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The intestinal estrobolome metabolic cross-talk with ER positive breast cancer

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Investigations in intestinal microbiome have revealed interconnected networks of interactions and feedback loops between gut bacteria and all critical mechanisms in the body via endocrinology. The perturbation of gut biota has been associated with the development of inflammatory, autoimmune and malignant diseases. The recently discovered connection of the gut biome to steroid hormone control and reception now termed the estrobolome is cutting-edge information. There are unique colonies in the gut that have the ability to metabolize certain estrogens (other groups of microbiota can handle other steroid hormones) back into circulation. The question becomes: which estrogens? Bacterial microbiome interactions with steroid hormones can lead to negative feedback loops in over 9,000 gene pathways and the expression of receptors and serum sex steroid levels that change over the female lifecycle. This decline, due to aging, which results in increased risk of cancer, provokes compensatory response from the estrobolome. Studies have shown bi-directional interactions between the amount of endogenously produced estrogen and the percentage re-conjugated back into circulation by various groups of gut biota. Studies have even shown changes in the estrobolome in response to monthly cycles. Knowing that these menstrual cycles disappear at mid-life, we present the hypothesis that the reinstatement of accurate exogenous bio-mimetic HRT and timing will restore the bi-directional microbiome crosstalk and interactions at the genomic level, lowering these overall risk factors for the diseases of aging.

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