Global Health Day

Association of PIN3 16-bp Duplication Polymorphism of TP53 with Breast Cancer Risk in Mali and Meta-analysis

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Background: Breast cancer, the most common tumor in women in Mali and worldwide has been linked to several risk factors, one of which includes genetic factors such as the PIN3 16-bp duplication polymorphism of TP53. The aim of our study was to evaluate the role of the PIN3 16-bp duplication polymorphism in the susceptibility to breast cancer in the Malian population and to perform a meta-analysis to better understand the correlation with data from other population groups.

Methods: Using PCR, we analyzed the PIN3 16-bp duplication polymorphism in blood samples of 60 Malian women with breast cancer and 60 healthy Malian women. In addition, we performed a metaanalysis of case-control study data from international databases, including Pubmed, Harvard University Library, Genetics Medical Literature Database, Genesis Library and Web of Science. Overall, odds ratio (OR) with 95% CI from fixed and random effects models were determined. Inconsistency was used to assess heterogeneity between studies and publication bias was estimated using the funnel plot.

Results: In the studied Malian patients, a significant association of PIN3 16-bp duplication polymorphism with breast cancer risk was observed in dominant (A1A2+A2A2 vs. A1A1: OR = 2.26, Cl 95% = 1.08-4.73; P = 0.02) and additive (A2 vs. A1: OR =1.87, Cl 95% = 1.05-3.33; P = 0.03) models, but not in the recessive model (P = 0.38). In the meta-analysis, nineteen (19) articles were included with a total of 6,018 disease cases and 4,456 controls. Except for the dominant model (P = 0.15), an increased risk of breast cancer was detected with the recessive (OR = 1.46, 95% Cl = 1.15-1.85; P = 0.002) and additive (OR = 1.11, 95% Cl = 1.02-1.19; P = 0.01) models.

Conclusion: The case-control study showed that PIN3 16-bp duplication polymorphism of TP53 is a significant risk factor for breast cancer in Malian women. These findings are further supported by data from the meta-analysis carried out on different ethnic groups around the world.

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