P133-T | Ultra-processed food consumption and the incidence of depression in a mediterranean cohort: the seguimiento universidad de navarra project

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Background: Some available evidence suggests that high consumption of ultra-processed foods (UPFs) is associated with a higher risk of obesity, hypertension and metabolic syndrome. A growing body of research on the link between depression and other non-communicable diseases suggests that UPFs might also be associated with depression, which is among the leading causes of ill health and disability worldwide.

Material and methods: We prospectively evaluated the relationship between UPF consumption and the risk of depression in the SUN (Seguimiento Universidad de Navarra) project, a dynamic, prospective and multipurpose Spanish cohort. We included 14 907 Spanish university graduates initially free of depression, who were followed for a mean of 10·2 years. Consumption of UPFs (defined as food and drink products ready to eat, drink, or heat and made predominantly or entirely from processed items extracted or refined from whole foods or synthesized in the laboratory) was assessed at baseline through a validated semi-quantitative 136-item food-frequency questionnaire. Participants were classified as incident cases of depression if they reported a physician diagnosis or the use of antidepressant medication in at least one of the follow-up questionnaires.

Cox proportional hazards models were used to estimate adjusted hazard ratios (HRs) and 95% confidence intervals (CIs) for depression incidence.

Results: During follow-up, 608 incident cases of medically-diagnosed depression were identified. Participants in the highest quintile of UPF consumption had a higher risk of developing depression (adjusted HR [95% CI] = 1·55 [1·17–2·06]; P for trend = 0·002) than those in the lowest quintile after adjusting for potential confounders.

Conclusions: In a large prospective Spanish cohort, a significant positive association between UPF consumption and depression risk was observed among middle-aged adult university graduates. Findings were in line with expectations and previous results on dietary habits and risk of depression in the SUN project.

P134-T | Changes in gene expression of selected genes related with weight loss and cardiovascular risk after intervention with an energy-restricted Mediterranean diet and physical activity in the PREDIMED PLUS-Valencia study. Modulation by genetic variants

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Background: Mediterranean diet can produce favourable changes in the expression of genes related to cardiovascular risk. Our objective was to analyze if additional weight loss can increase the favourable changes in the expression of selected genes related to obesity, oxidative stress and diabetes. We also tested whether polymorphisms in the selected genes modulate gene expression.

Methods: We analyzed a subsample of participants (men and women aged 55–75 years) in the PREDIMED PLUS-Valencia randomized controlled trial. We selected 25 subjects in the intervention group (intensive intervention with energy restricted Mediterranean diet plus physical activity) and 25 subjects from the control group (Mediterranean diet advice). Weight was measured at baseline and after 6-months (M) intervention. RNA was isolated at baseline and 6M from blood. Gene expression was validated by individual RT-qPCR and fold change between control group and intervention group was calculated using the 2-ΔΔCt method. Selected genes were PER1 and CLOCK (circadian rhythm); CAT and GPX3 (oxidative stress); DDIT4 (DNA repair) and ARRDC3 (diabetes). We also analyzed polymorphisms in the selected genes genotyped by the Illumina Human OmniExpress Array.

Results: There were significant differences in weight loss at 6M between the intensive intervention and the control group (−5·06 and −0·62 kg, respectively; $P < 0·01$). We detected an increase in gene expression at 6M for the analyzed genes, but this increase was lower and not statistically significant in the control group separately. However, in the intervention group, we detected statistically significant changes in gene expression in a multivariate model for