There were 13 separate SNP effects (three at ABCG2, three at SLC2A9, two at SLC22A11/A12 and one at each of ADH1B, GCKR, MLXIPL, CNBD1, PDX1). Conditional analysis at each of the ABCG2 and SLC2A9 loci, adjusting the logistic regression analysis by the lead SNPs, rs2231142 and rs16890979, respectively (figure 1), revealed evidence for an independent signal at SLC2A9 approaching genome-wide significance, but not at ABCG2. At ABCG2, of the seven variants reported as independent signals by Sandoval-Plata et al, only rs13120400 retained nominal significance (p<0.01) after conditioning on rs2231142, with p value reducing from 1.3×10⁻¹² to 8.8×10⁻⁸. This variant maps within ABCG2 (~19 kb from rs2231142). Conversely, rs2231142 retained strong evidence for association with gout (p<1×10⁻⁹⁰) after conditioning by each of the seven other ABCG2 locus variants reported by Sandoval-Plata et al (not shown). We therefore conclude that there are no genome-wide significant independent effects associated with gout using asymptomatic controls with hyperuricaemia at the genes MEPE, PPM1K-DT and LOC105377323 within the ABCG2 locus.

Repeating the LD clumping using a more stringent threshold of r²<0.01, we detected 11 separate SNP effects: two at ABCG2 (rs2231142 and rs148356273), three at SLC2A9 (rs16890979, rs3796834—r²=0.78 with rs16891234 reported by Sandoval-Plata et al - and rs6833292), one at GCKR (rs780093—r²=1.00 with rs1260326 reported by Sandoval-Plata et al), one at ADH1B (rs1229984, reported by Sandoval-Plata et al), one at SLC22A11 (rs7943154—r²=0.93 with rs2078267 reported by Sandoval-Plata et al), one at PDX1 (rs182200427, not reported by Sandoval-Plata et al), one at MLXIPL (rs7805304, not reported by Sandoval-Plata et al), and one downstream from CNBD1 (rs181604403, not reported by Sandoval-Plata et al).
We detected all genetic loci detected by Sandoval-Plata et al and three additional loci (PDX1, MLXIPL, CNBD1).

Finally, we note that the Sandoval-Plata et al study reports three apparently novel genes from their GWAS comparing gout with normouricaemic controls (<6.0 mg/dL)—MTX1, PRSS16 and APSB1. However, both MTX1 and APSB1 are within established serum urate GWAS loci (‘TRIM46’ and ‘OVOL1’, respectively). It is important also when determining candidate causal genes not to assume that the closest gene is necessarily causal. At these loci, colocalisation of GWAS signals with expression quantitative trait loci implicates MUC1, GBAP1 and FAM189B genes as candidate causal genes at the TRIM46 locus and OVOL1-AS1 at the OVOL1 locus.6

Riku Takei, 1 Nicholas A Sumpter, 1 Amanda Phipps-Green, 2 Murray Cadzow, 2 Ruth K Topless, 2 Richard J Reynolds, 1 Tony R Merriman 1

1 Division of Clinical Immunology and Rheumatology, The University of Alabama at Birmingham, Birmingham, Alabama, USA
2 Department of Biochemistry, University of Otago, Dunedin, New Zealand

Correspondence to Dr Tony R Merriman, Division of Clinical Immunology and Rheumatology, The University of Alabama at Birmingham, Birmingham AL 35294, USA: trmerriman@uabmc.edu

Twitter Tony R Merriman @tonymerriman2

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