Omayma O. Abdelaleem, Olfat G. Shaker, Marwa N. AbdelHafez, Noha K. Abdelghaffar, Hanaa M. Eid, Mohamed Zaidan, Abeer A. Khalefa, Naglaa A. Ahmed, **Nada F. Hemeda**, Othman M. Zaki, Aeshah Ali A. Awaji and Shereen R. Mohammed **(2021)**. The Influence of rs1859168 Polymorphism on Serum Expression of HOTTIP and Its Target miR-615-3p in Egyptian Patients with Breast Cancer. Biomolecules, 11: 733. **https://doi.org/10.3390/biom11050733**	**البحث الثاني**
مشترك مع آخرين من خارج التخصص– منشور	**2**

Title	**The Influence of rs1859168 Polymorphism on Serum Expression of HOTTIP and Its Target miR-615-3p in Egyptian Patients with Breast Cancer**.
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ABSTRACT

Background: Polymorphisms of long noncoding RNAs are lately documented as hazardous factors for the development of numerous tumors. Furthermore, the evaluation of noncoding RNAs has emerged as a novel detector of breast cancer patients. We aimed to genotype the HOXA transcript at the distal tip (HOTTIP) rs1859168 and assess its relationship with the levels of the serum HOTTIP and its target miR-615-3p in patients with breast cancer (BC). Methods: One hundred and fifty-one patients with BC, 139 patients with fibroadenoma (FA), and 143

healthy participants were incorporated into the current study. The genotyping of rs1859168 and the measurements of the HOTTIP and miR-615-3p levels were assessed using quantitative real-time PCR. Results: We revealed a significant association between each of the CC genotypes, C allele, dominant and recessive models, and the increased risk of BC ($p = 0.013$, $p < 0.001$, $p < 0.001$, and $p < 0.001$, respectively) relative to the healthy controls. Similarly, the CC genotype, C allele, and recessive model were observed to be related to the increased incidence of BC with respect to FA ($p < 0.001$ for all). A significant upregulation of HOTTIP and a marked decrease of miR-615-3p were verified in patients with BC compared to each of the healthy individuals, patients with FA, and the non-BC group (healthy subjects + FA) ($p < 0.001$ for all). A significant negative correlation was demonstrated between the expression of HOTTIP and miR-615-3p in the serum of patients with BC. The HOTTIP expression was upregulated, while that of miR-615-3p was downregulated in patients with BC who carried the CC genotype with respect to those who carried the AA or AC genotypes ($p < 0.05$ for all).
Conclusions:
The genetic variants of rs1859168 are linked to an increased susceptibility to BC. Moreover, HOTTIP and miR-615-3p may be used as novel indicators and targets for the treatment of patients with BC.