

Genetic Variants of Hormone Receptors and Their Clinical Implications

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Introduction

Hormone receptors are essential mediators of endocrine signaling, translating hormonal messages into cellular responses that regulate growth, metabolism, reproduction, and homeostasis. Genetic variants within hormone receptor genes can significantly alter receptor structure, expression, or function, leading to a spectrum of clinical outcomes ranging from subtle physiological differences to overt endocrine disorders. Understanding these genetic alterations provides valuable insights into disease mechanisms and opens avenues for personalized medicine in endocrinology. One of the best-studied examples is the estrogen receptor (ER), encoded by the *ESR1* and *ESR2* genes. Polymorphisms and mutations in these genes influence estrogen signaling and are associated with variations in bone density, cardiovascular risk, and breast cancer susceptibility [1].

Description

Certain variants, such as the *ESR1* PvuII and XbaI polymorphisms, have been linked to osteoporosis and differential responses to hormone replacement therapy. Clinically, these insights guide risk stratification and may inform individualized treatment strategies in hormone-dependent conditions. Androgen Receptor (AR) variants also have profound clinical implications. The CAG trinucleotide repeat length within the AR gene modulates receptor sensitivity to testosterone. Shorter repeats enhance receptor activity, while longer repeats reduce it, contributing to conditions such as androgen insensitivity syndrome, male infertility, and variations in prostate cancer risk. This genetic variability explains differences in androgenic effects among individuals and serves as a basis for tailoring therapeutic interventions, including testosterone replacement therapy [2].

Similarly, variants in the thyroid hormone receptor (THR) genes can disrupt thyroid hormone action despite normal

hormone levels, a condition known as resistance to thyroid hormone (RTH). Patients with RTH may present with goiter, tachycardia, or learning difficulties, reflecting tissue-specific resistance to thyroid hormone. Genetic characterization of THR mutations has improved diagnostic precision and avoided unnecessary interventions such as inappropriate thyroid ablation or overtreatment with antithyroid drugs. In addition, glucocorticoid receptor (GR) polymorphisms influence individual sensitivity to cortisol. Variants such as N363S and ER22/23EK are associated with altered metabolic profiles, obesity, and cardiovascular risk. These genetic differences contribute to variable responses to glucocorticoid therapy, posing challenges in managing conditions like asthma, autoimmune diseases, and adrenal insufficiency. Personalized dosing strategies based on receptor genotype may improve therapeutic outcomes and reduce adverse effects [3].

The study of genetic variants in hormone receptors is entering a new era, driven by advances in genomics, molecular biology, and precision medicine. Large-scale genome-wide association studies (GWAS) and next-generation sequencing are expected to uncover novel receptor variants, broadening our understanding of their roles in endocrine disorders. Integration of these genetic insights with transcriptomics, proteomics, and metabolomics will allow a systems-level view of receptor-mediated pathways and their clinical outcomes. Pharmacogenomics represents another promising frontier, where receptor genotyping could guide individualized treatment strategies. Tailoring hormone therapies, such as selective estrogen or androgen receptor modulators, based on genetic variants may optimize efficacy while minimizing adverse effects. Similarly, identifying receptor polymorphisms that affect sensitivity to glucocorticoids, thyroid hormones, or other endocrine agents will improve dosing precision and therapeutic safety [4].

Gene editing technologies, including CRISPR-Cas9, may eventually allow correction of pathogenic receptor mutations,

offering curative strategies for rare but severe endocrine disorders such as androgen insensitivity or thyroid hormone resistance. Meanwhile, advances in artificial intelligence and predictive modeling could help clinicians integrate receptor genetic data into routine decision-making, enabling earlier diagnosis and risk prediction. In the long term, incorporating receptor variant analysis into personalized medicine frameworks has the potential to transform endocrinology. By combining genetic information with clinical, lifestyle, and environmental factors, healthcare providers can deliver more holistic and targeted care, ultimately improving outcomes for patients with hormone-related conditions [5].

Conclusion

Genetic variants of hormone receptors play a pivotal role in shaping endocrine physiology and pathology. By influencing receptor function, these variants contribute to disease susceptibility, therapeutic responses, and clinical heterogeneity among patients. Advances in genetic testing and molecular profiling are enabling more precise identification of receptor variants, laying the foundation for personalized medicine in endocrinology. Ultimately, integrating receptor genetics into clinical practice holds promise for optimizing treatment strategies and improving outcomes across a wide range of hormone-related disorders.

Acknowledgement

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Conflict of Interest

None.

References

1. Conforti A, Tüttelmann F, Alviggi C, Behre HM, Fischer R, et al. (2022). Effect of genetic variants of gonadotropins and their receptors on ovarian stimulation outcomes: a Delphi consensus. *Front Endocrinol* 12: 797365.
2. Sudo S, Kudo M, Wada SI, Sato O, Hsueh AJ, et al. (2002). Genetic and functional analyses of polymorphisms in the human FSH receptor gene. *Mol Hum Reprod* 8: 893-899.
3. Behre HM, Greb RR, Mempel A, Sonntag B, Kiesel L, et al. (2005). Significance of a common single nucleotide polymorphism in exon 10 of the Follicle-Stimulating Hormone (FSH) receptor gene for the ovarian response to FSH: a pharmacogenetic approach to controlled ovarian hyperstimulation. *Pharm Genom* 15: 451-456.
4. Alviggi C, Pettersson K, Longobardi S, Andersen CY, Conforti A, et al. (2013). A common polymorphic allele of the LH beta-subunit gene is associated with higher exogenous FSH consumption during controlled ovarian stimulation for assisted reproductive technology. *Reprod Biol Endocrinol* 11: 51.
5. Haavisto AM, Pettersson K, Bergendahl M, Virkamäki ANTTI, Huhtaniemi I (1995). Occurrence and biological properties of a common genetic variant of luteinizing hormone. *J Clin Endocrinol Metab* 80: 1257-1263.