SRD5A2 Gene Polymorphisms and the Risk of Prostate Cancer: A Meta-Analysis

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Abstract
Several polymorphisms in the 5α-reductase type 2 (SRD5A2) gene have been implicated as risk factors for prostate cancer. We performed a meta-analysis of 9 studies (12 comparisons) with V89L genotyping (2558 prostate cancer cases and 3349 controls), 7 studies (8 comparisons) with A49T genotyping (1594 cases and 2137 controls), and 4 studies with TA repeat genotyping (1109 cases and 1378 controls). The random effects odds ratio (OR) for the \( L \) versus \( V \) allele was 1.02 [95% confidence interval (CI), 0.94–1.11]. There was no suggestion of an overall effect either in recessive or dominant modeling, and comparison of \( L/L \) versus \( V/V \) also showed no differential prostate cancer susceptibility (OR, 1.03; 95% CI, 0.83–1.28). The random effects OR for the \( T \) versus \( A \) allele was 1.56 (95% CI, 0.93–2.62). However, excluding the first published study there was no evidence for any effect (OR, 1.08; 95% CI, 0.72–1.61). Moreover, the \( T \) allele had a low prevalence (0%, 1%, and 2% in Asian, African and European controls, respectively). The random effects OR for longer \( T \) versus short \( T \) \( A \) alleles was 0.88 (95% CI, 0.74–1.05). Longer \( T \) \( A \) allele homozygotes were nonsignificantly under-represented among prostate cancer cases (OR, 0.53; 95% CI, 0.26–1.06). We exclude a role for the \( V89L \) allele in conferring susceptibility to prostate cancer. The \( A49T \) and \( TA \) repeat polymorphisms may have a modest effect on prostate cancer susceptibility, but bias and chance findings cannot be excluded; any genuine genetic effects would account only for a small proportion of prostate cancer in the population.

Introduction
High levels of endogenous androgens have long been considered as risk factors for prostate cancer (1, 2). Therefore, it has been postulated that variants in the genes of the enzymes involved in androgen biosynthesis and metabolism may be associated with the development of prostate cancer. Among these genes, \( SRD5A2 \) is located on chromosome 2 and encodes the steroid 5α-reductase type 2 enzyme expressed primarily in the androgen-sensitive cells of genital skin and the prostate gland (3, 4). This enzyme irreversibly converts testosterone into the main prostatic androgen, DHT (5). The binding affinity to the prostatic androgen receptor of DHT is five times higher than that of testosterone (5). Ross et al. (6) demonstrated that young Japanese men have lower 5α-reductase activity than young Caucasian-American and African-American men. Similarly, Wu et al. (7) reported that the DHT:testosterone ratio was highest in African-Americans, intermediate in Caucasians, and lowest in Asian-Americans, corresponding to the respective risk of developing prostate cancer in these groups.

Certain \( SRD5A2 \) polymorphisms may encode for 5α-reductase enzyme variants with different activities, probably because of altered mRNA stability (8). Makridakis et al. (9) reported a missense substitution in the \( SRD5A2 \) gene, which replaces valine at codon 89 with leucine (V89L). This substitution is associated with a reduced 5α-reductase activity both in vitro and in vivo (9). In another variant of the \( SRD5A2 \) gene (10), an alanine residue at codon 49 is replaced with threonine (\( A49T \)). This missense mutation increases steroid 5α-reductase activity 5-fold in vitro (10). Thus, these polymorphisms might alter DHT levels and consequently the risk of prostate cancer. A polymorphism in the 3’ untranslated region has also been reported, with different numbers of \( TA \) dinucleotide repeats (11).

Molecular epidemiological studies have presented seemingly contradictory results concerning a potential role of the \( V89L \) (12–20), \( A49T \) (10, 16–21), and \( TA \) repeat (17, 18, 20, 22) polymorphisms in prostate cancer susceptibility. Single studies may have been underpowered to detect dose-response relationships or even overall effects. Given the amount of accumulated data, a quantitative synthesis of the evidence was deemed important to perform. In this meta-analysis we aimed to obtain summary estimates for the strength of the postulated genetic association, as well as to quantify and explain the potential between-study heterogeneity.

Materials and Methods
Identification and Eligibility of Relevant Studies. We considered all of the studies that examined the association of the \( V89L \), \( A49T \), and \( TA \) repeat polymorphisms with prostate cancer. Sources included MEDLINE and EMBASE (last search update January, 2003). The search strategy was based on combinations of “prostate cancer,” “\( SRD5A2 \),” “androgens,” “pol-
morphism,” “allele,” and “genetics.” References of retrieved articles were also screened.

Nonfamilial case-control studies were eligible if they had determined the distribution of genotypes for any of the three polymorphisms in prostate cancer cases and in a concurrent control group of prostate cancer-free subjects using a molecular method for genotyping. We accepted disease-free controls regardless of whether they had BPH or not. Cases with prostate cancer were eligible regardless of whether they had a first-degree relative with prostate cancer or not. However, we excluded family-based studies of pedigrees with several affected cases per family, because their analysis is different (based on linkage considerations).

**Data Extraction.** Two investigators independently extracted data and reached consensus on all of the items. The following information was sought from each report: authors, journal and year of publication, country of origin, selection and characteristics of prostate cancer cases and controls, demographics, racial descent of the study population (categorized as European, African, and Asian descent), eligible and genotyped cases and controls, and number of cases and controls for each SRD5A2 genotype. For studies including subjects of different racial descent, data were extracted separately for each race, whenever possible. Furthermore, we examined whether matching had been used, whether there was specific mention of blinding of the personnel who performed the genotyping to the clinical status of the subjects, and whether the genotyping method had been validated. Whenever key information was missing in a published report, we obtained the pertinent data directly from primary study investigators.

**Meta-Analysis.** The primary analysis for the V89L polymorphism compared prostate cancer patients against controls for the contrast of L versus V alleles. This analysis aims to detect overall differences. We also examined the contrast of homozygotes (LL versus LV). Finally, we examined the contrast of L/L versus (V/L+LV) and (V/L+LL) versus V/V. These contrasts correspond to recessive and dominant effects, respectively, of the L allele. Similar contrasts were analyzed for the A49T polymorphism. For the TA repeat polymorphism, we contrasted the longer alleles (TA(18) combined) versus the shorter allele TA(0), as originally proposed (22). Genotype contrasts used the same longer versus shorter allele classification.

Because case-control studies were involved, the OR was used as the metric of choice. Studies with subjects of different races were split into separate race-specific comparisons. For each genetic contrast, we estimated the between-study heterogeneity across all of the eligible comparisons using the \( \chi^2 \)-based Q statistic (23). Heterogeneity was considered significant for \( P < 0.10 \). Data were combined using both fixed effects (Mantel-Haenszel) and random effects (DerSimonian and Laird) models (23). Random effects incorporate an estimate of the between-study variance and provide wider CIs, when the results of the constituent studies differ among themselves. Random effects are more appropriate when heterogeneity is present (23). Subgroup analyses estimated race-specific ORs for each allele contrast.

We also performed cumulative meta-analysis (24) and recursive cumulative meta-analysis (25, 26) to evaluate whether the summary OR for the allele contrasts changed over time as more data accumulated. Inverted funnel plots and the Begg-Mazumdar publication bias diagnostic (nonparametric \( \tau \) correlation coefficient; Ref. 27) evaluated whether the magnitude of the observed association was related to the variance of each study. Finally, we evaluated whether the summary results were different when the analyses were limited to studies with rigorous selection of cases and controls (those that confirmed histologically all of the prostate cancer cases and specifically screened all of the controls to rule out prostate cancer).

Analyses were conducted in SPSS 11.0 (SPSS, Inc., Chicago, IL), StatXact (Cytel Inc., Boston, MA), and Meta-Analyst (Joseph Lau, Boston, MA). All of the \( P \) values are two-tailed.

**Results**

**Eligible Studies**

We identified 12 eligible reports (Refs. 10, 12–22; Table 1), 2 of which (13, 22) were derived from the same cohort, but presented complementary data on different polymorphisms. The number of studies with V89L (12–20), A49T (10, 16–21), and TA repeat data (16, 17, 19, 22) was 9, 7, and 4, respectively. After splitting data per racial descent in 3 studies (10, 14, 15), there were 12, 8, and 4 available comparisons for the three polymorphisms, respectively. There was a considerable diversity of ethnic groups.

Nine reports (12, 13, 15–20, 22) selected prostate cancer patients based on a histological diagnosis from biopsy or prostatectomy, whereas the other 3 (10, 14, 21) did not clarify the exact diagnostic criteria. One report (19) mentioned positive family history of prostate cancer in 11.9% of patients, 4 reports (10, 17, 20, 21) specifically included patients without a family history of prostate cancer, whereas the remaining did not clarify the background of family history. Controls did not have a clinical diagnosis of prostate cancer at study entry, but the amount of additional screening [with digital rectal examination, prostate-specific antigen (<4 ng/ml), needle biopsy, or prostate resection] to exclude prostate cancer differed substantially across studies (Table 1).

With one exception (10) where the mean age of controls and cases differed by 5 years, the reported mean or median age of cases and controls was very similar (difference =2 years) and specific matching for age was described in 6 studies (13, 16–19, 22). Six reports (10, 12–14, 18, 22) mentioned specifically blinding of the personnel who performed the genotyping. Appropriate molecular methods for genotyping were used. All of the studies used PCR. Some studies performed in addition sequencing (13, 17, 22), single-strand conformational polymorphism analysis (10, 18, 20), or ASO-hybridization and sequencing (21). The distribution of genotypes in control groups was consistent with Hardy-Weinberg equilibrium for all three of the polymorphisms in all of the studies.

**Meta-Analyses Databases (Table 2)**

**V89L.** The eligible studies included 2662 patients with prostate cancer and 3573 controls of whom 2558 and 3349, respectively, had genotype data. The L allele was more highly represented among controls of Asian descent (50%; 95% CI, 48–52) than in controls of European descent (31%; 95% CI, 30–32) or African descent (25%; 95% CI, 22–28). Overall, the prevalence of L/L homozygosity was 25%, 10%, and 5% in control subjects of Asian, European, and African descent, respectively. The respective prevalence rates of V/L heterozygosity were 49%, 42%, and 39%.

**A49T.** The eligible studies included 1720 patients with prostate cancer and 2415 controls of whom 1594 and 2137, respectively, had genotype data. The prevalence of the T allele was 2% (95% CI, 1–3) and 1% (95% CI, 0.1–2) in control subjects of European and African descent, respectively. Overall, the
prevalence of \( T/T \) homozygosity was 0.2% and 0.3% in control subjects of European and African descent, respectively. The respective prevalence rates of \( A/T \) heterozygosity were 4% and 1%. The \( T \) allele was not detected in any subjects of Asian descent, thus the 2 comparisons on Asian subjects were excluded from the quantitative synthesis.

**TA Repeats.** The eligible studies included 1192 patients with prostate cancer and 1574 controls of whom 1109 and 1378, respectively, had genotype data. The prevalence of longer \( TA \) repeat alleles was 14% (95% CI, 12–15) and 9% (95% CI, 7–12) in control subjects of European and Asian descent, respectively. Overall the prevalence of homozygosity for longer \( TA \) repeat alleles was 2.3% and 0.7%, in the two groups, respectively. No study included African descent subjects.

**Quantitative Synthesis (Table 3)**

**V89L.** There was no evidence that the \( L \) allele modified the risk of prostate cancer (Fig. 1). The summary OR was 1.02 by both random \((P = 0.61)\) and fixed effects \((P = 0.64)\). In subgroup analyses, no differences were observed in allele distribution between prostate cancer patients and controls of European, Asian, and African descent. We found no evidence of an association of the \( L/L \) genotype with the risk of prostate cancer relative to the \( V/V \) genotype. The 95% CIs excluded a large effect. No susceptibility effect was seen in either recessive or dominant models. There was no between-study heterogeneity in any of these analyses.

**A49T.** There was a trend suggesting that the \( T \) allele may modify the risk of prostate cancer (Fig. 2). The summary OR was 1.56 by random effects \((P = 0.089)\) and 1.44 by fixed effects \((P = 0.029)\). However, no clear effect was seen in subjects of European descent. There was a trend for an association of the \( T/T \) genotype with the risk of prostate cancer relative to the \( A/A \) genotype, with an approximate doubling of the odds of cancer, but this was not formally statistically significant \((P = 0.25)\) and \( P = 0.13 \), by random and fixed effects, respectively. No clear effect was seen in recessive or dominant models. There was no between-study heterogeneity in any of these analyses.
**TA Repeats.** The contrast of alleles did not suggest any strong genetic effect \((P = 0.15; \text{ Fig. 3})\). There was a suggestion that homozygotes for longer TA repeats may have a smaller risk for prostate cancer with almost a halving of the odds as compared with subjects with other genotypes. However, this association was not formally statistically significant \((P = 0.07\) by both random and fixed effects). There was no between-study heterogeneity in any of these analyses.

**Bias Diagnostics**

**V89L.** The magnitude of the summary OR had been stable over time (by random effects, summary OR for \(L\) versus \(V\); 0.96 at the end of 1999, 0.97 at the end of 2000, 1.01 at the end of 2001, and 1.02 at the end of 2002). Smaller studies did not show different results from larger studies. Analyses limited to studies with rigorous selection of cases and controls yielded similar results from larger studies. Analyses limited to studies with rigorous selection of cases and controls yielded similar
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Fig. 1. Effect of the L versus V allele on the risk of prostate cancer. Each comparison is presented by the name of the first author, and the year of publication. Lf signifies subjects of African descent, As signifies subjects of Asian descent. For each comparison, the point estimate of the OR and the accompanying 95% CI are shown. Also shown is the summary random effects estimate for the comparison along with the respective 95% CI. Values 1 denote an increased risk for prostate cancer. Otherwise, figure set-up as per Fig. 1.

Fig. 2. Effect of the T versus A allele on the risk of prostate cancer. Values 1 denote an increased risk for prostate cancer with the T allele. Otherwise, figure set-up as per Fig. 1.

Discussion

This meta-analysis examined three well-characterized polymorphisms of the SRD5A2 gene in their relationship to prostate cancer susceptibility. The current evidence definitively excludes any increased risk conferred by the V89L polymorphism. No additional studies are needed on this postulated association. One cannot exclude that the T allele in the A49T polymorphism may increase modestly the risk for prostate cancer, and homozygosity for the longer TA repeat alleles may decrease modestly this risk. Given the relative rarity of these two variants on a population basis, larger studies with many thousands of subjects would be needed to verify such effects. However, the meta-analysis clearly demonstrates that the contribution of these polymorphisms to prostate cancer at a population level is probably small, if at all present. Thus very large studies, if ever conducted, should be carefully designed to avoid dilution of the observed effects, and the cost of running such studies should be carefully weighted against the anticipated small gain of information. For A49T, the attributable fraction of prostate cancer in subjects of European descent is probably ≤1%, whereas the polymorphism is completely absent in subjects of Asian descent. Even the observed effect may be spurious, because it was largely driven by the first reported study in the field, i.e., from data that are mostly hypothesis-generating. Longer TA repeat homozygosity also occurs in only 2.3% of European descent subjects, and <1% of Asian subjects. No data have been generated on the association of this polymorphism with prostate cancer on African subjects, where the prevalence of longer TA repeat alleles may be higher (8).

The meta-analysis did not address whether these three polymorphisms may have an effect on the clinical behavior of prostate cancer or other clinicopathological attributes. A few studies have generated some relevant data, but their results have been contradictory. Nam et al. (12) claimed a 3.3-fold significantly increased risk of disease recurrence with the V/V and V/L genotypes. Conversely, Soderstrom et al. (19) claimed a significant 5.7-fold increased risk of metastatic disease with the
The SRD5A2 gene may also have other polymorphisms that were not considered in the meta-analysis. One of them, the R227Q polymorphism, is already known, but is very rare: Q heterozygotes have a prevalence of only 0.2% in Asian descent subjects where this polymorphism has been studied (18). Nevertheless, we should note that linkage studies (30–32) based on genome scans have not identified overall any significant linkage of prostate cancer with the region of 2p23, the chromosomal location of the SRD5A2 gene.

The biochemical evidence for a putative relationship of SRD5A2 polymorphisms with androgen levels is also controversial. Hsing et al. (18) found that of all these polymorphisms, only the L allele had a statistically significant relationship with higher testosterone and lower 5α-androstan-3α,17β-diol glucuronide levels, but was not associated with apparent differences in DHT, estradiol, or steroid hormone binding globulin levels. A more marginal effect of the TA dinucleotide repeat polymorphism on DHT levels was also claimed (18). However, other investigators (33, 34) found actually lower testosterone levels with L/L and in 2 studies (13, 33), the V89L polymorphism was not significantly associated with the levels of androstanediol glucuronide. Even if SRD5A2 is an important enzyme in androgen biosynthesis and even if the identified polymorphisms regulate its activity under certain experimental circumstances (8–11), there is no conclusive evidence that hormone levels are eventually affected in the serum, or more importantly, in the prostate tissue. Moreover, the exact role of androgens in the pathogenesis of prostate cancer has been a contentious issue (1, 35, 36), so serum hormone levels may not provide definitive proof for the presence or not of genetic predisposition to prostate cancer. Polymorphisms in genes coding for other enzymes of the androgen biosynthesis and metabolism pathway have also been postulated as prostate cancer determinants (2), but associations may also be refuted on scrutiny of the available evidence (37).

Postulated genetic associations for prostate cancer need to be carefully validated across several studies, because early and small genetic association studies may come up with spurious findings (38–40). Furthermore, genetic associations for such a multigenetic disease are likely to have relatively small ORs that would require large sample sizes to clarify. Some other limitations of this meta-analysis should be acknowledged. First, some nondifferential misclassification bias is possible. The majority of the considered studies could not exclude latent prostate cancer cases in the control group, and some controls may have developed prostate cancer during the subsequent years. However, the lifetime risk of prostate cancer among Americans is ~16% (41), so the OR dilution would probably be small. Furthermore, control groups included a large, often unknown proportion of subjects with BPH. BPH may be also androgen-dependent, and affected by these same polymorphisms. However, one would then refer to a genetic factor conferring risk for prostate enlargement rather than cancer per se, a hypothesis with completely different connotations. Two (42, 43) of 3 studies (34, 42, 43) to date do not support this hypothesis. Finally, the meta-analysis did not address familial prostate cancer, i.e., the hereditary forms where several members of the same family may be affected. One study (21) has found no association between A49T and familial prostate cancer. Moreover, such hereditary forms account for a very small portion of prostate cancer (31) and, thus, even strong genetic associations would have a limited impact on the incidence of prostate cancer at the population level.

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References


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