

Lowbush blueberries, *Vaccinium angustifolium*, modulate the functional potential of nutrient utilization and DNA maintenance mechanisms in the rat proximal colon microbiota

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ABSTRACT:

Background: The core gut microbiota encodes for a metabolic capacity that often surpasses the metabolic potential of its host. Lowbush wild blueberries (LWB) are a rich source of bioactive compounds, and the gut microbiota is an important modulator of their activity. The objective of this research is to study the effect of a diet enriched with LWB on the gastrointestinal microbiota's metabolic potential.

Methods: Nine three-week-old male Sprague Dawley rats were randomly assigned to two groups. The control group ($N=4$) was placed on the AIN93 diet, and the treatment group ($N=5$) was fed the same diet with 8% (w/w) LWB powder substituting for dextrose. The animals consumed the diets for six weeks, after which they were sacrificed. Functional profiles and metabolic potential of the colon microbiota in response to diet were analyzed using deep whole genome sequencing (WGS).

Results: Proteins predicted from WGS DNA sequences were assigned to 3,746 COG, 5,577 KEGG, and 4,474 Pfam families. Statistical comparisons of the protein-coding genes revealed significant changes in 25 Gene Ontology (GO), 186 KEGG, and 20 Pfam protein families representing 2.1%, 3.3%, and 0.02% of all hits identified, respectively. Overall, the combined inquiries into these databases represented an emphasis on membrane trafficking, DNA regulation, modification and repair, and nutrient metabolism. Protein families that significantly increased by the enrichment of LWBs were involved with amino acid metabolism, 2,4-dienoyl-CoA reductase, metal ion binding, glutamate synthase, REDOX homeostasis, and aryl transferases. In

contrast, protein families involved with integrase/recombinase, reverse transcriptase, and transposon/transposase were at a lower abundance.

Conclusions: The results from this study reflect the potential impact that LWBs have on the functional repertoire of bacterial communities in the proximal colon. The results demonstrate a higher potential for the metabolism of amino acids and a lower potential for horizontal integration of plasmids and lower phage/transposon activity in the LWB diet, suggesting that the genome at the time of sampling was more stable. This study helps unravel diverse mechanisms of microbial adaptation to LWBs in the diet of mammals and can provide guidance in optimizing functional diets.