Candidate gene analysis supports a role for polymorphisms at *TCF7L2* as risk factors for type 2 diabetes in Sudan

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Background

Type 2 diabetes (T2D) is emerging as an important international health problem. The International Diabetes Federation (IDF) report that 382 million people worldwide are living with diabetes, with a further 316 million with impaired glucose tolerance and therefore at high risk from the disease [1]. Evidence published in the IDF Diabetes Atlas [1] disproves the misconception that diabetes is a disease of the wealthy. Indeed, more than 80 % of people with diabetes live in low and middle-income countries, with emerging hotspots including countries in the Middle East and Sub-Saharan Africa [1]. In Sudan, Awad et al. [2] reported a prevalence of 3.4 % and considered diabetes as the commonest cause of hospital admission and morbidity due to a non- communicable disease. The highest prevalence is reported in northern Sudan [3] and the lowest in the western desert regions [4], with data reported in the IDF Diabetes Atlas [1] suggesting prevalence varying from 6-10 % and 60 % of deaths due to diabetes occurring in people under 60 years of age.

Since the introduction of genome-wide association studies (GWAS) a large number of genes have been shown to be associated with T2D at genome-wide significance (generally accepted to be $P \leq 5\text{x}10^{-8}$ [5]), including many that have been shown to have effects across multiple ethnicities [6–19] and in trans-ancestry meta-analysis of large-scale GWAS [20]. Only a few studies have looked at these genes in Arab [16, 18, 19, 21–23] or Sub-Saharan African populations [8, 17]. In this study we looked for association between 14 single nucleotide polymorphisms (SNPs) in 7 of the top GWAS genes (*TCF7L2*, *CDKAL1*, *HHEX*, *IGF2BP2*, *KCNJ11*, *PPARG* and *CAPN10*) and risk of T2D in Sudan.

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