las variantes genéticas encontradas.

Resultados: Se observaron 57 (12.6%) pacientes con resultado positivo para una mutación de 452 (100%), entre estos predominó el género femenino con el 99.3% (449) y el 0.7% (3) para el sexo masculino, las mutaciones identificadas en la secuenciación de próxima generación (NGS) fueron de tipo sustitución con el 5.8% (26), seguidas de la deleciones con el 4.6% (21), largas deleciones o duplicaciones del gen BRCA1 y PALB2 con el 1.8% (8) y por ultimo las duplicaciones con el 0.4% (2).

Conclusiones: La tasa de prevalencia de las mutaciones en el panel multigénico fue mayor en las sustituciones identificando genes de alta penetrancia BRCA1/2, TP53, genes de moderada penetrancia ATM, CHEK2, PALB2, y genes de baja penetrancia RAD51C, MLH1, MUTYH en casos de cáncer de mama no seleccionados de la región de Córdoba en Colombia y es de aproximadamente 5.8%.

Palabras clave: Cáncer de mama, BRCA 1, BRCA 2, Panel de genes.

ABSTRACT

Introduction: Breast cancer is a neoplastic disease that affects one in every 8 women (12.5%), this being the most frequent pathology in women in terms of cancer. Its causes are multifactorial, so they confer a variable risk in different populations, due to sporadic conditions, or a hereditary or polygenetic predisposition. About 10% of tumors are hereditary due to germline mutations in genes with a variable degree of susceptibility in the development of breast cancer. The identification of pathogenic variants by next generation sequencing is very useful in decision making. Therefore, this study carried out a descriptive analysis of genetic variants of a multigenic panel performed on patients diagnosed with breast cancer, focused on evaluating the prevalence of germline mutations in a cancer institute to determine the variants found in the population of Córdoba.

Objective: To determine the prevalence of genetic variants of the multigenic panel and to characterize the clinical-epidemiological variables of patients diagnosed with hereditary breast cancer at the IMAT-Oncomedica clinic in Montería during the period 2016-2020.

Methods: Using the results of a multigenic panel performed on 452 patients with breast cancer not selected by age or family history, who have attended the IMAT-Oncomedica cancer institute, a statistical analysis of the prevalence of the genetic variants found was made.

Results: 57 (12.6%) patients with a positive result for a mutation of 452 (100%) were observed, among them the female gender predominated with 99.3% (449) and 0.7% (3) for males, the mutations identified in Next generation sequencing (NGS) were of the substitution type with 5.8% (26), followed by deletions with 4.6% (21), long deletions or duplications of the BRCA1 and PALB2 gene with 1.8% (8) and by last duplications with 0.4% (2).

Conclusions: The prevalence rate of mutations in the multigenic panel was higher in the substitutions identifying high penetrance genes BRCA1/2, TP53, moderate penetrance genes ATM, CHEK2, PALB2, and low penetrance genes RAD51C, MLH1, MUTYH in cases of unselected breast cancer from the Córdoba region in Colombia and is approximately 5.8%.

Keywords: Breast cancer, BRCA 1, BRCA 2, Gene panel.

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