



A brief overview of the genes involved in acute lymphoid leukemia

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Background

Acute lymphoid leukemia (ALL) is a type of cancer that causes a decrease in all three types of blood cells and often affects children under 15 years of age. ALL is divided into two categories: T_ALL and B_ALL.

Materials and Methods

I searched for articles in scientific databases such as Google Scholar and PubMed and read more than 100 articles.

Results

Genes involved in the disease can be divided into several categories:

1. Tumor suppressors like *P53*, *PTPN11* In which loss of mutations occur in them.
2. Oncogenes like *Ras*, *TAL1*, *C_myc*, that most of the proteins involved in the signaling pathway associated with cell growth and cell death, proliferation and survival, have been found to contain gain of function mutations.
3. Epigenetic regulators such as members of the histone methyl transferase family also develop inactivating mutations in ALL.
4. Transcription factors such as *ETV6* and *PAX5* are also mutated in a number of patients with ALL.
5. Genes that repair cell cycle, repair and maintain genome integrity, such as *ATM*, also cause genomic instability if they mutate, paving the way for more mutations.
6. The last group of genes that can cause acute lymphoid leukemia if mutated, Genes are the factors of genesis in which mutations have been observed with low frequency in patients.

Conclusion

- One of the genetic markers of acute lymphoid leukemia is the occurrence of translocation, which is caused by hybrid genes. These genes encode fusion proteins that have increased activity or high expression and production, like *BCR_ABL*, *RUNX1_ETV6*, *KUT2A_AFF1*.
- It should be noted that all these genes are involved in the main messaging paths such as *RAS/MAPK*, *WNT*, *JAK/STAT*.

References

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