An Epidemiological Reappraisal of the Familial Aggregation of Prostate Cancer: A Meta-Analysis

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Abstract

Studies on familial aggregation of cancer may suggest an overall contribution of inherited genes or a shared environment in the development of malignant disease. We performed a meta-analysis on familial clustering of prostate cancer. Out of 74 studies reporting data on familial aggregation of prostate cancer in unselected populations retrieved by a Pubmed search and browsing references, 33 independent studies meeting the inclusion criteria were used in the analysis performed with the random effects model. The pooled rate ratio (RR) for first-degree family history, i.e. affected father or brother, is 2.48 (95% confidence interval: 2.25–2.74). The incidence rate for men who have a brother who got prostate cancer increases 3.14 times (CI:2.37–4.15), and for those with affected father 2.35 times (CI:2.02–2.72). The pooled estimate of RR for two or more affected first-degree family members relative to no history in father and in brother is 4.39 (CI:2.61–7.39). First-degree family history appears to increase the incidence rate of prostate cancer more in men under 65 (RR:2.87, CI:2.21–3.74), than in men aged 65 and older (RR:1.92, CI:1.49–2.47), p for interaction = 0.002. The attributable fraction among those having an affected first-degree relative equals to 59.7% (CI:55.6–63.5%) for men at all ages, 65.2% (CI:57.7–71.4%) for men younger than 65 and 47.9% (CI:37.1–56.8%) for men aged 65 or older. For those with a family history in 2 or more first-degree family members 77.2% (CI:65.4–85.0%) of prostate cancer incidence can be attributed to the familial clustering. Our combined estimates show strong familial clustering and a significant effect-modification by age meaning that familial aggregation was associated with earlier disease onset (before age 65).

Introduction

Prostate cancer is one of the most common cancers among males in developed countries [1]. A lot of evidence shows that a family history of the disease is an important risk factor [1,2]. In 2003, three meta-analyses evaluated the increase in the risk of prostate cancer in relatives of affected men [3–5]. Since then, familial clustering has been assessed in a number of new populations. Furthermore, more recent data is available from the big cohorts in Sweden [6] and the US [7]. We studied all the data available up to September 2010 to assess the strength of prostate cancer familial aggregation. In order to evaluate the impact of a family history of prostate cancer on the disease incidence, we also estimated the attributable fractions among men with affected relatives.

Methods

Searching

We browsed the PubMed database using the search term ‘(prostate cancer) and (family history)’. The last update was performed September 21, 2010. Out of 801 initially identified articles, 53 reports provided data on the relationship between family history and risk of prostate cancer in an unselected population of men (see Figure S1). Case-control studies using selected populations as cases (example: patients undergoing prostatectomy [8,9]) and cohort studies with a specific cohort (example: smokers [10]) were excluded to avoid bias or heterogeneity due to these population characteristics. Additional 21 study reports were found through the references of the studies identified via the PubMed database.

Selection

74 relevant articles were coded. As quality control, we considered study design, control for age and the way family history was ascertained. Cohort studies and case-control studies reporting age-adjusted estimates or using age-matched controls were included. Cross-sectional studies [11–17] were excluded. Two studies in which the attempt to match for age did not result in a similar age of the cases and the controls [18,19] and one study in which the controls were not age-matched and age-adjusted estimates were not reported [20] were excluded. Additionally, one case-control study was excluded [21], because none of the participants reported a family history of prostate cancer. The study of McCahy et al. [22] was not used in the main analysis, because it was characterized by clearly outlying results (odds ratio for first-degree family history 17.83). The influence of exclusion of this study on the estimates was assessed in the sensitivity analysis.

Five studies [23–27] were excluded, because the investigated type of familial clustering did not correspond to any of the
exposures and reference categories considered in this meta-analysis (affected first-degree relatives, i.e. father and/or brother(s), versus not, affected father versus not, affected father versus no affected first-degree relatives, affected brother(s) versus not, affected brother(s) versus no affected first-degree relatives, affected first or second-degree relative(s) versus not, two or more affected first-degree relatives versus no history in first-degree relatives). Two articles [28,29] were excluded because of the lack of definition of ‘family history’.

Duplications in study populations were avoided so that each pooled estimate was based on independent studies. In case of an overlap between populations from several studies using the same design, a case-control study with the largest number of participants or the most recent cohort study was included. The case-control study reported by Negri et al. [30] was preferred over Gallus et al. [31] and Randi et al. [32], and Krain, 1974 [33] over Krain, 1975 [34]. Out of many reports based on the Swedish cancer register [6,35–45], only the most recent [6] was used. Similarly, the most recent findings were included from the studies using the Utah population database [7,46,47] and the US Health Professionals Cohort [48,49]. When there was a population overlap between studies using a different design, the cohort study [6] was preferred over the case-control studies [50–53], and the nested case-control study [7] over the study of West et al. [54]. A summary of the 25 case-control studies [30,33,55–77] and 8 cohort-based studies [6,7,49,78–82] included in the analysis is presented in Table 1 and Table 2.

Data analysis
The combined estimates were expressed with the ratio of incidence rates (RR) among those exposed and those not exposed. The hazard ratios, the odds ratios from the logistic regression models, and the odds ratios calculated from the contingency tables were assumed to estimate the rate ratios. This measure of association was considered appropriate to express the combined estimates for several reasons. Firstly, the hazard ratios, which can be estimated in cohort studies and density sampling case-control studies [83], are valid estimates of the rate ratios [84]. Also the odds ratios from the logistic regression models from density sampling case-control studies can be used to estimate the rate ratios without any adjustments [85]. Moreover, the bias introduced by estimating the rate ratios with the odds ratios is in

Table 1. Summary of the case-control studies included in the analysis.

| First author and reference | Date            | Place                     | Race          | Mean age at diagnosis | No. cases | No. controls | Controls |
|----------------------------|-----------------|---------------------------|---------------|-----------------------|-----------|--------------|----------|
| Beebe-Dimmer55             | 1996–2002       | USA: Michigan             | African       | 65                    | 121       | 179          | P C      |
| Fincham56                  | 1981–1983       | Canada: Alberta           | Caucasian     | NA, age 45 or older   | 382       | 625          | P C M    |
| Ghadirian57                | 1989–1993       | Canada: Montreal, Toronto, Vancouver | Caucasian | NA, median 70         | 640       | 639          | P D M    |
| Glover58                   | 1998           | Jamaica: Kingston         | African       | 73.3                  | 263       | 263          | H C M    |
| Hayes59                    | 1986–1989       | USA: Atlanta, Detroit, New Jersey | Mixed       | 61.5                  | 905       | 1264         | P C M    |
| Honda60                    | 1979–1982       | USA: Los Angeles County   | Caucasian     | NA, 60 or younger     | 216       | 216          | P C M    |
| Justine61                  | 2001–2002       | Australia: Perth          | Caucasian     | 63.8 C                | 560       | 450          | P C M    |
| Kolonel62                  | 1977–1983       | USA: Hawaii               | Mixed         | NA                    | 452       | 899          | P C M    |
| Krain33                    | 1971–1972       | USA: Los Angeles          | Mixed         | median 69             | 210       | 215          | H C M    |
| Lesko63                    | 1992–1994       | USA: Massachusetts        | Caucasian     | NA, median 65, age 70 or less | 563 | 703          | P D M    |
| Magura64                   | 2004–2006       | USA: North Dakota         | Caucasian     | 64.2 C                | 312       | 319          | H C M    |
| Mettlin65                  | 1995           | USA: Buffalo              | Caucasian     | 67.6                  | 1271      | 1909         | H C M    |
| Negri50                    | 1991–2002       | Italy                     | Italian       | 65.7 C                | 1294      | 1451         | H C      |
| Rovito66                   | 1998–2001       | USA: New York             | Caucasian     | 63.3 C                | 152       | 161          | H C M    |
| Bybicki67                  | 2001–2004       | USA: Detroit              | Mixed         | NA, median 63         | 637       | 244          | P C M    |
| Salinas68                  | 1993–1996, 2002–2005 | USA: King County, Washington | Caucasian | 59.9                  | 1211      | 1208         | P C M    |
| Schuman69                  | 1977           | USA: Minnesota            | Caucasian     | NA, median 64         | 36        | 41           | H D M    |
| Spitz70                    | 1985–1989       | USA: Texas                | Caucasian     | 66.2                  | 378       | 383          | H C M    |
| Staples71                  | 1994–1998       | Australia: Melbourne, Sydney, Perth | Caucasian | 60                    | 1475      | 1405         | P D M    |
| Steele72                   | 1968–1969       | Canada: Ontario           | Caucasian     | 69                    | 39        | 39           | H C M    |
| Stone73                    | 1994–1995       | USA: New Mexico           | Mixed         | 66.1                  | 244       | 526          | P C M    |
| Strom74                    | 1998–2005       | USA: Texas                | Hispanic      | 62.2                  | 176       | 174          | P C M    |
| Suzuki75                   | 1988–2004       | Japan                     | Japanese      | NA                    | 257 in total |                       | H C M    |
| Whittemore76              | 1987–1991       | USA, Canada               | Mixed         | NA, mean age at interview: 71 | 1500 | 1581         | P C M    |
| Zhu77                      | 1989–1991       | USA: Washington State     | Caucasian     | 64                    | 175       | 258          | P D M    |

PA-population based controls, H-hospital based controls, C-cumulative sampling, D-density sampling, M-age-matched controls.

The year of publishing. The period of collecting the data not reported.

Calculated from the reported distribution of age of the cases at diagnosis.

NA—not available.

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Table 2. Summary of the cohort-based studies included in the analysis.

| Author      | Date                | Place               | Race     | Mean age at diagnosis | Design                          | Cohort                                      |
|-------------|---------------------|---------------------|----------|-----------------------|----------------------------------|---------------------------------------------|
| Brandt6     | 1961–2006 Sweden    | Caucasian           | NA, aged younger than 75 | Cohort study | 3,900,000 men from the Swedish cancer registry |
| Chen69      | 1990–2004 USA       | Caucasian           | NA       | Prospective cohort study | 43494 men from the Health Professionals Follow-Up Study cohort |
| Kalish70    | 1987–1997 USA, Boston area | Caucasian        | 65,2 A  | Prospective cohort study | 1149 men from the Massachusetts Male Aging Cohort |
| Kerber7     | 1966–2000 USA, Utah | Caucasian           | NA       | Nested case-control, density sampling | 11572 cases and 11572 controls from the Utah Population Database |
| Park60      | 1993–2006 USA, California | Mixed             | NA       | Nested case-control, cumulative sampling | 729 cases and 729 controls from the Multiethnic Cohort |
| Schuurman81 | 1986–1992 The Netherlands | Caucasian     | 64,2 A  | Prospective cohort study | 52879 men from the Municipal population registries |
| Sun82       | 1992–2006 USA       | Caucasian           | NA       | Nested case-control, density sampling | 1157 cases and 1157 controls from the Prostate Lung and Ovarian Cancer Screening Trial cohort |

*Data calculated from the reported distribution of age of the cases at diagnosis.

In order to assess the public health implications of our findings, we estimated the attributable fractions among those with a family history of prostate cancer [86]. The measure was defined as the proportion of the disease incidence attributable to the exposure. The attributable fraction among those exposed can be expressed as: \( AF_E = \frac{RR-1}{RR} \) [84]. We estimated \( AF_E \) by plugging in our estimates of the rate ratios in the equation, which is often referred to as the Mantel-Haenszel approach [87]. The confidence bounds were obtained using the Wald method [88], with the standard deviations estimated by the Monte Carlo simulation [89].

The results from the individual studies were combined on the log scale. The Cochran’s Q statistic showed evidence of heterogeneity greater than expected by the sampling variance alone. Therefore, we used the random effects model to obtain the combined estimates. For every combined estimate the funnel plot, i.e. a plot of effects estimates versus their standard error, was visually examined and the Egger's asymmetry test [90] was used in order to assess the presence of a publication bias. A meta-regression was carried out to investigate the effect of study design (cumulative sampling case-control versus other), ethnicity (Caucasian versus other), country (US versus other) and publication year (cumulative sampling case-control versus other), and ethnicity on the combined estimate was estimated using the mixed effects model. To evaluate the effect of using the odds ratios from the cumulative-sampling case-control studies as estimates of the rate ratio, we also estimated the rate ratio for first-degree family history using only the cumulative-sampling case-control studies and compared it with the rate ratio based only on the density-sampling case-control studies. Sensitivity of the findings was examined by recalculation of the pooled association sizes after exclusion of studies one by one. As all studies reporting familial aggregation for men under 65 years old also provided data for the age group 65 and older, the paired t-test was used to assess the significance of the difference. The analysis was conducted in SAS (version 9.2; Cary, NC, USA). The rmeta package of the R software (version 2.11.1) was used for the plots.

Results

Pooled estimates

The pooled rate ratio for men with first-degree family history, i.e. affected father or/and brother(s), was based on 19 case-control [30,57–60,62–68,70–72,74–77], 3 nested case-control [7,80,82] and 4 cohort studies [6,49,78,81]. 18 independent studies [6,30,49,55–57,60,61,63–66,70,71,73,75,78,81] provided data for men with history of prostate cancer in father and 16 [6,30,49,57,61,63–66,70,71,73,75,78,79,81] for men with history of prostate cancer in a brother(s). The combined estimate for history of prostate cancer in a second-degree relative was based on 5 studies [7,58,64,66,70]. Seven studies [6,57,62,63,66,71,76] were used to estimate the rate ratio for 2 or more affected first-degree family members. Five studies [6,49,63,65,71] provided data for the different age groups.

The combined rate ratios and the corresponding attributable fractions among those exposed are reported in Table 3. The rate ratios for first-degree family history, i.e. affected father or/and brother(s) (Figure 1), affected father (Figure 2), and affected brother(s) (Figure 3) were bigger than 2, with the confidence level 95%. The estimated rate ratio for two or more affected first-degree relatives equaled 4.39 (95% confidence interval: 2.88–6.73).
The rate ratio for first-degree family history was significantly higher for men younger than 65, than for men aged 65 or older, \( p = 0.002 \).

59.7\% of the incidence of prostate cancer in men with an affected first-degree relative could be attributed to this risk factor (CI: 55.6–63.5\%). When two or more first-degree family members were affected, the attributable fraction equaled 77.2\% (CI: 63.4–85.0\%). For men younger than 65, the estimated attributable fraction equaled 65.2\% (CI: 57.7–71.4\%) and for men 65 or older 47.9\% (CI: 37.1–56.8\%).

Publication bias and sensitivity analysis

The results of the Egger’s test for first-degree family history (\( p = 0.99 \)), affected father (\( p = 0.86 \)), affected brother(s) (\( p = 0.33 \)), and affected second-degree relative (\( p = 0.06 \)) did not indicate a publication bias. The funnel plot for first-degree family history suggests a potential publication bias (see Figure 4). In particular, the rate ratio for the study by Suzuki et al. [75], a relatively small study, is by far the largest from all the studies included in the analysis. The sensitivity analysis showed that neither a decision to include this study, nor any other shifted the estimate of the rate ratio for first-degree family history or affected father more than by 0.1. Analysis conducted without the study by Chen et al. [49] gave the rate ratio for affected brother(s) 0.18 bigger than the estimate based on all the studies. Excluding none of the other studies led to a change by more than 0.12.

The combined estimate for men aged 65 or older did not change by more than 0.1, when one of the studies it was based on was excluded. For the age category of men younger than 65, it increased from 2.87 to 3.38 when the study by Chen et al. [49] was not included, which was the largest change of the estimate when one of the studies it was based on was excluded. The rest of the estimates appeared to be more sensitive to changes in the sample of studies. The studies by Magura et al. [64] and Kerber et al. [7] had the largest effect on the estimate of the rate ratio for affected second-degree family members. Excluding them changed the estimate from 2.52 to 2.08 and 3.29 respectively. Not including the study by Staples et al. [71] in the sample used to estimate the rate ratio for two or more affected first-degree relatives led to a decrease of the estimate from 4.39 to 3.89, and not using the study by Lesko et al. [63] to an increase to 4.96, which were the largest changes of the estimate when one of the studies it was based on was excluded. Including the study by McCahy et al. [22] would not change any of the combined estimates by more than 0.1.

Table 3. Estimates of the rate ratios and the attributable fractions among men with different types of family history.

| Type of clustering          | RR (95% CI) | AF<sub>F</sub> (95% CI) | N  |
|----------------------------|-------------|----------------------|----|
| 1st degree relatives       |             |                      |    |
| For all men                | 2.48 (2.25–2.74) | 59.7% (55.6–63.5%) | 26 |
| For men before the age of 65 | 2.87 (2.21–3.74) | 65.2% (57.7–71.4%) | 5  |
| For men aged 65 or older   | 1.92 (1.49–2.47) | 47.9% (37.1–56.8%)  | 5  |
| Affected father             | 2.35 (2.02–2.72) | 57.4% (50.7–63.1%)  | 18 |
| Affected brother(s)        | 3.14 (2.37–4.15) | 68.1% (58.1–75.7%)  | 16 |
| 2+ 1st degree relatives    | 4.39 (2.61–7.39) | 77.2% (65.4–85.0%)  | 7  |
| 2nd degree relatives       | 2.52 (0.99–6.46) | 60.4% (19.8–80.4%)  | 5  |

RR: Rate Ratio, AF<sub>F</sub>: attributable fraction among those exposed, N: number of studies the estimates are based on.

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Figure 1. Rate ratio of prostate cancer for first-degree family history, i.e. affected father or brother relative to no first-degree family history. Estimates from the case-control studies are presented at the top. They are separated from the estimates from the cohort-based studies with a line break.

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The meta-regressions showed that neither the study design, country, nor year of publication had a significant influence on the combined estimates for first-degree relatives (\( p = 0.40 \) for study design, \( p = 0.08 \) for country, and \( p = 0.29 \) for publication year). The estimated multiplicative effect of ethnicity on the rate ratio equaled 1.04 (CI:0.83–1.30). The estimated rate ratio equaled 2.50 for Caucasian populations and 2.41 for other populations. This difference was not significant, \( p = .75 \). The estimated rate ratio based only on the cumulative-sampling case-control studies and only on the density-sampling case control studies equaled 2.61 (CI:2.25–3.02) and 2.44 (CI:2.08–2.87) respectively.

Discussion

We identified 74 articles reporting information on the association between family history and prostate cancer from...
studies conducted in 16 countries in North America, Europe, Asia
and Australia. The identified studies differed regarding the study
design, the analysis, the way family history was ascertained, the
investigated type of clustering, and the reference category that they
used. 25 case-control studies and 8 cohort-based studies with non-
overlapping populations from 8 countries and 4 continents met the
inclusion criteria and reported data on the considered types of
clustering. According to our estimates, almost 60% of the prostate
cancer incidence among men with first-degree family history is
attributable to this risk factor.

The sensitivity analysis showed that the individual study results
had a small influence on the pooled estimates of the rate ratio for
first-degree family history, affected brother(s), and affected father.
The results for affected second-degree relatives and to 2 or more
affected first-degree family members, which are based on a small
number of studies, are more sensitive to changes in the sample of
studies used in the analysis and, therefore, should be treated with
cautions. The meta-regression and the similarity between the
combined estimates based only on the cumulative-sampling case-
control studies and only on the density-sampling case-control
studies suggested that using the odds ratios from the cumulative-
sampling case-control studies as estimates of the rate ratios did not
substantially bias our estimates.

We did not attempt to identify unpublished studies. However,
neither the visual examination nor the statistical procedures
suggested that publication bias could have an important effect on
the estimates. With the exception of the study by Glover et al. [58],
the studies included in the analysis were conducted in developed
countries, most of them in the USA. Our analysis did not suggest

Figure 2. Rate ratio of prostate cancer for a history of prostate
cancer in father. Estimates from the case-control studies are
presented at the top. They are separated from the estimates from the
cohort studies with a line break.
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Figure 3. Rate ratio of prostate cancer for a history of prostate
cancer in brother(s). Estimates from the case-control studies are
presented at the top. They are separated from the estimates from the
cohort studies with a line break.
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Figure 4. Funnel plot for affected first-degree relatives. The
study of Suzuki et al., which may be subject to publication bias, is
indicated with a square.
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that a difference in the strength of familial clustering between the USA and other countries exists. However, generalizing the results to males not living in developed countries may be inappropriate. The population in most of the considered studies was Caucasian. However, the meta-regression showed that the effect of ethnicity on the rate ratio for first-degree family history was small and not significant. This finding suggests that the strength of the association between family history and prostate cancer for Caucasian males is similar as in other populations.

The amount of evidence on the relationship between family history and prostate cancer that was available in our study was much larger, than in the previous meta-analysis. Since 2003, the strength of the associations has been investigated in a number of new populations and a more recent data has been reported from the Swedish cancer register and the Utah population database. This allowed using stringent inclusion criteria and at the same time retaining a substantial number of studies. In contrast to the previous works, several measures were taken in order to improve the quality of the analysis. To avoid a possible bias caused by confounders the studies among specific populations such as smokers [10] were excluded. As referring to prostate examination may occur more frequently among men with prostate cancer family history, the cross-sectional data gathered among males referred to examination by a doctor [11,12,14] was not used. Homogeneity of the studies was assured by including only the studies in which family history was defined and corresponding to one of the investigated types of clustering. Finally, as pooling of the studies required the assumption of independence, overlaps in study populations were avoided.

The results confirm the conclusions made in the previous meta-analyses [3–5] and support the American Cancer Society guidelines. We observed more than a 2-fold increase in the incidence rate of the disease for all of the investigated types of familial clustering, meaning that over 50% of prostate cancer cases among men with a certain type of family history are attributable to familial clustering of the disease. Having a brother with prostate cancer appears to be associated with a larger increase in the incidence rate than being a son of a father with prostate cancer. The incidence rate increases with an increasing number of affected family members. Family history appears to increase the incidence rate of prostate cancer for males younger than 65 more, than for males aged 65 and older, which suggests the relative importance of genetic factors and/or shared environment and/or food factors in an early onset of prostate cancer. In line with our conclusions, the American Cancer Society (ACS) recommends that men at average risk should be offered testing beginning at age 50, and that men at increased risk for prostate cancer, such as those with a history of the disease in a father or brother at a young age, should begin testing with both the prostate specific antigen blood test and the digital rectal examination at age 45, or even younger if they have multiple relatives with the disease.

Supporting Information

Figure S1 Flow of Included Studies. (DOC)

Author Contributions

Conceived and designed the experiments: JV MK TM. Performed the experiments: MK TN. Analyzed the data: JC MK TN. Contributed reagents/materials/analysis tools: MK TN. Wrote the paper: JV MK TN.

References

1. Damber JE, Aus G (2008) Prostate cancer. Lancet 371: 1710–21.
2. Noe M, Schroy P, Marie-Francois D, Babayan R, Geller A (2007) Increased cancer risk for individuals with a family history of prostate cancer, colorectal cancer, and melanoma and their associated screening recommendations and practices. Cancer Causes and Control 19: 1–12.
3. Bruner DB, Moore D, Parulian A, Doogan J, Engstrom P (2003) Relative risk of prostate cancer for men with affected relative: systematic review and meta-analysis. Int J Cancer 107: 797–803.
4. Johns LE, Houlston RS (2003) A systematic review and meta-analysis of familial prostate cancer risk. BJU International 91: 799–804.
5. Zeegers MPA, Jellema A, Ostrer H (2003) Empiric risk of prostate carcinoma for relatives of patients with prostate carcinoma. A meta-analysis. Cancer 97: 1894–1903.
6. Brandt A, Bermejo JL, Sundquist J, Hemminki K (2010) Age-specific risk of incident prostate cancer and risk of death from prostate cancer defined by the number of affected family members. European Urology 58: 275–280.
7. Kerber RA, O’Brien EO (2005) A cohort study of cancer risk in relation to family histories of cancer in the Utah population database. Cancer 103: 1906–1915.
8. Isaacs SD, Kimmey N, Balfour-Bonnie A, Beatty TH, Walsh PC (2005) Risk of cancer in relatives of prostate cancer prohbands. J Natl Cancer Inst 87: 991–996.
9. Strobat GD, Carter BS, Beatty TH, Chilis B, Walsh PC (1996) Family history and the risk of prostate cancer. The pro 17: 337–347.
10. Ahn J, Modelli R, Weinstein J, Snyder K, Virtamo J, et al. (2000) Family history of prostate cancer and prostate cancer risk in the alpha-tocopherol, beta-carotene cancer prevention (ATBC) study. Int J Cancer 123: 1154–1159.
11. Aprikian AG, Raisz M, Plante M, Meshoul A, Troudh C, et al. (1995) Family history and the risk of prostate carcinoma in a high risk group of urological patients. The journal of urology 154: 494–406.
12. Hernandez DJ, Han M, Humphreys EB, Mansfield LA, Tanzer SS, et al. (2000) Predicting the outcome of prostate biopsy: comparison of a novel logistic-regression-based model, the prostate cancer risk calculator and prostate-specific antigen level alone. BJU International 100: 609–614.
13. Makinen T, Tammeela TL, Stenman U, Maattainen L, Rannikko S, et al. (2002) Familial history and prostate cancer screening with prostate-specific antigen. J Clin Oncol 20: 2656–2663.
14. Nam RK, Toi A, Laurence HK, Trachtenberg J, Jettew MA, et al. (2007) Assessing individual risk for prostate cancer. J Clin Oncol 25: 3582–3589.
