OPEN ACCESS Freely available online

Journal of Women Health

Perspective

Comparative Transcriptomics of SSCs and FGSCs Identifies c-Kit as a Hub Gene in EGFR1 Signaling

Nima Ghasemi[1] and Hossein Azizi[2*]

[1]*Department of Applied Biotechnology and System Biology, College of Biotechnology, Amol University of Special Modern Technologies, Amol, Iran.*

[2]*Department of Stem Cells and Cancer, College of Biotechnology, Amol University of Special Modern Technologies, Amol, Iran.*

DESCRIPTION

The discovery of Female Germline Stem Cells (FGSCs) has transformed the field of reproductive biology, challenging the established notion that female mammals possess a fixed, non-renewable reserve of oocytes at birth [1]. Unlike Spermatogonial Stem Cells (SSCs), which continuously produce sperm throughout a male's reproductive life, FGSCs are believed to maintain the ability to produce eggs after birth, opening exciting possibilities for fertility restoration and regenerative therapies. Nevertheless, the molecular mechanisms that regulate FGSC maintenance and differentiation are still not well understood. One key regulator of germline development is c-Kit (KIT proto-oncogene, receptor tyrosine kinase), a membrane-bound receptor known for its essential role in primordial germ cell (PGC) survival, proliferation, and migration during embryogenesis [2]. While SSCs downregulate c-Kit expression to maintain an undifferentiated state [3]. The sustained expression of c-Kit in female germline cells suggests a distinct role in FGSCs, likely associated with their differentiation.

Keywords: Female germline stem cells; Spermatogonial stem cells; c-Kit; EGFR1 signaling pathway; Differential gene expression.

MATERIALS

To investigate the molecular differences between male and female germline stem cells, we analyzed gene expression differences using microarray data from the GSE51313 dataset, generated using the Illumina MouseWG-6 v2.0 platform, which comprises three biological replicates for both SSCs and FGSCs [4]. Data processing was performed using GEO2R, applying a log2 fold change threshold of >2 and an adjusted p-value <0.05 (Benjamini-Hochberg correction). Differentially expressed genes (DEGs) were visualized using the EnhancedVolcano package in R. We subsequently built Protein-Protein Interaction (PPI) networks utilizing the STRING database, analyzed network centrality using Cytoscape with the Centiscape plugin, and performed modularity clustering using Gephi (v0.10.1). The gene c-Kit, significantly upregulated in FGSCs, was selected as a key node for further module-based enrichment analysis.

RESULTS

Enrichment of the c-Kit module revealed the EGFR1 Signaling Pathway (WP572) as the most significantly enriched pathway (adjusted p-value = 0.00001037, combined score = 733.55), suggesting a functional interaction between c-Kit and EGFR-mediated signaling in FGSC biology. Given that EGFR signaling is critical for cell survival, proliferation, and differentiation, its enrichment highlights a potential regulatory axis supporting FGSC maintenance or early differentiation.

CONCLUSION

In summary, our combined transcriptomic and network-based analysis highlights c-Kit and EGFR1 signaling as critical elements in the molecular profile differentiating FGSCs from SSCs. These findings provide novel insights into the sex-specific regulation of germline stem cells, offering a foundation for future studies aimed at harnessing FGSCs for therapeutic applications in reproductive medicine.

REFERENCES

1. Zou, K., et al. Production of offspring from a germline stem cell line derived from neonatal ovaries. Nature Cell Biology. 2009;11(5): 631-636.
2. Chen, L., et al. Primordial germ cells and gastrointestinal stromal tumors respond distinctly to a cKit overactivating allele. Hum Mol Genet. 2013;22(2):313-327.
3. Zhang, L., et al. c-kit and its related genes in spermatogonial differentiation. Spermatogenesis. 2011;1(3):186-194.
4. Xie, W., H. Wang, and J. Wu. Similar morphological and molecular signatures shared by female and male germline stem cells. Sci Rep. 2014;4:5580.

***Correspondence to:** Hossein Azizi, Department of Stem Cells and Cancer, College of Biotechnology, Amol University of Special Modern Technologies, Amol, Iran, Tel: +98-911-220-6741; E-mail: h.azizi@ausmt.ac.ir

Received: June 09, 2025; **Manuscript No:** JWHS-25-8582; **Editor Assigned:** June 12, 2025; **PreQc No:** JWHS-25-8582(PQ); **Reviewed:** June 20, 2025; **Revised:** June 30, 2025; **Manuscript No:** JWHS-25-8582(R); **Published:** July 09, 2025

Citation: Ghasemi N, Azizi H (2025). Comparative Transcriptomics of SSCs and FGSCs Identifies c-Kit as a Hub Gene in EGFR1 Signaling. J Women's Health. 1:2.