Basal Expression of ACK1 within Luminal Breast Cancer Subtypes compared to other Breast Cancer Subsets

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Background

- Breast cancer remains as one of the most common cancers in women globally, as well as one of the most significant contributors to total global cancer-related morbidity.
- The non-receptor tyrosine kinase **ACK1** has been found to **be significantly overexpressed in both prostate and breast cancer**[2] and strongly involved in breast cancer pathology.

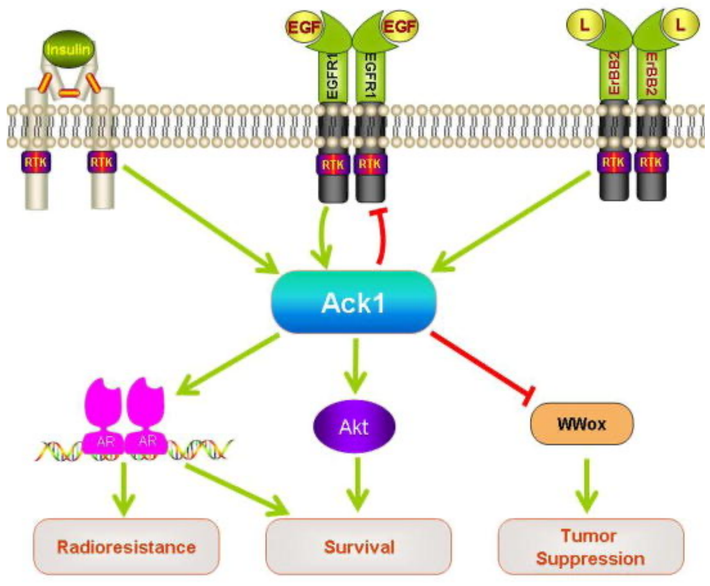

Figure 1. A schematic for the downstream targets and cellular actions of ACK1 within breast cancer [1].

- **However, the relative expression levels of ACK1 in different subsets of breast cancer is not well-known.**

Objective

We aimed to analyze basal ACK1 expression levels in various breast cancer cell lines and assess for variations by breast cancer subtype.

Methods

- **In Vitro**: Quantitative reverse-transcriptase polymerase chain reaction (Q-RT-PCR) and western blot analysis were conducted to analyze ACK1 gene and protein expression in several breast cancer cell lines.
- **Clinical**: Patient tumor sample data was extracted from the METABRIC, TCGA, and HORSEFIRE breast cancer projects from the TCGA database and analyzed for ACK1 expression.
- Statistical analysis using a one-way ANOVA and unpaired two-tailed student's T-test using excel and GraphPad prism.

Results

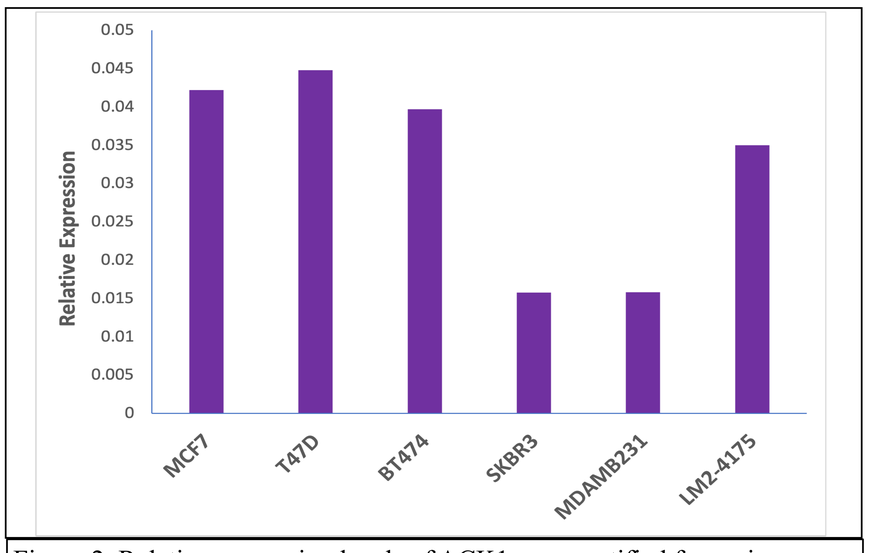

Figure 2. Relative expression levels of ACK1 are quantified for various luminal and triple negative breast cancer cell lines through Q-RT-PCR, revealing increased expression of ACK1 in MCF7 (Luminal A), T47D (Luminal A), and BT474 (Luminal B) cell lines.

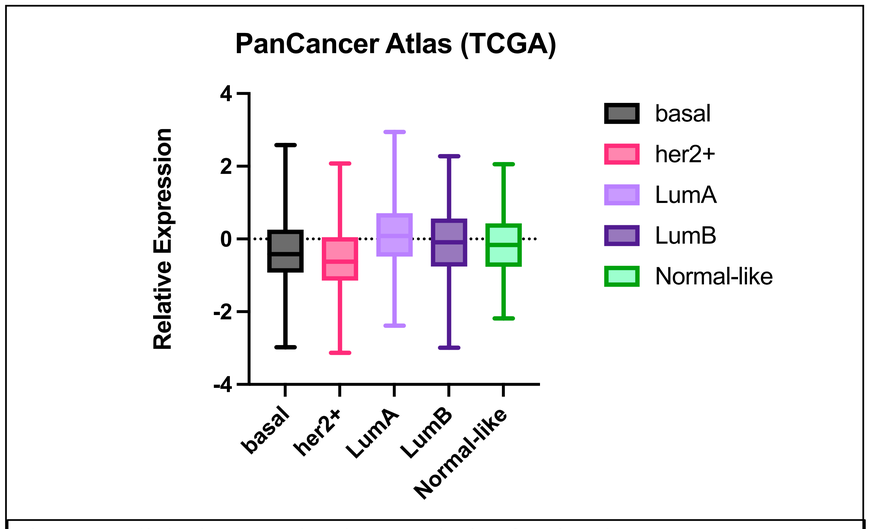

Figure 3. Clinical TCGA data base analysis of patient breast tumor samples of the TCGA breast cancer project yielded significantly increased expression of ACK1 in luminal breast cancer subtypes ($p < 0.01$).

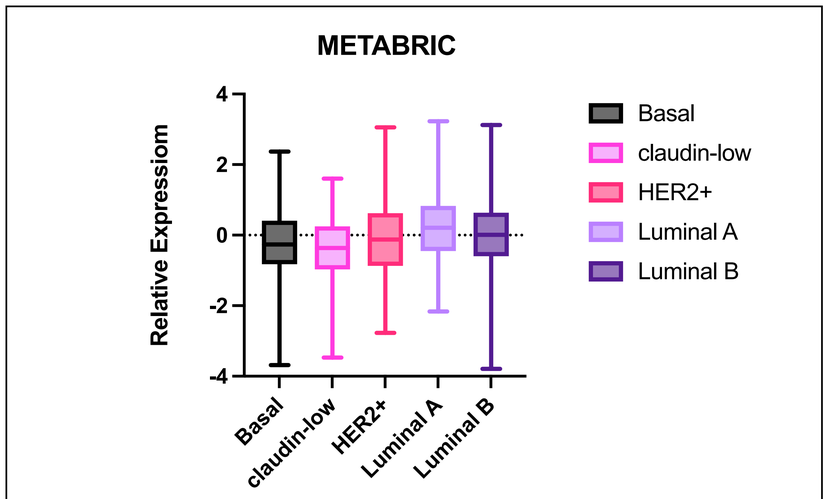

Figure 4. Similarly, clinical TCGA data base analysis of patient breast tumor samples of the METABRIC breast cancer project yielded significantly increased expression of ACK1 in luminal breast cancer subtypes ($p < 0.01$).

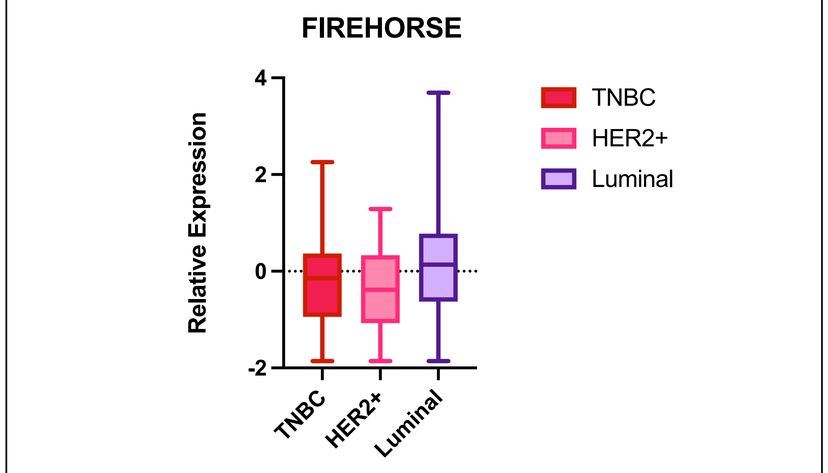

Figure 5. TCGA data base analysis of patient breast tumor samples of the FIREHORSE breast cancer project also yielded significantly increased expression of ACK1 in luminal breast cancer subtypes ($p < 0.03$).

Conclusion

- Q-RT-PCR analysis findings of **increased ACK1 expression in luminal breast cancer subtypes** were corroborated by TCGA analysis of three collective breast cancer projects.
- Further studies are needed to strongly support increased expression of ACK1 among more luminal subtypes and larger clinical data collections.
- Increased ACK1 expression in luminal subtypes could provide *novel targets/strategies for selective treatment*.

References

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This work would not have been possible without the amazing guidance and invaluable assistance of doctoral student Maninder Khosla and principal investigator Suresh K. Alahari, PhD. This research project was supported through the LSU Health Sciences Center, LSU School of Medicine.