

SYSTEMS-LEVEL ANALYSIS OF ANDROGEN IN AGING AND AGE-RELATED DISEASES: A NETWORK PHARMACOLOGY, MOLECULAR DOCKING AND MICROBIOTA-INTEGRATED APPROACH

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Aging has been associated with hormonal changes, namely in androgen signaling, which contribute to the development of age-related disorders such as Parkinson’s disease and osteoporosis[1]. Network pharmacology and molecular docking were utilized in this study combined with gut microbiota data and bioinformatics databases to study the role of principal androgens-testosterone, dihydrotestosterone, androstenedione, dehydroepiandrosterone, and its sulfate ester in processes of aging. The SwissTarget Prediction and ChEMBL were utilized to predict the androgen-related targets. Disease genes were downloaded from the GeneCards and OMIM for the aging process, Parkinson’s disease, and osteoporosis. The overlap analysis was carried out by the Venny software, and protein-protein interaction networks were cre-

ated by the STRING and Cytoscape [2, 3]. The GO and KEGG analyses revealed the enrichments in the xenobiotic metabolism, calcium signaling, androstenedione neuroactive ligand-receptor pathways[4]. Molecular docking demonstrated strong interactions between testosterone and hub targets such as CYP19A1 and IL6[5]. Integration of gut microbiota genes further had a visual impact on enrichment profiles, emphasizing the gut-brain and gut-bone axes. This comprehensive analysis highlights the major roles of androgen-responsive pathways in aging process and aging-related diseases’ development. Our findings provide a basis for further experimental evaluation and therapeutic exploration targeting endocrine and microbial regulators to alleviate age-related disorders.

Key words: network pharmacology, androgen, aging, metabolites, age-related diseases.

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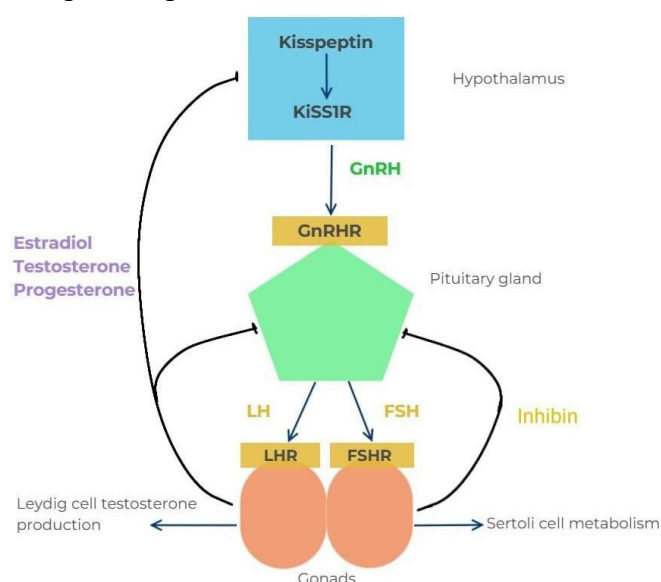


Figure 1. The HPT axis controls male reproduction through hormones: kisspeptin stimulates GnRH, which triggers LH and FSH release, affecting the testes. Testicular hormones then provide negative feedback.

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