Erratum to: Genome-wide association and HLA fine-mapping studies identify risk loci and genetic pathways underlying allergic rhinitis (Nature Genetics, (2018), 50, 8, (1072-1080), 10.1038/s41588-018-0157-1)
In the version of this article initially published, in Fig. 3, the y-axis numbering did not match the log scale indicated in the axis label. The error has been corrected in the HTML and PDF version of the article.
Aberrant intestinal microbiota in individuals with prediabetes

Aims/hypothesis: Individuals with type 2 diabetes have aberrant intestinal microbiota. However, recent studies suggest that metformin alters the composition and functional potential of gut microbiota, thereby interfering with the diabetes-related microbial signatures. We tested whether specific gut microbiota profiles are associated with prediabetes (defined as fasting plasma glucose of 6.1–7.0 mmol/l or HbA1c of 42–48 mmol/mol [6.0–6.5%]) and a range of clinical biomarkers of poor metabolic health. Methods: In the present case–control study, we analysed the gut microbiota of 134 Danish adults with prediabetes, overweight, insulin resistance, dyslipidaemia and low-grade inflammation and 134 age- and sex-matched individuals with normal glucose regulation. Results: We found that five bacterial genera and 36 operational taxonomic units (OTUs) were differentially abundant between individuals with prediabetes and those with normal glucose regulation. At the genus level, the abundance of Clostridium was decreased (mean log2 fold change −0.64 (SEM 0.23), p_adj = 0.0497), whereas the abundances of Dorea, Ruminococcus, Sutterella and Streptococcus were increased (mean log2 fold change 0.51 (SEM 0.12), 0.51 (SEM 0.11), 0.51 (SEM 0.21), 0.60 (SEM 0.11), 0.51 (SEM 0.11), 0.60 (SEM 0.21), and 0.92 (SEM 0.21), p_adj = 4 × 10^{-44} respectively). The two OTUs that differed the most were a member of the order Clostridiales (OTU 146556) and Akkermansia muciniphila, which both displayed lower abundance among individuals with prediabetes (mean log2 fold change −1.74 (SEM 0.41), p_adj = 2 × 10^{-44} and −1.65 (SEM 0.34), p_adj = 4 × 10^{-44}, respectively). Faecal transfer from donors with prediabetes or screen-detected, drug-naive type 2 diabetes to germfree Swiss Webster or conventional C57BL/6 J mice did not induce impaired glucose regulation in recipient mice. Conclusions/interpretation: Collectively, our data show that individuals with prediabetes have aberrant intestinal microbiota characterised by a decreased abundance of the genus Clostridium and the mucin-degrading bacterium A. muciniphila. Our findings are comparable to observations in overt chronic diseases characterised by low-grade inflammation.

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Investigating the causal effect of smoking on hay fever and asthma: a Mendelian randomization meta-analysis in the CARTA consortium

Observational studies on smoking and risk of hay fever and asthma have shown inconsistent results. However, observational studies may be biased by confounding and reverse causation. Mendelian randomization uses genetic variants as markers of exposures to examine causal effects. We examined the causal effect of smoking on hay fever and asthma by using the smoking-associated single nucleotide polymorphism (SNP) rs16969968/rs1051730. We included 231,020 participants from 22 population-based studies. Observational analyses showed that current vs never smokers had lower risk of hay fever (odds ratio (OR) = 0.68, 95% confidence interval (CI): 0.61, 0.76; P <0.001) and allergic sensitization (OR = 0.74, 95% CI: 0.64, 0.86; P <0.001), but similar asthma risk (OR = 1.00, 95% CI: 0.91, 1.09; P = 0.967). Mendelian randomization analyses in current smokers showed a slightly lower risk of hay fever (OR = 0.958, 95% CI: 0.920, 0.998; P = 0.041), a lower risk of allergic sensitization (OR = 0.92, 95% CI: 0.84, 1.02; P = 0.117), but higher risk of asthma (OR = 1.06, 95% CI: 1.01, 1.11; P = 0.020) per smoking-increasing allele. Our results suggest that smoking may be causally related to a higher risk of asthma and a slightly lower risk of hay fever. However, the adverse events associated with smoking limit its clinical significance.
Readout for intersatellite laser interferometry: Measuring low frequency phase fluctuations of high-frequency signals with microradian precision

Precision phase readout of optical beat note signals is one of the core techniques required for inter-satellite laser interferometry. Future space based gravitational wave detectors like eLISA require such a readout over a wide range of MHz frequencies, due to orbit induced Doppler shifts, with a precision in the order of µ rad/√Hz at frequencies between 0.1 mHz and 1 Hz. In this paper, we present phase readout systems, so-called phasemeters, that are able to achieve such precisions and we discuss various means that have been employed to reduce noise in the analogue circuit domain and during digitisation. We also discuss the influence of some non-linear noise sources in the analogue domain of such phasemeters. And finally, we present the performance that was achieved during testing of the elegant breadboard model of the LISA phasemeter, which was developed in the scope of a European Space Agency technology development activity. (C) 2015 AIP Publishing LLC.

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Effects of temperature on domain-growth kinetics of fourfold-degenerate (2×1) ordering in Ising models

Computer-simulation techniques are used to study the domain-growth kinetics of (2×1) ordering in a two-dimensional Ising model with nonconserved order parameter and with variable ratio $\alpha$ of next-nearest- and nearest-neighbor interactions. At zero temperature, persistent growth characterized by the classical growth exponent $n=1/2$ is found for $\alpha=1$, whereas the domain boundaries become pinned and the growth stops for $\alpha

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