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MOBILITY AND PHYSICAL FUNCTION IN OLDER ADULTS

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ASSOCIATIONS BETWEEN WALKING SPEED AND GUT MICROBIOME DIVERSITY IN OLDER MEN FROM THE MROS STUDY

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While gut dysbiosis has been linked to frailty in aging, its association with early mobility impairments is unclear. Here, our primary goal was to determine the cross-sectional associations between walking speed and gut microbiome in 740 older men (84±4y) from MrOS with available stool samples and 400m walking speed measured in 2014–16. We also analyzed the retrospective longitudinal associations between changes in 6-meter walking speed (from 2005-06 to 2014-16) and gut microbiome composition among participants with available data (702/740). The gut microbiome composition was determined by 16S sequencing (DADA2 and SILVA). We examined diversity, taxa abundance (by ANCOM-BC), and performed network analysis (by NetCoMi) to uncover microbial communities interactions by walking speed levels. Higher walking speed (m/s) was associated with greater microbiome Shannon α-diversity (R=0.11; P=0.004). Decline in walking speed was associated with lower Shannon α-diversity (R=0.07; P=0.054). Faster walking speed and less decline in walking speed were associated with higher abundance of genus-level bacteria that produce short-chain fatty acids, and possess anti-inflammatory properties, including Paraprevotella, Fusicatenibacter, and Alistipes, adjusting for age, race, site, education, health, marital status, weight, height, physical activity, batch, medications, energy, and fiber intake (P<0.05). The gut microbiome networks of participants in the first vs. last quartile of walking speed (≤0.9 vs. ≥1.2 m/s) exhibited distinct characteristics, including different cluster numbers, hubs, and centrality measures (P<0.05). Faster walking speed and its less decline were associated with higher gut microbiome diversity, suggesting potential role of microbiome in preserving mobility in aging.
We examined cross-sectional associations of mtDNAcn estimated by whole genome sequencing with gait speed and grip strength in the Baltimore Longitudinal Study of Aging (BLSA). First, we estimated mtDNAcn in 688 participants using single-nucleotide polymorphism genotyping data. The sex-stratified associations of mtDNAcn with gait speed were compared using linear regression, with age, sex, and race as co-variates. In a sex-stratified analysis, we tested the mtDNAcn-by-sex interaction using linear regression in a model adjusted for age, sex, and race. We also tested the mtDNAcn-by-sex interaction using logistic regression in a model adjusted for age, sex, race, and autosomal coverage. Specifically, in men, we found a significant mtDNAcn-by-sex interaction for gait speed (β = −0.23, p = 0.02). In men, the odds of reporting slow walking pace increased with mtDNAcn (β = −0.129, p = 0.002). In women, there was a significant sex-by-mtDNAcn interaction for slow walking pace (β = -0.173, p = 0.007). The odds of reporting slow walking pace increased with mtDNAcn (β = −0.253, p = 0.0003). The interaction for grip strength was stronger in men than in women (both p > 0.05). There was a significant sex-by-mtDNAcn interaction for grip strength (β = −0.23, p = 0.01). The odds of reporting weak grip strength increased with mtDNAcn (β = −0.22, p = 0.04). There was no significant sex-by-mtDNAcn interaction for gait speed (β = 0.0, p = 0.22). There was no significant sex-by-mtDNAcn interaction for grip strength (β = 0.0, p = 0.22). We additionally tested sex differences in handgrip strength measured using a hand dynamometer in UK Biobank. Handgrip strength was measured using a hand dynamometer. We additionally tested sex differences in handgrip strength measured using a hand dynamometer in UK Biobank. Handgrip strength was measured using a hand dynamometer.

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