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Summary

GUT MICROBIOTA IS ASSOCIATED WITH PERSISTENCE OF LONGER-TERM VACCINE IMMUNOGENICITY AFTER TWO DOSES OF BNT162B2

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UEG Week Copenhagen 2023 Poster

October 15, 2023

A prospective cohort study of 242 BNT162b2 recipients identified baseline gut microbiota composition associated with sustained neutralising antibody response at day 180, with specific bacterial species predicting persistent high vaccine immunogenicity independent of clinical factors.

KEY POINTS

- Among 242 adult BNT162b2 two-dose recipients, 95.9% remained seropositive at day 180, with 25.2% classified as persistent high-responders (median NAb 205.4 AU/mL) and 74.8% as low-responders (median NAb 40.9 AU/mL) based on 75th percentile cutoff.
- Baseline stool samples showed Ruminococcus bicirculans, Parasutterella excrementihominis, and Streptococcus salivarius were more abundant in high-responders, while Bacteroides thetaiotaomicron was less abundant, with no difference in overall alpha or beta diversity.
- Multivariable analysis adjusting for age, sex, diabetes mellitus, and overweight/obesity found R. bicirculans (aOR 1.87), P. excrementihominis (aOR 2.20), and S. salivarius (aOR 2.09) were associated with persistent high response, while clinical factors were not.
- R. bicirculans positively correlated with metabolic pathways including L-cysteine biosynthesis and L-isoleucine biosynthesis I that benefit immune function, and validation by qPCR is planned.

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