RAMASAMY, D.P.K. **Constructing Signaling Pathways with Bioinformatics tools using as model the basal-like breast cell lines overexpressing (MCF10A/CD90+) or silenced (Hs578T/shCD90) for CD90/Thy-1.** 2022. 136 p. Tese (Doutorado em Ciências) - Faculdade de Medicina Veterinária e Zootecnia, Universidade de São Paulo, São Paulo, 2022.

Breast cancer is the most prevalent cancer among women. Among the subtypes of breast cancer, the basal-like Triple Negative Breast Cancer (TNBC) is the most aggressive type and it displays the poorest prognosis within the ductal carcinoma subtype. Due to the lack of adequate molecular targets, the diagnosis and treatment of patients with TNBC phenotype have been a great challenge. To understand the biology of TNBC, our laboratory has studied the difference in the expression of CD90/Thy-1 which is overexpressed in the malignant Hs578T basal-like TNBC cell line and no expressed in the non-malignant MCF10A. Further, the study has been extended to investigate the role of CD90, in that CD90 was overexpressed in MCF10A non-malignant epithelial cell line (MCF10A/CD90) and silenced in Hs578T highly malignant cell line (Hs578T/CD90sh) based on the functional genetic approach. This study has shown the involvement of CD90 in several cellular processes which take part in malignant transformation. In this context, based on a systematic literature review, we first construct the signaling pathway of target genes and proteins involved in TNBC signalling pathways. Applying the quantitative mass spectrometry-based proteomic approach to identify the differential proteins in breast epithelial MCF10A cells, cancerous Hs578T cells, and functionally modified cell lines with CD90 (MCF10A/CD90+ and Hs578T/CD90sh). The proteomic data were analyzed using downstream bioinformatics approaches (MaxQuant and Perseus) to find the differentially quantified proteins in modified cell lineages (MCF10A/CD90+ and Hs578T/CD90sh) compared to the respective cells without modification (wildtype control cells). The quantitative proteomics data analysis have shown forty-four differential expressed proteins (DEPs) in MCF10A overexpressing CD90 and sixty-eight proteins in Hs578T silencing CD90. Finally, the comparison between CD90-associated differential expressed proteins with the constructed signalling pathway associated with TNBC have shown the dysregulation of signalling pathways such as EGFR, VEGFR, HIF1α, WNT, TGF-β, and STAT3. Hence, CD90 can be considered the promising TNBC tumor marker, indicating new therapeutic targets to interfere with.