of similar analyses, and this certainly could result from differences in phenotype definition, environmental exposures, or study design (Pajukanta et al. 2000; Francke et al. 2001; Broeckel et al. 2002; Harrap et al. 2002; Chiodini and Lewis 2003). Replication of linkage analyses for complex cardiovascular traits has often proven challenging, and the difficulty in achieving replication for MI underscores the many difficulties in the conduct and interpretation of such linkage analyses (Altmuller et al. 2001).

Identifying genetic factors underlying linkage peaks in this and related studies of MI will require considerable expenditure of resources and should proceed on the basis of the strongest possible evidence. We encourage the systematic comparison of available and accruing linkage data across studies in various CAD phenotypes, including continued assessment of the most appropriate linkage methods.

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0002-9297/2004/7501-0020$15.00

Am. J. Hum. Genet. 75:152–154, 2004

Reply to Newton-Cheh et al.

To the Editor:

Newton-Cheh et al. (2004 [in this issue]) raise the issue of some methodological concerns in our genomewide-scan study that identified significant linkage on chromosome 1p34-36 for premature myocardial infarction (MI). We would like to systematically address their concerns. First, we do explicitly report that the genomewide significance for the chromosome 1p34-36 linkage as $P < .05$ ($P = .030$–$.038$), derived from Wiltshire et al. (2002). This point was duly emphasized in the abstract and the "Results" and "Discussion" sections (Wang et al. 2004). Second, with respect to the high number of loci with asymptotic P values (pP) that were suggestive of linkage, we performed permutation tests and reported empirical P values. As we reported, only the chromosome 1p34-36 locus fulfilled the criteria of genomewide significance. Third, MI is a dichotomous phenotype. Either patients have an MI or do not have this acute ischemic event. As reported by Altmuller et al. (2001), studies of 101 genomewide scans in 31 different diseases revealed that quantitative "intermediate" traits did not have any advantages over dichotomous traits for linkage analysis. Furthermore, several methodological investigations indicated that, in practice, treatment of ordinal (or binary) data as continuous with standard linear models for genetic mapping of categorical traits is feasible, with marginal

Table 1

Five Genomewide Scans for CAD

Study	Population	No. of Families	Mean Age (years)	Locus/Loci	Analysis Programs
Pajukanta et al. 2000	Finnish	156	<55	2q21 and Xq23	MAPMAKER/SIBS, and SIBPAIR in the ANALYZER package
Francke et al. 2001	Mauritian	99	47	16p13	Genehunter 2.1
Broeckel et al. 2002	European	513	52	14q32	SOLAR
Harrap et al. 2002	Australian	61	62	2q36	MAPMAKER/SIBS
Wang et al. 2004	American	428	44	1p34-36	SAGE

loss of statistical powers (Hackett and Weller 1995; Rao and Xu 1998; Rao and Li 2000; Rebai 2000). Fourth, we did indeed use permutation testing, and it was a significant computational burden. In addition, the results of genomewide significance fully incorporated the criteria as set forth by Wiltshire et al. (2002). Fifth, the fine-mapping study is ongoing; we agree that the 10-cM analysis will not maximally extract the identity-by-descent information. Since two markers at the chromosome 1p34-36 locus showed asymptotic multipoint P values of $<10^{-12}$, it is unlikely that further fine mapping will be informative for confirming the finding of this positive linkage. Beyond fine mapping, the most convincing evidence of linkage will be the replication of our findings in an independent population. Sixth, our primary analysis was for both premature MI and coronary artery disease (CAD). No additional subgroups were analyzed by phenotype.

Our population has the most restrictive demographic features of any cohort with CAD to date (Pajukanta et al. 2000; Francke et al. 2001; Broeckel et al. 2002; Harrap et al. 2002; Wang et al. 2004) (table 1). (Not only were our patients the youngest, probably representing the most aggressive phenotype, but the exclusion of other important risk factors, such as insulin-dependent diabetes mellitus or significant hypercholesterolemia, also helped define a cohort with the highest likelihood of genetic underpinning.) Although it is true that our findings of a chromosome 1p locus are not concordant with those of the other four genomewide scans (table 1), our population of young Americans is unique, and it is noteworthy that three of the other four studies (Pajukanta et al. 2000; Francke et al. 2001; Harrap et al. 2002) had a relatively small number of families. Furthermore, each of the studies used a different statistical method implemented in separate programs, and none of the loci recorded to date have been replicated by the other studies.

In summary, we reported a locus with high genomewide significance for linkage of premature MI through use of state-of-the-art analysis, including permutation testing. We look forward to identification of the specific gene(s) underlying this linkage peak and replication of this linkage in an independent population.

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0002-9297/2004/7501-0021$15.00