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28568 – MUTATIONS IN THE FANCC AND CREBBP GENES DIFFERENTIATE A CASE OF A PATIENT WITH TRIPLE-NEGATIVE BREAST TUMOR AND FAVORABLE CLINICAL PROGRESSION

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Introduction: Triple-negative breast cancer (TNBC) accounts for approximately 15% of diagnosed cases. Characterized by the lack of tumor expression of estrogen, progesterone, and HER2 receptors, it is the most aggressive subtype with the poorest prognosis, exhibiting heterogeneous behavior given the limited available systemic therapies. The heterogeneity of TNBC was first studied by Lehmann et al. in 2011, and with ongoing research, the disease is now divided into five distinct groups: basal-like 1 (BL1), basal-like 2 (BL2), immunomodulatory (IM), luminal androgen receptor-positive (LAR), and mesenchymal/magnetic stem-like (M/MSL). Each subtype has unique molecular features and suggests the possibility of different therapeutic options. Several biomarkers have been studied as potential targets for TNBC treatment, but there has yet to be a significant change in the prognosis of these patients. **Methodology:** Three patients with TNBC were studied, recruited through one of the projects of the National Oncology Care Support Program (PRONON) from the Mário Penna Institute (Ministry of Health, NUP 25000.079266/2015-09), approved by the Research Ethics Committee (Ethics Submission Certificate – CAEE: 82703418.8.0000.5121). Tumor DNA samples from these patients were extracted from material obtained via fine-needle biopsy or primary breast surgery using the AllPrep DNA/RNA Kit. Next-generation sequencing (NGS) was performed using the QIAseq® Pan-cancer Multimodal panel kit (UHS-5000Z). The generated data were analyzed using the QIAGEN CLC Genomics Workbench 22 software. All sequences were mapped, and a list of mutations (both synonymous and non-synonymous) for each patient was determined, referencing the human genome version GRCh38/hg38. These data were correlated with the patients' clinical outcome data. **Conclusion:** In this study, variants of uncertain significance (VUS) were identified in the FANCC and CREBBP genes in a patient with TNBC who showed a favorable clinical course. No variants in these genes were found in the other two patients with poorer prognoses analyzed. These findings, combined with the roles of these genes in processes related to carcinogenesis, suggest a potential genetic signature associated with good prognosis for TNBC, which should be validated in future complementary studies. With further analysis and the sequencing of tumor DNA from a larger number of patients, it is expected to confirm these findings or even identify other pathways with prognostic or predictive value.