[BIOINFO 2023]

Utilizing Mendelian Randomization to Investigate the Therapeutic Efficacy of Drugs Associated with Androgenetic Alopecia with DEEPCT

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The objective of the study was to use a deep-learning-based algorithm called Deep-learning-based Clinical Trial (DEEPCT) to simulate the therapeutic effects of Finasteride and Minoxidil on Androgenetic Alopecia (AGA). The DEEPCT algorithm consisted of a genome-wide association study (GWAS) and a genetic score calculation, followed by a Mendelian Randomization (MR) analysis. The study aimed to elucidate the causal relationships between the expression of the target genes of these drugs and the progression of AGA. Our research involved using a GWAS to identify variants linked to the expression of the target gene. To calculate the genetic score, we summed up the weights of significant alleles from GWAS (p-value <0.05). We aimed to establish a cause-and-effect relationship between the expression of Finasteride's and Minoxidil's target genes and cases of AGA. The expression of target genes was used as the exposure to emphasize significant causality. SRD5A2, a target of Finasteride, showed a robust causative connection with AGA progression. The SRD5A2 genetic score for lowering transcriptome level by 1SD was associated with a decrease of 23% (odds ratio) in the risk of AGA event (OR [95% CI] = 0.77 [0.69, 0.86]; p-value < 0.001). Similarly, REN, Minoxidil's target gene, exhibited a causal relationship with AGA progression. The REN genetic score for lowering transcriptome level by 1SD was associated with a decrease of 15% (odds ratio) in the risk of AGA event (OR [95% CI] = 0.72 [0.77, 0.99]; p-value < 0.05). Through the implementation of the DEEPCT algorithm, this study uncovered a significant causal relationship between both Finasteride and Minoxidil and the progression of AGA. In addition to supporting further studies for more in-depth therapeutic exploration of AGA, this study presents the possibility of drug repurposing and utilizing side effects of DEEPCT.