Longitudinal association of green tea consumption and cognitive function after 16 years

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Background : Mild cognitive impairment (MCI) is a precursor to dementia and needs to be prevented. Although previous studies reported the association between green tea consumption and subsequent cognitive function, its domain-specific associations remain unclear.

Methods : This longitudinal study followed a subset of 270 retired participants from the Aichi Worker's Cohort Study (215 male and 55 female) who are 60-79 years of age in 2018. In 2002 participants were asked about their green tea intake which was categorized as <1, 1, or ≥2 cups/day. In 2018, cognitive status was assessed using the Japanese version of the Montreal Cognitive Assessment (MoCA-J) which evaluates seven cognitive domains, including visuospatial/executive function, naming, attention, language, abstraction, delayed recall, and orientation. MCI was defined as a MoCA-J score ≤25. Poisson regression was used to estimate multivariable-adjusted risk ratios (RRs) for MCI. Linear regression was applied to MoCA-J total and domain scores. The models were progressively adjusted for age, sex, education, smoking, alcohol use, physical activity, sleep duration, body mass index, hypertension, diabetes, and use of hyperlipidemia. All analyses were conducted with Python.

Results : MCI was present among nearly half (47.3%) of the participants in 2018. A significant inverse association was observed between green tea consumption and proportion of MCI (67.2%, 56.8%, and 40.6% for <1, 1, and ≥2 cups/day, respectively). Participants drinking ≥2 cups/day had significantly lower risk of MCI (RR 0.58; 95% CI: 0.37, 0.90) compared to those drinking <1 cup/day. Those consuming ≥2 cups/day were associated with high MoCA-J total scores (β -coef 1.17; 95% CI: 0.34, 2.00) and with high delayed recall scores (β -coef 0.46; 95% CI: 0.01, 0.92).

Conclusions : The study demonstrates longitudinal association between green tea consumption in middle age and the risk of MCI and delayed recall domain in later life.

Trends in prevalence of vitamin D deficiency over a 10-year period in Japan: The ROAD study

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Purpose : To clarify the 10-year trend in the prevalence of vitamin D (VD) deficiency.

Methods : In the baseline survey of the population-based cohort entitled Research on Osteoarthritis/Osteoporosis Against Disability (ROAD) study conducted between 2005 and 2007, serum 25-hydroxyvitamin D (25D) levels were measured in 1,683 participants (595 men and 1,088 women). Ten years later, in the fourth survey, 1,902 participants (636 men and 1,266 women) underwent the same examinations as in the baseline survey. Serum 25D levels in the baseline and fourth surveys were compared to examine temporal trends. VD deficiency was defined as a serum 25D level <20 ng/mL.

Results : The mean serum 25D levels were 23.3 ng/mL at baseline and 25.1 ng/mL in the fourth survey, showing a significant increase (baseline vs. fourth survey, $p < 0.0001$). The prevalence of VD deficiency was 29.5% at baseline and 21.6% in the fourth survey, demonstrating a significant decrease over the 10-year period ($p < 0.001$).

Conclusion : In this population-based cohort observed over 10 years, the prevalence of VD deficiency decreased significantly. This favorable change may contribute to a future reduction in the incidence of osteoporosis and osteoporotic fractures.

Metabolic profiling of familial hypercholesteremia related genetic variants in Hong Kong's "Children of 1997" birth cohort

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Background : Familial hypercholesterolemia (FH) is a genetic disorder, characterized by early life elevated low-density lipoprotein cholesterol (LDL-C), which leads to premature cardiovascular disease. However, few studies explored whether different FH gene mutations have distinctive perturbation in lipid subtractions and other metabolic markers in late adolescent, which helps inform disease mechanism and targets of screening.

Methods : We identified functional variant of FH by screening for corresponding genetic variants in FH related gene region (LDLR, APOB, PCSK9, and LDLRAP1) based on LDL-C GWAS summary statistics data from GLGC (East Asian, n=146492), with validation using the Hong Kong's "Children of 1997" birth cohort (n=3443). In the birth cohort, externally weighted overall and gene specific polygenic risk scores (PRS) were constructed as exposures. Outcomes included 250 metabolic markers measured by NMR spectroscopy. Associations of PRS, in standard deviation (SD), with metabolic markers were assessed using multivariable linear regression, correcting for multiple comparison using Bonferroni correction.

Results : Higher overall PRS was associated with increment in majority of the cholesterols except HDL-C, such as LDL-C and apolipoprotein B (ApoB). The pattern with lipids were similar across APOB and LDLR PRS (e.g., LDLR PRS β : 0.072 SD for LDL-C and 0.074 SD for ApoB, and APOB PRS β : 0.072 SD for LDL-C and 0.081 SD for ApoB). Whilst PCSK9 and LDLRAP1 PRS also showed similar pattern, these associations did not survive multiple comparison.

Conclusion : Our study suggested the impact of FH related mutations in lipid traits is already evident in late adolescents, such as LDL-C and ApoB, which the latter is an emerging cause of cardiovascular disease risk. Effects appear more evident for APOB and LDLR. These findings will help inform screening for genetic and lipid targets for downstream management to reduce elevated cardiovascular risk amongst people with FH.

Identification of nutrient–proteome relationships with TG:HDL-C: UKB and YMoC study

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Background : Plasma proteomics captures Insulin Resistance (IR)-related pathways, where the triglycerides to high-density lipoprotein cholesterol ratio (TG/HDL) serves as a pragmatic surrogate aligned with clamp-derived sensitivity.

Objective : Identify TG/HDL-associated plasma proteins with replication, and characterize their nutrient correlates.

Methods : We analyzed baseline data from the UK Biobank (UKB; discovery; n=37,997; age 56.8 ± 8.2 years; female 53.9%) and the Yamanashi multi-omics cohort (YMoC; validation; n=162; age 54.2 ± 7.3 years; female 40.1%). Participants with diagnosed diabetes were excluded. The outcome was TG/HDL. Proteins were quality-controlled, log2 transformation, and z-standardization. In UKB, covariate-adjusted linear regressions (age, sex, BMI, smoking, alcohol, physical activity, lipid-lowering drugs) tested associations between each protein and TG/HDL, with significance determined by Benjamini–Hochberg FDR control ($q<0.05$). Replication required concordant direction and $q<0.05$ in YMoC. For replicated proteins, partial Spearman correlations with food frequency questionnaire (FFQ)-derived nutrients were calculated after energy adjustment by the residual method, with FDR controlled at 0.1.

Results : Of 2,919 proteins assayed, 143 showed concordant associations with TG/HDL in both UKB and YMoC (e.g., CHI3L1, GGT1; $q<0.05$ respectively). In particular, CHI3L1 correlated with saturated fatty acid intake ($r=0.26$), and GGT1 correlated with ethanol intake ($r=0.30$).

Discussion : These nutrient–protein links are consistent with prior evidence implicating CHI3L1 in liver fibrosis and GGT1 in incident type 2 diabetes risk, suggesting that ethanol and saturated fatty acid intake may play a role in diabetes risk through IR-related proteomic alterations.

Conclusion : We identified candidate nutrient–protein pairs along the diet–proteome–IR axis. Intervention studies and external validation are needed to strengthen causal inference.

Cross-cohort profiling of BMI-associated plasma proteome and diet in the UKB and the YMoC

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Background : Obesity increases the risk of type 2 diabetes and cardiovascular disease. Plasma proteomics can capture metabolic, inflammatory, and hormonal pathways associated with BMI, and diet is a key contributor to BMI-related proteomic variation.

Objective : To identify BMI–protein associations consistently observed across the UK Biobank (UKB) and the Yamanashi Multi-Omics Cohort (YMoC), and to evaluate protein–diet associations using food-frequency questionnaire (FFQ).

Methods : In UKB, associations between BMI and each of 2,919 proteins were examined using linear models adjusted for age, sex, smoking, activity, and income. Replication required concordant effect direction and $q<0.05$ in YMoC after BH-FDR. FFQ nutrients were energy-adjusted by the residual method. Within the replicated protein set, partial Spearman correlations between nutrients and proteins were estimated with adjustment for age, sex, smoking, physical activity, and income. FDR was controlled at $q<0.10$.

Results : Of 2,919 proteins, 88 showed concordant associations with BMI in UKB and YMoC (both $q<0.05$). Within the replicated set, mushroom intake was inversely associated with KRT18 ($r=-0.320$, $q=0.001$), GSTA1 ($r=-0.235$, $q=0.035$), and GSTA3 ($r=-0.219$, $q=0.052$). Alcohol (ethanol) intake was positively associated with GGT1 ($r=0.215$, $q=0.063$) and inversely associated with CCN3 ($r=-0.249$, $q=0.031$).

Discussion : The observed inverse associations of mushroom intake with KRT18 and GSTA1/3 suggest reductions in hepatocyte injury and oxidative or xenobiotic stress. In contrast, the alcohol-related pattern—higher GGT1 and lower CCN3—aligns with mechanisms of metabolic stress and early tissue remodeling.

Conclusions : Across two cohorts, a subset of BMI-associated plasma proteins was consistently identified, with dietary associations observed in the replication cohort. Mechanistic and interventional studies are needed to test causality and assess clinical relevance.