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Meeting Report

Cancer Research

National Cancer Institute Prostate Cancer Genetics Workshop

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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.*

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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

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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.

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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

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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 methods 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 troublesome, and validation is problematic. Bioinformatics issues are extremely difficult; high errors generate too many false-positive rates for efficient follow-up with variants; because the bioinformatics tools for predicting actual functionally, important 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 comparisons. 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 logistical 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 validation) 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 management]. 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 complicated.

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 development 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. Cancer Epidemiol Biomarkers Prev 2010;19:2869–76.
2. Palanisamy N, Ateeq B, Kalyana-Sundaram S, Pflueger D, Ramnarayanan K, Shankar S, et al. Rearrangements of the RAF kinase pathway in prostate cancer, gastric cancer and melanoma. Nat Med 2010;16:793–8.
3. Witte JS, Goddard KA, Conti DV, Elston RC, Lin J, Suarez BK, et al. Genomewide scan for prostate cancer-aggressiveness loci. Am J Hum Genet 2000;67:92–9.

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4. Stanford JL, McDonnell SK, Friedrichsen DM, Carlson EE, Kolb S, Deutsch K, et al. Prostate cancer and genetic susceptibility: a genome scan incorporating disease aggressiveness. Prostate 2006;66:317–25.
5. Mitra AV, Bancroft EK, Barbachano Y, Page EC, Foster CS, Jameson C, et al. Targeted prostate cancer screening in men with mutations in BRCA1 and BRCA2 detects aggressive prostate cancer: preliminary analysis of the results of the IMPACT study. BJU Int 2011;107:28–39.
6. Fitzgerald LM, Kwon EM, Koopmeiners JS, Salinas CA, Stanford JL, Ostrander EA. Analysis of recently identified prostate cancer susceptibility loci in a population-based study: associations with family history and clinical features. Clin Cancer Res 2009;15:3231–7.
7. Cheng I, Plummer SJ, Neslund-Dludas C, Klein EA, Casey G, Rybicki BA, et al. Prostate cancer susceptibility variants confer increased risk of disease progression. Cancer Elpidemiol Biomarkers Prev 2010; 19;2124–32.
8. Gudmundsson J, Besenbacher S, Sulem P, Budbjartsson DF, Olafsson I, Arinbjamarson S, et al. Genetic correction of PSA values using sequence variants associated with PSA levels. Sci Transl Med 2010;2:62ra92.
9. Witte JS. Personalized prostate cancer screening: improving PSA tests with genomic information. Sci Transl Med 2010;2:62.
10. Schaid DJ, McDonnell SK, Zarfas KE, Cunningham JM, Hebbring S, Thibodeau SN, et al. Pooled genome linkage scan of aggressive prostate cancer: results from the International Consortium for Prostate Cancer Genetics. Hum Genet 2006;120:471–85.
11. Johanneson B, McDonnell SK, Karyadi DM, Quignon P, McIntosh L, Riska SM, et al. Family-based association analysis of 42 hereditary prostate cancer families identifies the apolipoprotein L3 region on chromosome 22q12 as a risk locus. Hum Mol Genet 2010;19:3852–62.