

Genome-Wide Linkage Analysis of 1,233 Prostate Cancer Pedigrees From the International Consortium for Prostate Cancer Genetics Using Novel sumLINK and sumLOD Analyses

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BACKGROUND. Prostate cancer (PC) is generally believed to have a strong inherited component, but the search for susceptibility genes has been hindered by the effects of genetic heterogeneity. The recently developed sumLINK and sumLOD statistics are powerful tools for linkage analysis in the presence of heterogeneity.

METHODS. We performed a secondary analysis of 1,233 PC pedigrees from the International Consortium for Prostate Cancer Genetics (ICPCG) using two novel statistics, the sumLINK and sumLOD. For both statistics, dominant and recessive genetic models were considered. False discovery rate (FDR) analysis was conducted to assess the effects of multiple testing.

RESULTS. Our analysis identified significant linkage evidence at chromosome 22q12, confirming previous findings by the initial conventional analyses of the same ICPCG data. Twelve other regions were identified with genome-wide suggestive evidence for linkage. Seven regions (1q23, 5q11, 5q35, 6p21, 8q12, 11q13, 20p11–q11) are near loci previously identified in the initial ICPCG pooled data analysis or the subset of aggressive PC pedigrees. Three other regions (1p12, 8p23, 19q13) confirm loci reported by others, and two (2p24, 6q27) are novel susceptibility loci. FDR testing indicates that over 70% of these results are likely true positive findings. Statistical recombinant mapping narrowed regions to an average of 9 cM.

CONCLUSIONS. Our results represent genomic regions with the greatest consistency of positive linkage evidence across a very large collection of high-risk PC pedigrees using new statistical tests that deal powerfully with heterogeneity. These regions are excellent candidates for further study to identify PC predisposition genes. *Prostate* 70: 735–744, 2010.

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INTRODUCTION

Prostate cancer (PC) is believed to have a complex environmental and genetic etiology potentially involving numerous genes [1]. The identification of PC genes has proven to be very difficult; genetic heterogeneity is a major issue that hinders progress [2]. Confirmations of reported PC susceptibility loci are infrequent and some of the loci that have been confirmed by multiple researchers are in chromosomal regions with very few promising candidate genes [3,4]. Luo and Yu [5] reported that evidence for PC susceptibility variants had been reported on all but two human chromosomes. These two remaining chromosomes, 21 [6,7] and 22 [8,9], have subsequently both been implicated. The International Consortium for Prostate Cancer Genetics (ICPCG) was formed by a large and diverse group of researchers who have pooled their resources with the intent of deciphering the principal genetic factors underlying this pervasive disease [10]. The ICPCG published the findings of a conventional linkage analysis using the well-known heterogeneity LOD (HLOD) statistic and multiple subset analyses based on 1,233 high-risk PC pedigrees. The study identified several susceptibility loci for further study [8].

Here, we present the results of a secondary analysis of the ICPCG pooled pedigree resource using new genome-wide linkage-based statistics, the sumLINK and sumLOD, to identify PC susceptibility loci. These new statistics have been shown in simulation studies to be powerful and robust tools for identifying susceptibility loci in the presence of genetic heterogeneity [11]. The sumLINK/sumLOD approach is well-suited to analysis of pooled data resources such as this, because it requires only summary data from each constituent group which is logistically easier to attain (there are often data privacy and confidentiality concerns associated with sharing individual raw genotype data and pedigree structures). Secondary analyses of existing data that are more powerful at addressing genetic heterogeneity have the potential to refine the original analyses, and identify additional evidence for PC predisposition genes.

METHODS

The sumLINK approach focuses on "linked" pedigrees, which we define to be a pedigree-specific $\text{LOD} \geq 0.588$ ($P \leq 0.05$). The aim is to identify regions with extreme consistency of linkage evidence across pedigrees. The sumLINK statistic is the sum of multi-

point LOD scores for all pedigrees that meet the threshold of $\text{LOD} \geq 0.588$ at a given point in the genome. This value is computed at intervals of 1 cM throughout the genome. We assess the significance of the sumLINK empirically using a unique genome randomization and shuffling method that simulates the expected consistency of linked pedigrees under null conditions [11]. Briefly, for each pedigree, the vectors of LOD scores for each chromosome are connected in random order, with the first and last values connected to form a "loop," and the loop is broken at a random position to create a randomized, shuffled "genome-wide" vector of LOD scores. These vectors are then aligned across pedigrees and values of the sumLINK statistic are calculated. This procedure is designed to maintain each pedigree's potential for linkage signals across the genome, but randomizes consistency of linkage evidence across pedigrees. Observed peaks are compared with peaks occurring in 1,000 iterations of the randomized data in order to establish the expected frequency of peaks with a similar or greater magnitude for the data in question. This expected frequency may be called a false positive rate (FPR).

The sumLOD statistic is a complimentary companion to the sumLINK statistic. The sumLOD statistic is similar to the sumLINK statistic, but with a reduced inclusion threshold; all positive pedigree LOD scores at each point in the genome are summed to calculate the sumLOD statistic. Significance of the sumLOD is determined empirically by the same genome randomization procedure that is used for the sumLINK. In accordance with the standards for significant linkage evidence set by Lander and Kruglyak [12], peak sumLINK and sumLOD values are considered to represent significant evidence of linkage, if the expected frequency of peaks of similar magnitude under null conditions is <0.05 per genome. Peak values are considered to be suggestive evidence of linkage if the expected frequency is <1 per genome.

We applied the sumLINK and sumLOD procedures to the 1,233 PC pedigrees in the ICPCG pooled pedigree resource. Pedigree characteristics and genotyping details have been described previously [8]. The two statistics were computed at 1-cM increments ($N = 3,502$) throughout the 22 autosomes based on LOD scores from the dominant and recessive inheritance models that were used in the original ICPCG analysis. The sex chromosomes were not included in the analysis. Five hundred seventy-two pedigrees achieved a maximum LOD score of at least 0.588 at

some point in the genome under the dominant inheritance model, and 533 pedigrees achieved a LOD score of at least 0.588 under the recessive model. Only these pedigrees contributed to the sumLINK analyses. One thousand two hundred thirty pedigrees contributed to the sumLOD analysis under each model. Empirical significance was computed based on 1,000 iterations of the genome randomization technique.

FPRs were calculated based on the empirical distributions for each of the four analyses (dominant and recessive, sumLINK and sumLOD). False discovery rate (FDR) *q*-values were estimated to account for the effects of multiple testing that are inherent in the usage of multiple models and statistics. Application of FDR methods to multipoint LOD scores have been shown to be valid provided no fine-mapping markers are used [13]. This requirement is met in the present analysis. The empirical FDR *q*-value represents the probability that a given result is a false positive based on the pooled distributions of all four analyses.

LOCALIZATION

Loci identified with the sumLINK approach have natural potential for subsequent gene localization using statistical recombinant mapping [14], as, by definition, there exist a statistical excess of linked pedigrees contributing to each peak. Hence, for all significant and suggestive sumLINK peaks we will pursue localization using statistical recombinant mapping. The genetic marker sets for which pedigrees were genotyped varied between institutions. Even though the resolution of each separate linkage study map was an average spacing of 10 cM, the disparity of different marker maps helps fine-mapping efforts. If pedigrees from different resources are linked to the same region, they can identify regions smaller than the resolutions of each independent marker map. These genomic segments are the most probable locations for finding a PC susceptibility gene.

Given the linkage evidence for each pedigree is based on a 10 cM map, most pedigrees will have a genotyped marker within 5 cM of any given cM position on the genetic map. Hence, when selecting pedigrees to consider "linked" to a significant or suggestive region, we identified all pedigrees that achieved $\text{LOD} \geq 0.588$ within 5 cM of the observed sumLINK peak. We then examined the LOD score curves for each of these pedigrees and determined the probable location of recombination events that mark the outer limits of the segregating chromosomal segment within each pedigree. Recombinant events are estimated to be at the outer point of an abrupt drop in LOD score, as these positions are statistical

evidence for a loss of genetic sharing by affected pedigree members. A shared chromosomal region bounded by two recombinant events on each side is an approximate 95% confidence interval for the consensus region [14].

RESULTS

Figure 1 shows the genome-wide sumLINK and sumLOD statistics for each model, together with lines representing the thresholds for significant and suggestive linkage as determined by the randomization procedure. Results are summarized in Table I. We identified one locus with significant linkage evidence, and 12 loci with suggestive linkage evidence. There were no significant or suggestive linkage peaks identified by the recessive sumLINK analysis.

Significant linkage evidence was observed at chromosome 22q12 by both the dominant sumLINK (FPR = 0.010, 46 contributing pedigrees) and the dominant sumLOD (FPR = 0.032, 454 contributing pedigrees). In addition to both of these findings being genome-wide significant in their respective single genome-wide screens (FPRs < 0.05), after correction for all four genome-wide analyses, the FDR was 0.186. This indicates that under the null hypothesis, the expected number of peaks at least as extreme as these two is only 0.4 ($= 0.186 \times 2$), and, therefore, that 1.6 of these two peaks are not likely to be from the null distribution. Since both peaks are at 22q12, this indicates that even after correction for the four genome-wide analyses performed here, there is excellent evidence that the 22q12 locus is a true positive.

Suggestive peaks are those that in a single genome-wide screen would only be expected once per genome under the null hypothesis. Twelve loci were identified within their respective single genome-wide analyses to have suggestive evidence for linkage. In decreasing order of significance, these regions were at chromosomes 5q11 (dominant sumLOD and sumLINK), 2p24 (dominant sumLINK), 6p21 (dominant sumLOD and sumLINK), 19q13 (dominant sumLINK), 8q12 (dominant and recessive sumLOD), 8p23 (dominant sumLOD), 11q13 (dominant sumLOD), 20p11-q11 (dominant and recessive sumLOD), 6q27 (recessive sumLOD), 1q23 (dominant sumLINK), 5q35 (dominant sumLINK), and 1p12 (dominant sumLOD). Loci at 5q11 and 2p24, are perhaps worthy of particular note because although strictly only suggestive, both were borderline significant (FPRs of 0.059 and 0.089, respectively). Accounting for the four genome-wide analyses, the FDR value associated with these 18 suggestive and significant peaks (distributed across 13 regions) was 0.262, indicating that only 4.7 (18×0.262) peaks would have been expected under the null. That is, we observed

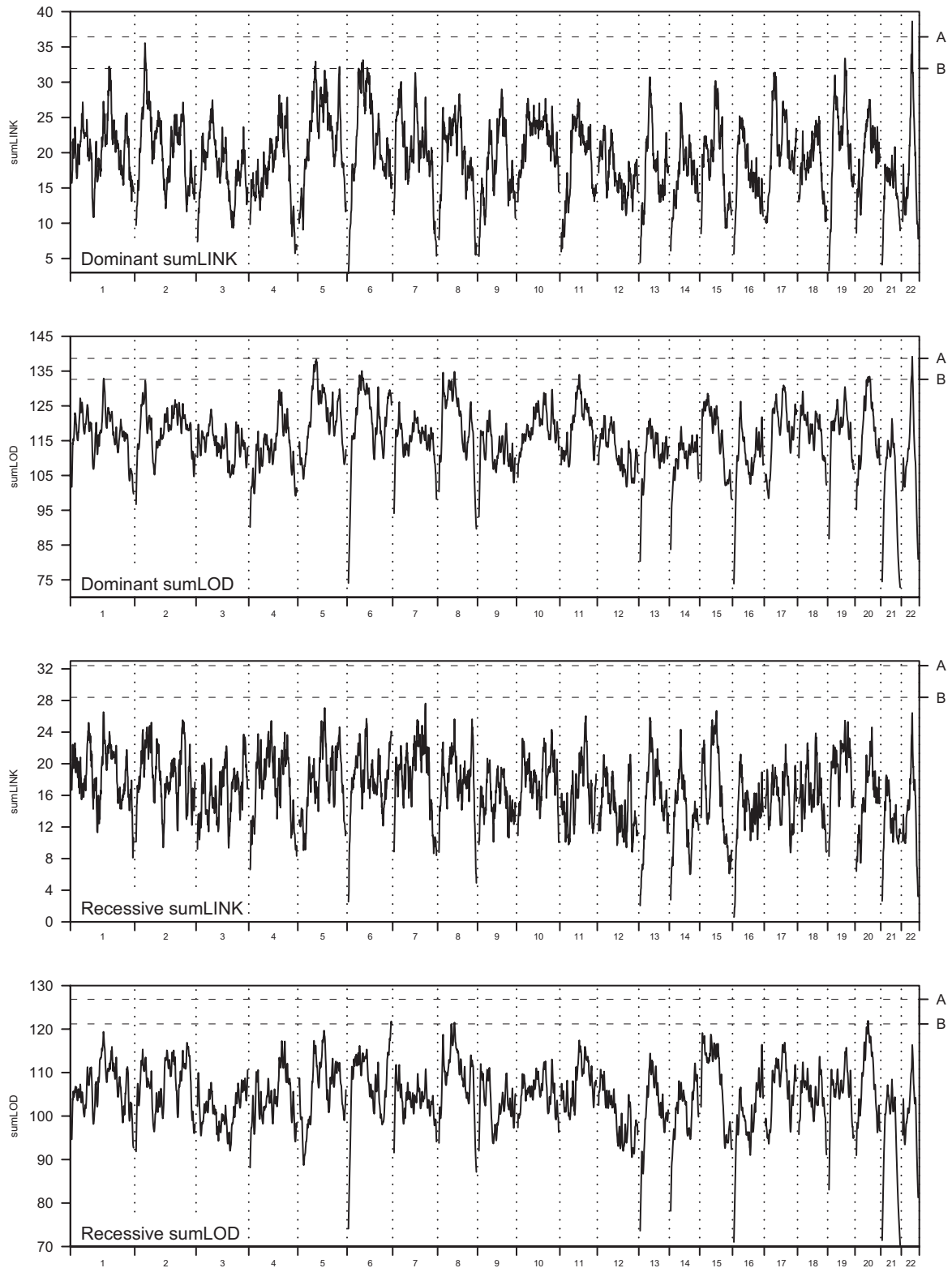


Fig. 1. Genome-wide sumLINK and sumLOD values for dominant and recessive inheritance models. The line marked “A” in each figure represents the threshold for significant linkage evidence determined by the genome shuffling process. The line marked “B” shows the threshold for suggestive linkage evidence. The data underlying this figure is contained in Supplementary Table I.

TABLE I. Chromosomal Regions With At Least Suggestive Linkage Evidence

Chr	Nearest marker	cM	No. of peds contributing	Analysis	Model	FPR	FDR		
							q-Val	Obs peaks	Exp peaks
22q12	D22S283	42	46	sumLINK	Dom	0.010	0.115	1	0.1
	D22S283	42	454	sumLOD	Dom	0.032	0.186	2	0.4
5q11	D5S2500	75	507	sumLOD	Dom	0.059	0.200	4	0.8
	D5S407	72	43	sumLINK	Dom	0.529	0.259	17	4.4
2p24	D2S1360	39	45	sumLINK	Dom	0.089	0.200	4	0.8
6p21	D6S2427	59	495	sumLOD	Dom	0.350	0.259	17	4.4
	D6S1017	64	40	sumLINK	Dom	0.445	0.259	17	4.4
19q13	D19S900	70	43	sumLINK	Dom	0.379	0.259	17	4.4
8q12	D8S285	68	487	sumLOD	Dom	0.393	0.259	17	4.4
	D8S285	68	449	sumLOD	Rec	0.851	0.259	17	4.4
8p23	D8S1130	18	467	sumLOD	Dom	0.442	0.259	17	4.4
11q13	D11S1314	79	491	sumLOD	Dom	0.558	0.259	17	4.4
20p11-q11	D20S912	51	484	sumLOD	Rec	0.688	0.259	17	4.4
	D20S195	58	489	sumLOD	Dom	0.736	0.259	17	4.4
6q27	D6S281	189	450	sumLOD	Rec	0.740	0.259	17	4.4
1q23	D1S2628	164	44	sumLINK	Dom	0.822	0.259	17	4.4
5q35	D5S400	177	43	sumLINK	Dom	0.852	0.259	17	4.4
1p12	D1S534	140	491	sumLOD	Dom	0.935	0.262	18	4.7

False positive rate (FPR) refers to the expected frequency of peaks of similar or greater magnitude based on the results of 1,000 repetitions of the genome randomization procedure. False discovery rate (FDR) results are based on the cumulative distribution of null *P*-values from all analyses. The q-value indicates the proportion of all results of similar or greater significance that are expected to be false positives.

13.3 more peaks than expected, and, thus, 13.3 are likely not from the null. Hence, there is good evidence that many, although not all, of these loci with suggestive evidence for linkage are also true positive findings.

Table II shows the results of our localization analysis for the seven significant and suggestive regions identified with the sumLINK analyses. Estimated regions are based on the observation of two recombination events at each end, indicating an approximate 95% support interval. The microsatellite markers flanking the two-recombinant region are also reported. These two-recombinant localization intervals range from 5 to 17 cM, with a mean of 9.1 cM. Since we

included information from all pedigrees with a $\text{LOD} \geq 0.588$ within 5 cM of the peak, there were some instances where pedigrees showed conflicting evidence about the location of the shared chromosomal region. In these instances, we selected the region where the greatest number of pedigrees agreed, and reported the number of conflicting pedigrees in the table together with the number of supporting pedigrees.

DISCUSSION

We have performed a secondary analysis of data from the largest collection of high-risk PC pedigrees

TABLE II. Localization Intervals for sumLINK Regions

Locus	Peak (cM)	2-recomb. interval (cM)	Supporting pedigrees ^a	Conflicting pedigrees ^b	Flanking markers
1q23	164	161–170	59	0	D1S1677–D1S452
2p24	39	29–40	53	0	D2S1400–D2S1360
5q11	72	72–79	52	2	D5S407–D5S647
5q35	177	168–185	52	0	D5S422–D5S1960
6p21	64	65–74	50	0	D6S1582–D6S1280
19q13	70	63–69	55	2	D19S570–D19S420
22q12	42	37–42	57	0	D22S280–D22S683

^aNumber of pedigrees with $\text{LOD} \geq 0.588$ within 5 cM of the peak.

^bPedigrees that exhibit $\text{LOD} \geq 0.588$ within 5 cM of the peak, but do not agree with the consensus 2-recombinant support interval due to recombination occurring outside the bounds of the interval.

ever assembled with new multipoint linkage-based statistics, sumLINK and sumLOD, which are specifically designed to address genetic heterogeneity. Three of the 13 loci that we identified in the present analysis (5q11, 5q35, and 22q12) correspond directly to peaks that were reported in the original ICPCG analysis using the conventional HLOD statistic [8]. In that analysis, a dominant LOD score of 1.95 was observed at 22q12, which increased to 3.57 in the subset of pedigrees with at least five affected family members. Additionally, a non-parametric LOD of 2.28 was reported at 5q12, and a dominant LOD of 2.05 was reported at 5q35 in the subset of families with mean age at diagnosis ≤ 65 years. Two other loci (1q23 and 8q12) are near peaks that were reported in the first analysis [8]. The loci on chromosomes 6p21, 11q13, and 20p11–q11 correspond to susceptibility loci previously identified in the ICPCG data resource in linkage scans for aggressive PC [11,15]. The remaining loci have not previously been identified in pooled ICPCG data, though many of them correspond to findings reported elsewhere in linkage studies by individual institutions.

The dominant and recessive sumLOD peaks on chromosome 20 appear to be supportive of the HPC20 locus [16], although it should be noted that the original HPC20 linkage peak was at 20q13, about 20–30 cM downstream from the peaks we report here. Our tentative replication of HPC20 is in contrast to an earlier ICPCG study using the same data and a conventional HLOD approach that failed to replicate this locus [10], although a later ICPCG study concentrating on aggressive PC pedigrees did find linkage evidence [15]. The ICPCG aggressive PC linkage study found a dominant LOD score of 2.49 midway between the dominant and recessive sumLOD peaks that we report here. The observed LOD score increased to 2.65 in the subset of pedigrees with mean age at onset > 65 years. The present study includes data from most of the pedigrees that were included in the ICPCG aggressiveness analysis, but the difference in phenotype definition prevents a direct comparison of the pedigrees that contribute to the results. HPC20 was originally identified by the Mayo Clinic site [16,17]; however, of the 45 pedigrees that exhibited $\text{LOD} \geq 0.588$ within 5 cM of the dominant sumLOD peak, only 6 were from Mayo Clinic. As seen from these comparisons, one distinct advantage of the sumLINK and sumLOD statistics is that the approach inherently identifies subgroups of pedigrees that are genetically alike, and hence one analysis can encompass what in conventional analyses may take many subset analyses and multiple testing corrections. It is therefore perhaps not surprising that our results more closely align with linkage findings for subset-based analyses such as aggressive PC [15].

In addition to the findings discussed above, three of the other suggestive linkage regions reported here support previously identified loci. Our peak at 1p12 falls within a region of interest reported by other ICPCG member-sites [17]. The peak at chromosome 1q23 approximates the HPC1 susceptibility region [18], although the *RNASEL* candidate gene proposed as the HPC1 gene [19] is located about 20 Mb beyond the boundary of our support interval. An ICPCG member-site previously reported linkage at 8p23 [20], a finding that was recently replicated and refined by combined somatic deletion and fine linkage mapping [21]. The suggestive sumLOD peak at 8p23 is about 4 Mb from the *MSR1* PC candidate gene. Our 19q13 region also corresponds to previously reported linkage for aggressive PC [22,23].

Our suggestive regions on chromosomes 2p24 and 6q27 appear to be new. Of particular interest of these new loci is perhaps 2p24. Statistical evidence for 2p24 was borderline significant, and recently a germline copy number variant at the 2p24 locus has been associated with aggressive PC [24]. Other notable association studies have focused on regions identified in this report. Copy number variations at 8p23 and 11q13 have been implicated in aggressive PC and PC recurrence, respectively [25]. Kallikrein genes *KLK2* and *KLK3* at chromosome 19q13 have been identified as PC candidate genes [26].

We did not identify linkage evidence to regions that have recently received much attention due to highly significant and replicable association evidence with PC in genome-wide association studies. The most compelling of these results are located on chromosomes 8q24, 17q12, and 10q11 [3]. It is perhaps not surprising that we did not find any evidence to support these regions because these SNPs have common minor allele frequencies and very small effect sizes. The sumLINK and sumLOD are linkage-based statistics, and linkage is most powerful for finding rarer, more highly penetrant variants.

The localization procedure we used here to delimit support intervals generated much more concise intervals than the 1-LOD drop regions reported previously by ICPCG for the four sumLINK peaks that overlapped with previous findings [8]. The intervals reported previously ranged from 12 to 30 cM with a mean length of 21.2 cM, substantially longer than the mean length of 9.5 cM, we report here for the same four regions. A particularly interesting example of the narrower intervals can be seen in the putative susceptibility locus at chromosome 5q11–12. The previous analysis of this data identified a suggestive HLOD peak at 77 cM, with a reported 1-LOD support interval extending from 66 to 96 cM. In the present analysis, the sumLINK statistic identified a suggestive linkage peak at 72 cM

and a two-recombinant support interval of only 7 cM, which includes the original HLOD peak. This ability to more narrowly define regions using statistical recombinant mapping was also illustrated by an earlier candidate region localization study for the chromosome 22q12 susceptibility locus [9]. That report had the advantage of LOD score data from several large pedigrees with fine-mapping markers, which were not included in the present results. Nonetheless, and as expected, the two-recombinant localization region we report here supports the region previously reported in that article.

CONCLUSION

A secondary reanalysis of 1,233 PC pedigrees using novel linkage statistics identified 13 regions with at least genome-wide suggestive evidence for linkage. Eight regions provide confirmation of loci previously identified by conventional linkage analyses in the same ICPCG data [8] or the subset of aggressive PC pedigrees [15], three are regions that confirm loci not seen in the original analyses, but are reported in other linkage studies [21–23,27], and two are novel loci. One distinct benefit of the sumLINK and sumLOD approach is that the statistics are based on the identification of pedigrees that are genetically alike at a locus, and the constituent set of pedigrees may change from locus-to-locus. This both addresses genetic heterogeneity directly and largely circumvents the need for subset and stratification analyses that are costly in terms of multiple testing. This is illustrated by the fact that several of the regions identified here replicate results that were originally found in stratification analyses. The second advantage for the sumLINK statistic is the natural progression to statistical recombinant mapping, which appears to hold much promise for narrowing linkage regions. Furthermore, the FDR approach for correction of multiple genome-wide analyses can better guide interpretation and aid prioritization of findings. Evidence here suggests that these statistics have the potential to further refine the results of original analyses, and provide new directions in the pursuit for PC susceptibility genes.

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