GENETICS, VITAMINS

GENETICS OF VITAMIN D

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A new GWAS of vitamin D serum level reports two new loci as sample size could be increased from 16K to 79K. While the previous GWAS hits had a reasonable biological function (GC transport protein, DHCR7 converting to cholesterol, CYP2R1 to calcidiol and CYP24A1 degradation) the new loci look more like statistical artifacts.
The authors tried some kind of dose effect estimates

SNP-by-diet interaction. We performed a genome-wide association screening of circulating 25-hydroxyvitamin D while accounting for potential interaction effect between SNP and dietary vitamin D intake. Our tests incorporating gene-diet interaction were based on the following model:

$$\ln(25(\mathrm{OH})D) = \beta_0 + \beta_1 \times G + \beta_2 \times E + \beta_3 \times G \times E + \beta_Z \times Z$$

where G is a SNP that was coded additively, E is the raw vitamin D intake, measured on a continuous scale. The parameters β_0, β_1, β_2, and β_3 are the intercept, the main effect of SNP, the main effect of dietary vitamin D intake, and the interaction effect between G and E. The model also included the same

where SNP effects on serum level became slightly weaker (which makes sense as diet is a clear environmental factor).

Unfortunately there are no statistical model that look into seasonal effect, although this is being the most important factor in vitamin D epidemiology. The authors correctly describe in their discussion that a

study conducted by Karohl et al. with 310 monozygotic and 200 dizygotic male twins observed a heritability of 70% during winter, whereas in summer, serum 25-hydroxyvitamin D concentrations appeared to be entirely determined by non-genetic factors (heritability: 0%). Comparable estimates were also identified in a slightly larger study conducted by Mills et al. (winter: 90% vs. summer: 56%). Consistent with season dependency, sex differences were also observed (males: 86% vs. females: 17%)1

Given these facts I think it is not sufficient to included just month of examination.

Association analysis. Genome-wide analyses were performed within each cohort according to a uniform analysis plan. We fit additive genetic models using linear regression on natural-log transformed 25-hydroxyvitamin D, and adjusted the models for month of sample collection (12 categories), age, sex, and body mass index, and principal components capturing genetic ancestry. Further adjustments included cohort-specific variables, such as geographical location and assay batch,

I know from at least two datasets that were obtained over more than one and a half year, that monthly effects can not be pooled. There was up to 20% variation between same months. This may be particular true this year where the Guardian wrote that this winter is one of darkest ever for parts of Europe.

the previous low of 13 hours, dating back to 1948, could well be beaten, Frédéric Decker of Météo News told La Voix du Nord this week. “The forecast isn’t looking too great,” he said. “The weather’s going to stay pretty damp and dull.” Rouen in Normandy had an even more depressing first half of the month, with just 2.5 hours of sunshine compared with a full-month norm of 58.6, Météo France said, while Paris’s 10 hours were also a far cry from the 62.5 hours the capital usually averages in January.

A winter only analysis could therefore shed more light into vitamin D genetics.