Identifying Inflammatory Bowel Disease causative genes through trans-eQTLs mapping within GWAS loci

From 2014-03-01 to 2016-02-29, closed project

Objective

Life-time prevalence of inflammatory bowel disease (IBD) is reaching an alarming rate of > 1/400 in industrialized societies. Improved understanding of disease pathogenesis is essential to develop more effective preventive, diagnostic and therapeutic measures. Genome-wide association studies (GWAS) have identified ~ 160 risk loci contributing to inherited predisposition to Crohn’s disease and/or ulcerative colitis. While this has already led to the identification of new perturbed pathways and potential drug targets, causative genes and variants remain unknown for the vast majority of risk loci. Moreover, the identified risk loci only account for an estimated 25% of inherited risk. GWAS loci are likely to be regulatory and therefore alter expression levels of other genes. In the present project we propose to apply an integrated genomic and transcriptomic approach to identify novel genes and pathways that are causally involved in inherited predisposition to IBD. We aim to detect causative genes implicated in IBD’s susceptibility through the evaluation of trans-eQTLs within GWAS loci. Trans_CEDAR is based on the generation of an integrated dataset of nine cell/tissue types collected on 350 healthy caucasians individuals, as well as on the use of next generation sequencing to identify rare variants in functionally-incriminated candidate genes. We expect to detect new causative variants that may constitute new drug targets. The present project will also generate a map of trans-eQTL in different tissues, equally useful for the study of other diseases, to be shared with the scientific community.

Related information

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