Meeting Report

National Cancer Institute Prostate Cancer Genetics Workshop


Abstract

Compelling evidence supports a genetic component to prostate cancer susceptibility and aggressiveness. Recent genome-wide association studies have identified more than 30 single-nucleotide polymorphisms associated with prostate cancer susceptibility. It remains unclear, however, whether such genetic variants are associated with disease aggressiveness—one of the most important questions in prostate cancer research today. To help clarify this and substantially expand research in the genetic determinants of prostate cancer aggressiveness, the first National Cancer Institute Prostate Cancer Genetics Workshop assembled researchers to develop plans for a large new research consortium and patient cohort. The workshop reviewed the prior work in this area and addressed the practical issues in planning future studies. With new DNA sequencing technology, the potential application of sequencing information to patient care is emerging. The workshop, therefore, included state-of-the-art presentations by experts on new genotyping technologies, including sequencing and associated bioinformatics issues, which are just beginning to be applied to cancer genetics. Cancer Res 71(10): 3442–6. ©2011 AACR

Introduction

William J. Catalona (Northwestern University, Chicago, IL) opened the workshop with a discussion of the public health problem caused by the heterogeneity of prostate cancer aggressiveness, that is, the inability to accurately identify those men destined to suffer and die from prostate cancer. Elucidation of genetic markers associated with aggressive disease is one of the most important endeavors in prostate cancer research today, as better markers to identify aggressive prostate cancer could substantially improve patient care.

Catalona presented the history of the Genetics Working Group (GWG) and outlined the goals of the workshop. The National Cancer Institute’s (NCI) Specialized Program of Research Excellence (SPORE) GWG was formed in 2007, with the aim to conduct a case–case association study of aggressive versus nonaggressive prostate cancers, genotyping the 30+ validated prostate cancer susceptibility single-nucleotide polymorphisms (SNP) in more than 20,000 patients from the prostate cancer SPORE sites. The SNPs associated with prostate cancer aggressiveness would then be tested for association with other disease characteristics and treatments. The NCI funded the proposal of the GWG to hold a workshop to (i) plan the proposal for funding the case–case study of the consortium, (ii) “fine-tune” the strategies for conducting future studies, and (iii) plan an expanded collaboration beyond the SPORE sites.

Matthew L. Freedman (Dana-Farber Cancer Institute, Boston, MA) commented that the combined SPOREs alone

Authors’ Affiliations: 1 Department of Urology, Northwestern University Feinberg School of Medicine; and 2 Department of Medicine, University of Illinois, Chicago, Illinois; 3 Division of Genetic Epidemiology, University of Utah, Salt Lake City, Utah; 4 National Human Genome Research Institute, NHl; and 5 Department of Urology and Oncology, Johns Hopkins Medical Institutions, Baltimore; 6 Division of Cancer Epidemiology and Genetics, National Cancer Institute, Rockville, and Core Genotyping Facility, SAIC-Frederick, Inc., National Cancer Institute, NIH, DHHS, Gaithersburg; and 7 Genome Technology Branch, National Human Genome Research Institute, NIH; and 8 Cancer Genetics Branch, National Human Genome Research Institute, Bethesda, Maryland; 9 Department of Internal Medicine, University of Michigan Medical School, Ann Arbor, Michigan; 10 Department of Public Health and Primary Care, University of Cambridge, Strangeways Research Laboratory, Cambridge, United Kingdom; and 11 The Institute of Cancer Research, Surrey, and The Royal Marsden NHS Foundation Trust, Sutton, United Kingdom; 12 Division of Public Health Sciences, Fred Hutchinson Cancer Research Center, and 13 Department of Epidemiology, School of Public Health, University of Washington, Seattle, Washington; 14 Department of Medical Oncology, Dana-Farber Cancer Institute, Boston, and The Broad Institute, Cambridge, Massachusetts; 15 deCODE Genetics, Inc., Reykjavik, Iceland; 16 Center for Clinical Epidemiology and Biostatistics, Abramson Cancer Center, University of Pennsylvania, Philadelphia, Pennsylvania; 17 Department of Laboratory Medicine and Pathology, Mayo Clinic, Rochester, Minnesota; and 18 Departments of Epidemiology and Biostatistics, and Urology, Institute for Human Genetics, University of California, San Francisco, California

Corresponding Author: William J. Catalona, Department of Urology, Northwestern University Feinberg School of Medicine, 675 North St. Clair Street, Suite 20-150, Chicago, IL 60611; Phone: 312-695-4471; Fax: 312-695-1482. E-mail: wcatalona@nmnff.org

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bring a tremendous potential to bear on prostate cancer biology. The characteristics distinguishing the SPORE populations from the other existing cohorts are the deep clinical annotation; their size; the potential to study multiple ancestral groups; the potential to study pharmacogenetics; in addition, because of the availability of thousands of tumor samples from the same patient population, studies of combined germ line and somatic abnormalities could be enhanced.

The GWG will leverage its combined resources to conduct research that otherwise would not be possible without this synergy. A large multi-institutional virtual biobank of clinically and genetically annotated samples would be extremely useful to a wide array of researchers for a number of activities including (i) discovery of rare, highly penetrant susceptibility variants, (ii) validation of discoveries in biomarker development, and (iii) identification of patients who are carriers of known genetic variants and thus potential candidates for clinical trials of targeted therapy.

Genetic determinants of lethal disease are likely to have small effect sizes, and larger studies may be necessary to identify them (1). Until research is directed at this area, identification of genetic variants that contribute to prostate cancer aggressiveness is unlikely. Many speakers echoed the need for establishing a broad-based consortium to provide the large sample sizes required for studies on prostate cancer aggressiveness.

Practical Issues

The workshop addressed the short- and long-term objectives of the GWG as well as possible future projects. The consensus was that it would be wise first to conduct a preliminary “meta-analysis” of aggressive versus nonaggressive prostate cancer from the existing studies, with genotype and clinical data available for the 30+ SNPs. It was also agreed that additional promising candidate SNPs, identified from ongoing genetic studies, should be analyzed, thereby constantly expanding the data set to validate newly discovered variants.

The effect sizes for genetic variants associated with prostate cancer risk are small, and it is currently unknown whether the effect size for variants associated with aggressive disease will be similar. From the prostate cancer genome-wide association study (GWAS) scans already available, it might be possible to estimate whether effect sizes are smaller or larger for aggressiveness than for risk; if the effect sizes are predicted to be larger, a smaller sample size might yield sufficient statistical power. However, if the effect sizes are smaller, many speakers echoed the need for establishing a broad-based consortium to provide the large sample sizes necessary to identify statistically significant associations. To generate reliable results, tens of thousands of samples are needed. In a complex disease such as prostate cancer, stratification for aggressiveness considerably reduces the number of usable samples. Because the variants associated with the less common aggressive phenotype may in turn be less common, very large numbers are needed to have a higher power to discover variants with a minor allele frequency (MAF) of more than 2.5%.

There was also agreement that, although the initial study to launch the consortium should include the 30+ SNPs as the model, ultimately the consortium should conduct larger case–case–control analyses of promising candidate SNPs identified from other genetic studies, and possibly even undertake a GWAS, constantly expanding the data sets to validate newly discovered variants.

Coordinating and harmonizing data were also noted as being critical issues. Although decentralized genotyping can be problematic and inefficient, other consortia have successfully used decentralized genotyping for small numbers of variants. Phenotype presents perhaps the greatest challenge for standardization and harmonization of data. Defining the aggressive phenotype has been problematic. Comparing patients from the tails of the aggressiveness distribution, without unduly compromising sample size and power, enhances the ability to detect the genetic associations; however, merely dividing patients into those one would predict would do well or poorly is not sufficient.

The proposed aim of the GWG was to conduct a case–case association study; however, several speakers suggested that comparing genotypes of cases to controls should be included. If the focus is only on cases and significant associations are found, one would not know whether the association represented increased risk in the more aggressive cases or decreased risk in the less aggressive ones. The use of publicly available control data was discussed in this context.

Functional Studies and Other Opportunities

Freedman pointed out that there are other important questions to ask on a genome-wide scale with either germ line or somatic tissues, using a variety of platforms. He discussed the need to decipher the relationships between the germ line and somatic genomes and how noncoding regions interact with other genes. He pointed out that gene expression itself is a heritable trait.

Genetics of Prostate Cancer Aggressiveness

Genetics of prostate cancer progression

William B. Isaacs (Johns Hopkins University, Baltimore, MD) emphasized that accumulation of mutations in key genes is a critical aspect of our current views on prostate cancer progression. The importance of somatic gene fusions has emerged as paramount (2), and understanding germ line factors that predispose to fusion events could be important for initiation or for early events in the carcinogenic process.

Family history is a known risk factor, and studies have reported familial concordance in prostate cancer survival. Isaacs cited studies in families that identified several chromosomal regions linked to prostate cancer aggressiveness (3, 4). An important association with aggressiveness is found in carriers of *BRCA1* and *BRCA2* mutations (5). Therefore, even though rare variants may account for a small fraction of prostate cancers, they may be more important determinants of aggressive disease. Isaacs and other speakers suggested that most of the prostate cancer susceptibility loci identified so far probably modulate early stages of disease rather than disease progression.
GWAS replications for aggressive disease

A study by Fitzgerald and colleagues (Fred Hutchinson Cancer Research Center, Seattle, WA) found only one GWAS risk allele (on chromosome X) associated with Gleason score (6). From a review of published studies from this group, more SNPs from candidate genes rather than from GWAS were associated with aggressiveness, and only rarely were the candidate gene SNPs for prostate cancer risk also associated with aggressiveness. John S. Witte (University of California San Francisco, San Francisco, CA) reported on a study that attempted to replicate GWAS risk SNPs for prostate cancer aggressiveness. They found that prostate cancer risk alleles on chromosomes 17 and X were also associated with biochemical failure after treatment; however, many other susceptibility variants were not associated with biochemical failure (7).

Proposed international GWAS of aggressive prostate cancer

Janet L. Stanford (Fred Hutchinson Cancer Research Center, Seattle, WA) discussed preliminary plans for an international collaborative GWAS focused on aggressive prostate cancer. The projected sample size is about 10,000 aggressive prostate cancer cases and 10,000 age-matched controls without diagnosed prostate cancer.

Early age-at-onset prostate cancer

Kathleen A. Cooney (University of Michigan, Ann Arbor, MI) reported evidence for a significant genetic component and more aggressive prostate cancer in young men. The GWAS scan conducted by Cooney and colleagues of early-onset cases versus publicly available controls revealed an association on 8q24 \( (P = 1.2 \times 10^{-8}) \) and 3 other SNPs on chromosomes 10q11, 11q13, and 11p15. The average number of prostate cancer risk alleles was higher in the early-onset cases than in older cases or population controls.

GWAS on variation in prostate-specific antigen values

Julius Gudmundsson (deCODE Genetics, Inc., Reykjavik, Iceland) presented results from a GWAS conducted on variation in prostate-specific antigen (PSA) values, which have high heritability. They identified 6 genome-wide significant loci associated with PSA levels; all but 2 were previously associated with prostate cancer risk (8). New loci on 10q and 12q were associated with basal PSA levels but not with prostate cancer risk. Genetic variants with an impact on basal PSA levels may affect the frequency of recommending a prostate biopsy and cause prostate cancer diagnosis to be delayed among men with genetically low PSA secretion; nevertheless, the improvement from incorporating these SNPs is modest (9).

Familial prostate cancer

Isaacs reported on the International Consortium for Prostate Cancer Genetics (ICPCG) group’s linkage signals on chromosomes 6, 11, and 20 in one large combined analysis of families with more aggressive disease (10) and on chromosomes 1, 4, 8, and 12 in a second set of such families. Follow-up fine-mapping (e.g., see Ostrander below) and whole-exome sequencing studies (e.g., see Thibodeau, Whole-Exome and Genome Sequencing) of some of these linkage signals are being pursued by ICPCG groups.

Ethnic heterogeneity

Rick A. Kittles (University of Illinois, Chicago, IL) noted that ethnic genetic heterogeneity must be considered in GWAS studies because regions associated with prostate cancer in one population cannot be assumed to confer the same level of association in other ethnic groups. Variation exists in allele frequency and in effect size across ethnic groups. Candidate genes and pathways in prostate cancer also have variants that differ significantly across different populations. Risk alleles in regions on 8q24 near MYC are more common in men of African descent and may account for much of the higher risk among men of African versus European descent. Most of the genotyping platforms used for GWAS to date have poor coverage of variants for African-descent populations. Timothy R. Rebbeck (University of Pennsylvania, Philadelphia, PA) reported that the MADCaP (Men of African Descent and Carcinoma of the Prostate) consortium validated the regions on 8q24 in African Americans but could validate only 2 other loci detected from GWAS on European-descent populations (MSMB and JAZF1). GWAS investigations of prostate cancer in African-American men are currently underway (Principal Investigators: Brian E. Henderson, University of Southern California, Los Angeles, CA, and John A. Witte).

Technical Aspects of DNA Sequencing

Several presentations dealt with current approaches to follow-up of promising loci and new DNA sequencing and genotyping technologies.

Fine-mapping studies

In discussing follow-up studies of promising loci, Elaine A. Ostrander (National Human Genome Research Institute, Bethesda, MD) described an example of how her group fine-mapped a susceptibility locus on 22q (10). She emphasized that they had many advantages (e.g., large amount of data from other groups and the ability to narrow the linkage signal to few hundred kilobases in a gene-poor region that was functionally easy to identify) and warned that with other loci, the challenges will be greater.

Whole-exome and genome sequencing

Stephen N. Thibodeau (Mayo Clinic, Rochester, MN) presented pilot studies in whole-exome sequencing in ICPCG families. Dr. Thibodeau selected families with a large number of affected individuals and available first cousins. At the meeting, Thibodeau described advances in sequencing and target capture technology and indicated that they are currently obtaining high-quality data containing up to 150 million reads, more than 70% of the sequences having more than 40× coverage, identifying ~35,000 filtered on-target SNPs of which ~16% were novel, including an average of ~30 splice and ~100 nonsense changes per individual. The remaining changes were missense and synonymous changes. He emphasized the need for considerable quality control and bioinformatics support.
for these projects. To identify candidate targets, they filter the
data initially at sharing across family members for nonsense
and splice variants.

Stephen J. Chanock (NCI, Bethesda, MD) emphasized how
quickly the technology is moving and how difficult it is to
analyze the vast amounts of data generated. Whole-exome
sequencing should be done in families in which multiple
members could also be sequenced for comparative purposes.
Coverage of sequence is the most important consideration.
Current versions of whole-exome sequencing capture meth-
ods provide approximately 70% of the coverage desired, and
up to 2,000 potentially important genes are missed, including
cancer genes. False-negative rates are particularly trouble-
some, and validation is problematic. Bioinformatics issues are
extremely difficult; high errors generate too many false-posi-
tive rates for efficient follow-up with variants; because the
bioinformatics tools for predicting actual functionally, impor-
tant coding shifts or terminations are imprecise, follow-up
analysis should include a large set of variants. An agnostic
testing approach is not feasible because of multiple compar-
isons. Dr. Chanock also questioned the wisdom of attempting
whole-genome sequencing for the opportunity of examining a
favored candidate region.

Bioinformatics

Elliott H. Margulies (National Human Genome Research
Institute, Bethesda, MD) also discussed bioinformatics issues,
explaining techniques for reducing false-positive rates and
statistical “noise.” The sequence reads he has obtained have
increased to 95% of the genome with a low false-positive rate.
He reported that somatic variants are suppressed in noncoding
functional regions and postulated that defining them may be
another way of segmenting the genome into various regions.

New gene chip technology

Pointing out that most of the known prostate cancer risk
alleles have a MAF of 10% or more, Chanock indicated that
more sophisticated technology is needed to find rarer variants
(MAF <5%). He described a new commercial 2.5 million SNP
chip that enables interrogation of less common SNPs, namely,
those with an MAF between 3% and 10%. The chip includes at
least 10% to 15% more common variant bins not captured in
the previous chips.

Prostate Cancer Genetics Consortia

Rosalind A. Eeles (Institute of Cancer Research and Royal
Marsden Hospital, London, UK) reviewed the multiple logis-
tical issues to be considered in setting up genetics research
consortia and highlighted the current activities of several
related consortia, including PRACTICAL (29 groups with
>56,000 samples for follow-up of genetic variants for valida-
tion) and ELLIPSE [NIH-funded U19 (Elucidation of Loci for
Prostate Cancer Susceptibility) investigating the role of SNP
profiles in different aspects of disease progression and man-
gement]. The GWG will coordinate its studies with these
efforts.

Summary

Multiple lines of evidence suggest a genetic component to
prostate cancer aggressiveness, but it has not been possible to
define it using variants identified from current studies. The
clinical importance of unraveling the molecular genetics of
prostate cancer aggressiveness cannot be overstated. This
work is urgently needed, as distinguishing between indolent
and aggressive prostate cancers would be of tremendous
clinical benefit. We propose undertaking genotyping-based
projects here, because, while undertaking sequencing is
appealing, it remains expensive and computationally compli-
cated.

The success of this workshop was evidenced by the number
and quality of scientists in attendance and by the strength of
their presentations. The information presented and the
thoughtful discussion will be valuable in planning the develop-
ment of the GWG consortium, the establishment of the large
prostate cancer patient cohort, and the implementation of the
large case–case–control association study of aggressive
prostate cancer.

Disclosure of Potential Conflicts of Interest

No potential conflicts of interest were disclosed.

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References

1. Penney KL, Pyne S, Schumacher FR, Sinnott JA, Mucci LA, Kraft PL,
et al. Genome-wide association study of prostate cancer mortality.
2. Palansammy N, Ateeq B, Kalyana-Sundaram S, Pfueger D, Ramnar-
ayan K, Shankar S, et al. Rearrangements of the RAF kinase
pathway in prostate cancer, gastric cancer and melanoma. Nat Med
Genomewide scan for prostate cancer-aggressiveness loci. Am J