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Gut microbiome alterations in dehydroepiandrosterone and high-fat diet-induced PCOS in rats: A shift from beneficial to harmful bacterial taxa

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Polycystic ovary syndrome (PCOS), a common endocrine disorder in women, involves complex interactions between hormonal imbalances, metabolic dysfunction, and gut microbiome dysbiosis. While hyperandrogenism and high-fat diets independently alter gut microbiota, their combined effects in PCOS remain unclear, limiting development of microbiome-targeted interventions. This study investigated how high-fat diet (HFD) and dehydroepiandrosterone (DHEA) affect gut microbiome and metabolic health in a PCOS rat model. We used immunoassays and other colorimetric assays to estimate various hormonal levels and metabolic parameters. Real time PCR was performed to quantify the relative abundance of the bacterial species using genus specific 16S rDNA primers and universal primer sequence was used as internal control. We found that DHEA alone reduced microbial diversity, while HFD plus DHEA exacerbated dysbiosis, increasing pathogenic bacteria linked to systemic inflammation. We also performed correlation analysis and it highlighted the significant impact of dietary and hormonal factors on PCOS pathophysiology. The comparison of gut microbiome composition between high-fat diet plus DHEA-fed PCOS rats and DHEA-only treated rats highlights the significant impact of diet on the gut microbiome and its subsequent influence on metabolic health in PCOS.

Keywords: Gut dysbiosis, Diet, Animal model