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Topic of Research: - Interactome Based Functional Insights Into the Dynamics of Turner Syndrome

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Turner Syndrome is a condition with partial understanding of its molecular basis where a large proportion of associated candidate genes are still unknown. Here, we investigated the underlying mechanism, key genes, and aberrations caused from TS through network biology approach. The power-law distribution analysis showed that the TS network carries scale-free hierarchical fractal attributes. Through local-community-paradigm (LCP) estimation, we found that a strong LCP is also maintained which means that networks are dynamic and heterogeneous. Functional interologs in different organisms from lower to higher levels were also studied. In a comparative study, we analysed co-expression networks (WGCNA) of TS and healthy individuals using data from 182 microarray of peripheral mononuclear blood samples from the GEO repository. We then tried to validate the role of resulting key gene, BDNF. For BDNF gene, a dynamic expression range across all TS patients along with the presence of G196A polymorphism in one TS patient was found. MD simulation analysis of BDNF protein showed significant changes due to Val66Met polymorphism that might lead to functional impairment. Further study on a greater number of samples will prove this point beyond doubts or otherwise enriching the much-desired repertoire of personalized medicine.