

Identifying role of N-myristoyltransferase in the mTOR signalling cascade of ER- α positive breast cancer cells (MCF-7)

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Breast cancer is the most common malignancy in women from the western world. Estrogen receptor (ER) is a key regulatory in the malignancy of breast cancer. The status of the ER- α of breast tumours is used for predicting response to endocrine therapy. ER- α can be post-translationally modified multiple ways including but not limited to phosphorylation, acylation and, ubiquitination. ER- α can be phosphorylated on multiple amino acid residues throughout the whole protein and within all major structural domains: the N-terminal A/B domain, the DNA-binding or C domain, the hinge or D domain and, the ligand-binding domain or E domain. When phosphorylation occurs in the N-terminal domain it is associated with good endocrine therapy outcome, while phosphorylation that occurs in the C-terminal domain leads to poor prognosis. For example, phosphorylation of the ER- α at S¹¹⁸, S¹⁶⁷, and S²³⁶ predict better prognosis whereas, T³¹¹, Y⁵³⁷, and S⁵⁵⁹ predict poor outcome. This has lead to a phosphorylation score called P7 score that more precisely predicts prognosis. Independent studies suggest ER- α phosphorylated at serine¹¹⁸ leads to good endocrine therapy prognosis while phosphorylation at tyrosine⁵³⁷ leads to poor outcome. N- myristoyltransferase (NMT) is an enzyme that modifies proteins by covalently attaching a myristic acid to their N-terminal end. The non-receptor tyrosine kinase pp60cSrc phosphorylates ER- α at tyrosine⁵³⁷ leading to poor prognosis. Myristoylation of pp60cSrc is essential for its activation. The mTOR pathway member Akt/PKB regulates NMT1 activity thus establishing a crosstalk between mTOR pathway and NMT mediated signalling pathways. Therefore, we investigated mTOR-NMT-cSrc mediated regulation of ER- α in ER- α positive MCF-7 cells by inhibiting mTOR and ER- α . Results suggest increased expression of NMT1 upon down-regulating mTORC1 activity and further activation of NMT mediated signalling pathway such as activation of c-Src. Understanding of ER- α activation mechanism would lead to identification of panel of surrogate markers, which would aid in designing treatment protocols for better endocrine therapy outcomes.

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