GENETICS

Known prostate cancer risk loci —guilty by association?

The results of the first study to assess a large number of susceptibility loci with respect to clinical end points in prostate cancer have been published in the *British Journal of Cancer*.

Sullivan and colleagues investigated the associations between 56 single nucleotide polymorphisms (SNPs) and biochemical recurrence, the development of castration-resistant prostate cancer (CRPC) or prostate-cancer-specific mortality (PCSM). They analysed a further five SNPs to see whether these were associated with PSA levels at disease diagnosis. Susceptibility loci for investigation were chosen on the basis of previously published reports of their association with clinical end points in prostate cancer or PSA levels.

Blood samples from 1,354 men treated for localized prostate cancer were prospectively collected and genotyped, then matched to phenotypic data. Univariate analysis revealed two SNPs were associated with

increased risk of biochemical recurrence and three with the development of CRPC. On multivariate analysis, seven SNPs showed associations with clinical end points: SNP rs4857841 was associated with PCSM, rs13385191 and rs339331 with biochemical recurrence and rs13385191, rs1894292, rs17178655 and rs11067228 with CRPC. However, none of these relationships remained significant after Bonferroni correction. The only association that was significant after this correction was between rs17632542 and PSA level at diagnosis.

These data provide further evidence that known SNPs that are associated with clinical end points in prostate cancer do not predict the risk of the disease progressing.

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Original article Sullivan, J. *et al.* An analysis of the association between prostate cancer risk loci, PSA levels, disease aggressiveness and disease-specific mortality. *Br. J. Cancer* doi:10.1038/bjc.2015.199