Significant genetic correlations among pain at different body sites – evidence from the UK Biobank

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Background

Pain is a global public health priority and it is recognised to have significant genetic contributions to its development. Although some genetic studies have focused on pain in specific body sites and have suggested that possible genetic variants associated with pain phenotypes, the overall understanding of the genetics of pain in different body sites remain unclear.

Objectives

To identify the genetic correlations of pain in different body sites using the UK Biobank cohort

Methods

The UK Biobank cohort has recruited over 500,000 individuals with genetic information available to researchers.

We first defined eight pain phenotypes based on a specific pain question used by the UK Biobank (Figure 1). Then, we performed eight genome-wide association studies using the UK Biobank dataset to identify the genetic variants for eight pain phenotypes (n = 151,922–226,683). Then we used the LDSC software to calculate the genetic correlations among eight pain phenotypes in the UK Biobank.

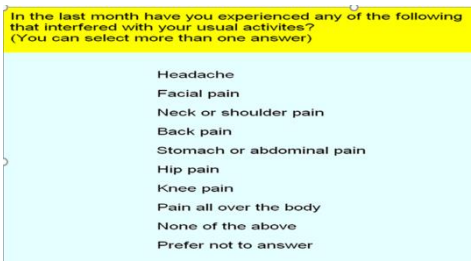

Figure 1: The pain question used by the UK Biobank

Pain phenotypes	Cases	Controls
Headache	74,761	149,312
Facial pain	2,610	149,312
Neck or shoulder pain	53,994	149,312
Stomach or abdominal pain	8,217	149,312
Back pain	43,991	149,312
Hip pain	10,116	149,312
Knee pain	22,204	149,312
Pain all over body	5,670	149,312

Table 1: GWAS numbers of the eight pain phenotypes in the UK Biobank

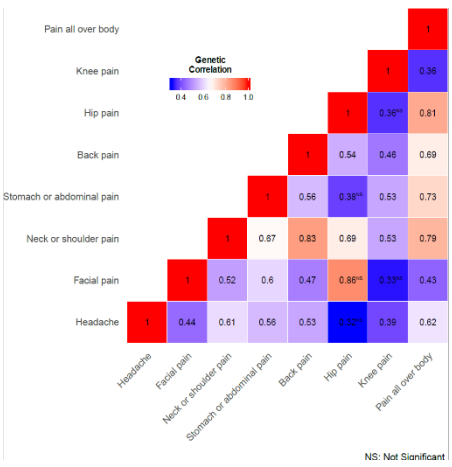

Figure 2: The genetic correlations among the eight pain phenotypes in the the UK Biobank

Results

The GWAS numbers of the eight pain phenotypes can be found in the Table 1. We identified multiple significant and positive correlations among eight pain phenotypes. (Figure 2) The largest positive and significant genetic correlation was between neck or shoulder pain and back pain ($rg = 0.83$, $P = 2.11 \times 10^{-100}$), followed by hip pain and pain all over the body ($rg = 0.81$, $P = 0.0004$). Neck or shoulder pain had positive and significant genetic correlations with all other pain phenotypes ($0.52 < rg < 0.83$), this was the same for pain all over the body ($0.36 < rg < 0.81$).

Discussion and Conclusions

We have shown that many pain phenotypes have positive and significant genetic correlations with each other. This indicates that common genetic risk factors confer liability to pain at many different sites across the body, suggesting shared risk factors and, potentially, disease mechanisms.

Relevance for patient care:

Improving our understanding of the genetic contributions to the experience of pain could help our understanding of its aetiology and prevention. It also can help to develop more targeted pain relieve drugs for patients.

References:

1. LDSC software: https://github.com/bulik/ldsc
2. The contents of this abstract were included in the paper: Meng W, Adams MJ, Reel P, Rajendrakumar A, Huang Y, Deary IJ, Palmer CNA, McIntosh AM, Smith BH. Genetic correlations between pain phenotypes and depression and neuroticism. Eur J Hum Genet. 2019 Oct 29. doi: 10.1038/s41431-019-0530-2