Pubertal development and prostate cancer risk: Mendelian randomization study in a population-based cohort

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We investigated whether pubertal development influences risk of prostate cancer in a population-based cohort. We used a genetic score comprised of single nucleotide polymorphisms (SNPs) associated with Tanner genital stage in adolescent boys [8, 9], as a surrogate for the onset and progression of pubertal changes, and we determined associations of this genetic score with prostate cancer risk, stage and grade.

The Tanner scale is a widely used 5-point scale that rates breast development in girls, genital development in boys, and pubic hair growth in both

Using a genetic score instead of directly assessed Tanner stage, in an approach known as Mendelian randomization (MR) [11], allows stronger causal inferences because genetic variants are usually unaffected by non-genetic confounding, reverse causality, or measurement error, which underlie the problematic interpretation of observational studies

This is a case-control study nested within a multicenter randomized controlled trial of treatments for prostatespecific antigen (PSA)-detected prostate cancer: the Prostate Testing for cancer and Treatment (ProtecT) study

We found evidence of an inverse association between our genetic score for pubertal development in boys and prostate cancer, i.e. the higher the score and, thus, the later the sexual maturation, the lower the risk for prostate cancer. The association was particularly strong for Gleason grade (odds ratio (OR) low- vs. high-grade disease, per tertile: 0.76; 95 % CI, 0.64–0.89; P = 0.001; Table 3). A dose-response effect of the genetic score in tertiles on high-grade prostate cancer was observed. Men in the highest score tertile (representing the most sexually immature individuals at a specific age) had a 43 % (95 % CI, 21–59 %) lower risk of high- versus lowgrade disease than men in the lowest tertile (Table 4).