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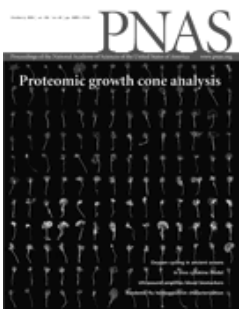

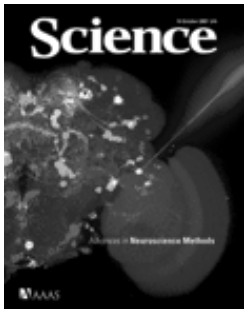

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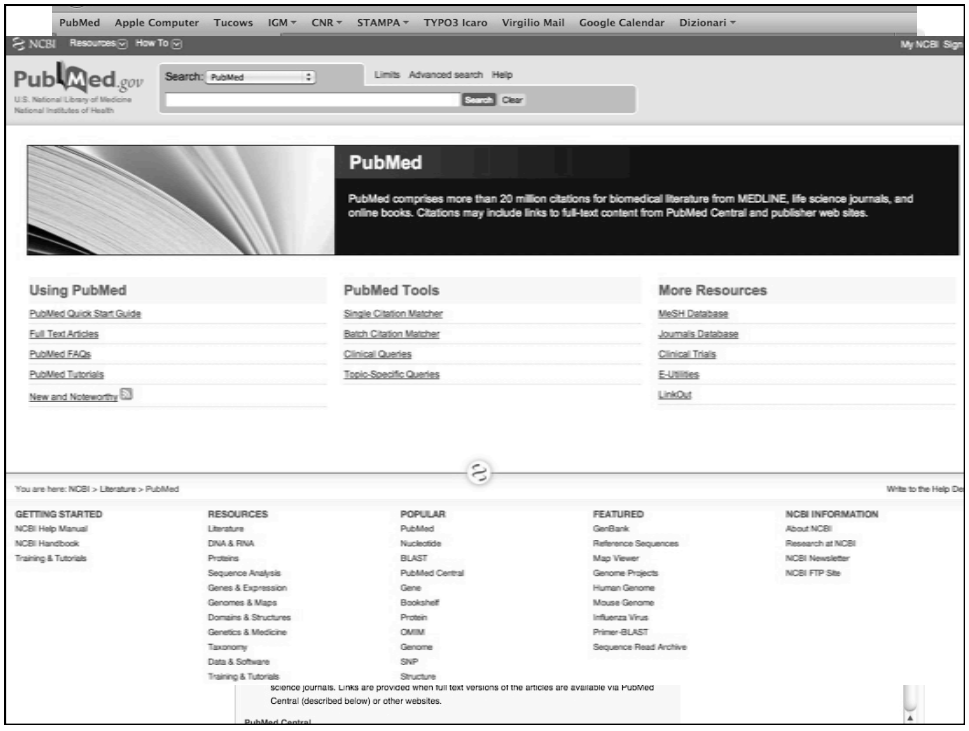

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Letters (also called communications): short descriptions of important current research findings which are usually fast-tracked for immediate publication because they are considered urgent.

Articles: usually between five and twenty pages and are complete descriptions of current original research findings, but there are considerable variations between scientific fields and journals

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nature genetics

Interpreting principal component analyses of spatial population genetic variation

John Novembre[1,3] & Matthew Stephens[1,2]

Nearly 30 years ago, Cavalli-Sforza *et al.* pioneered the use of principal component analysis (PCA) in population genetics and used PCA to produce maps summarizing human genetic variation across continental regions[1]. They interpreted gradient and wave patterns in these maps as signatures of specific migration events[1–3]. These interpretations have been controversial[4–7], but influential[8], and the use of PCA has become widespread in analysis of population genetics data[9–13]. However, the behavior of PCA for genetic data showing continuous spatial variation, such as might exist within human continental groups, has been less well characterized. Here, we find that gradients and waves observed in Cavalli-Sforza *et al.*'s maps resemble sinusoidal mathematical artifacts that arise generally when PCA is applied to spatial data, implying that the patterns do not necessarily reflect specific migration events. Our findings aid interpretation of PCA results and suggest how PCA can help correct for continuous population structure in association studies.

Cavalli-Sforza *et al.*'s classic text "The History and Geography of Human Genes"[1] synthesizes a decades-long survey of human genetic variation. These ground-breaking datasets stimulated development of methods that are now widely used, including application of principal component analysis (PCA) to population genetic variation. In essence, Cavalli-Sforza *et al.* collected count data for many genetic variants ("alleles") from population samples at many geographic locations, and produced for each allele an allele-frequency map, a spatially interpolated map representing variation in allele frequency across space. They then used PCA, a general method for summarizing high-dimensional data, to distill the many allele-frequency maps into a smaller number of "synthetic maps," which for brevity we refer to as PC maps. Intuitively, the first few PC maps summarize the many allele-frequency maps, in that each allele-frequency map can be well approximated by a linear superposition of PC maps.

Figure 1 shows PC maps for Asia, Europe and Africa from refs. 2,3. In interpreting these maps, Cavalli-Sforza and colleagues suggest that "if there is a radiation of circular or elliptic lines from a specific area, a [population] expansion is a possible explanation; and its place of origin must be the center of the radiation" (p. 295 of ref. 3). They also suggest centripetal population movements as an alternative explanation. Examples of their explanations for the European PC maps in **Figure 1** include expansion of agriculturalists out of the Near East (Europe PC1); migrations of Mongoloid Uralic speakers from northwestern Asia (Europe PC2); migration of the carriers of the proto-Indo-European Kurgan culture in Europe (Europe PC3); and an expansion from Greece (Europe PC4).

Because the basis for these interpretive guidelines is unclear, we performed simulations to investigate whether such specific migration events are necessary to explain the observed patterns. Specifically, we performed PCA on data simulated under equilibrium population genetic models without range expansions, assuming a constant homogeneous short-range migration process across both time and (two-dimensional) space. The results showed highly distinctive structure. For example, the first two PC maps show large-scale orthogonal gradients, and the next two show 'saddle' and 'mound' patterns (**Fig. 1**). The same four basic patterns occurred consistently in the first few PC maps across multiple simulations, although not always in the same order (**Supplementary Fig. 1** online). Results for the analogous one-dimensional habitat setting are even more structured, resembling sinusoidal functions of increasing frequency (**Fig. 2, Supplementary Fig. 2** online). Thus PC maps show local peaks and troughs *even when underlying migration patterns are homogeneous across time and space*. This suggests that the local features of the PC maps do not necessarily indicate specific localized historical migration events. Furthermore, many PC maps obtained by Cavalli-Sforza *et al.* in Asia, Europe and Africa show patterns strikingly similar to those from our simulations (**Fig. 1, Supplementary Fig. 1**).

In fact, these highly structured patterns are mathematical artifacts that arise generally when PCA is applied to spatial data in which covariance (similarity) between locations tends to decay with geographic distance. Such data produce highly structured covariance matrices (see, for example, **Supplementary Fig. 3** online), with special mathematical properties. In particular, they have eigenvectors related to sinusoidal waves of increasing frequency (for example, ref. 14). This produces sinusoidal patterns in PC maps because PC maps are visual representations of these eigenvectors (see **Supplementary Methods**

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The NEW ENGLAND JOURNAL of MEDICINE

Genomewide Association Analysis of Coronary Artery Disease

Nilesh J. Samani, F.Med.Sci., Jeanette Erdmann, Ph.D., Alistair S. Hall, F.R.C.P., Christian Hengstenberg, M.D., Massimo Mangino, Ph.D., Bjoern Mayer, M.D., Richard J. Dixon, Ph.D., Thomas Meitinger, M.D., Peter Braund, M.Sc., H.-Erich Wichmann, M.D., Jennifer H. Barrett, Ph.D., Inke R. König, Ph.D., Suzanne E. Stevens, M.Sc., Silke Szymczak, M.Sc., David-Alexandre Tregouet, Ph.D., Mark M. Iles, Ph.D., Friedrich Pahlke, M.Sc., Helen Pollard, M.Sc., Wolfgang Lieb, M.D., Francois Cambien, M.D., Marcus Fischer, M.D., Willem Ouwehand, F.R.C.Path., Stefan Blankenberg, M.D., Anthony J. Balmforth, Ph.D., Andrea Baessler, M.D., Stephen G. Ball, F.R.C.P., Tim M. Strom, M.D., Ingrid Braenne, M.Sc., Christian Gieger, Ph.D., Panos Deloukas, Ph.D., Martin D. Tobin, M.F.P.H.M., Andreas Ziegler, Ph.D., John R. Thompson, Ph.D., and Heribert Schunkert, M.D., for the WTCCC and the Cardiogenics Consortium*

ABSTRACT

BACKGROUND

Modern genotyping platforms permit a systematic search for inherited components of complex diseases. We performed a joint analysis of two genomewide association studies of coronary artery disease.

METHODS

We first identified chromosomal loci that were strongly associated with coronary artery disease in the Wellcome Trust Case Control Consortium (WTCCC) study (which involved 1926 case subjects with coronary artery disease and 2938 controls) and looked for replication in the German MI [Myocardial Infarction] Family Study (which involved 875 case subjects with myocardial infarction and 1644 controls). Data on other single-nucleotide polymorphisms (SNPs) that were significantly associated with coronary artery disease in either study ($P<0.001$) were then combined to identify additional loci with a high probability of true association. Genotyping in both studies was performed with the use of the GeneChip Human Mapping 500K Array Set (Affymetrix).

RESULTS

Of thousands of chromosomal loci studied, the same locus had the strongest association with coronary artery disease in both the WTCCC and the German studies: chromosome 9p21.3 (SNP, rs1333049) ($P=1.80\times10^{-14}$ and $P=3.40\times10^{-9}$, respectively). Overall, the WTCCC study revealed nine loci that were strongly associated with coronary artery disease ($P<1.2\times10^{-5}$ and less than a 50% chance of being falsely positive). In addition to chromosome 9p21.3, two of these loci were successfully replicated (adjusted $P<0.05$) in the German study: chromosome 6q25.1 (rs6922269) and chromosome 2q36.3 (rs2943634). The combined analysis of the two studies identified four additional loci significantly associated with coronary artery disease ($P<1.3\times10^{-6}$) and a high probability (>80%) of a true association: chromosomes 1p13.3 (rs599839), 1q41 (rs17465637), 10q11.21 (rs501120), and 15q22.33 (rs17228212).

CONCLUSIONS

We identified several genetic loci that, individually and in aggregate, substantially affect the risk of development of coronary artery disease.

From the University of Leicester, Leicester (N.J.S., M.M., R.J.D., P.B., S.E.S., H.P., M.D.T., J.R.T.); University of Leeds, Leeds (A.S.H., J.H.B., M.M.I., A.J.B., S.G.B.); University of Cambridge and National Health Service Blood and Transplant, Cambridge (W.O.); and the Wellcome Trust Sanger Institute, Hinxton (P.D.) — all in the United Kingdom; Universität zu Lübeck, Lübeck (J.E., B.M., I.R.K., S.S., F.P., W.L., I.B., A.Z., H.S.); Universität Regensburg, Regensburg (C.H., M.F., A.B.); GSF—Nationales Forschungszentrum für Umwelt und Gesundheit, Neuherberg (T.M., H.-E.W., T.M.S., C.G.); Technische Universität München, Munich (T.M.); Ludwig Maximilians University, Munich (H.-E.W., C.G.); and Johannes Gutenberg University Mainz, Mainz (S.B.) — all in Germany; and INSERM, UMR S525, Université Pierre et Marie Curie, Paris (D.-A.T., F.C.). Address reprint requests to Dr. Samani at the Department of Cardiovascular Sciences, University of Leicester, Glenfield Hospital, Leicester LE3 9QP, United Kingdom, or at njs@le.ac.uk or to Dr. Schunkert at Medizinische Klinik II, Universität zu Lübeck, 23538 Lübeck, Germany, or at heribert.schunkert@innere2.uni-luebeck.de.

*Members of the Wellcome Trust Case Control Consortium (WTCCC) and the Cardiogenics Consortium are listed in the Supplementary Appendix, available with the full text of this article at www.nejm.org.

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LETTERS

Journal name nature genetics

Title Interpreting principal component analyses of spatial population genetic variation

John Novembre[1,3] & Matthew Stephens[1,2] **Authors**

Abstract

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Journal name The NEW ENGLAND JOURNAL of MEDICINE

Title Genomewide Association Analysis of Coronary Artery Disease

Authors

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N Engl J Med 2007;357:

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MATERIALS AND METHODS

RESULTS

DISCUSSION

ACKNWOLEDGMENTS

SUPPLEMENTAL DATA

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5. Karlin S.
Proc Natl Acad Sci U S A. 2005 102(38):13355-62.

Karlin S. 2005.Statistical signals in bioinformatics.Proc Natl Acad Sci USA.102(38):13355-62

1: Karlin S. Statistical signals in bioinformatics. Proc Natl Acad Sci U S A. 2005 102(38):13355-62.

2: Sierotzki H, Frey R, Wullschleger J, et al. Cytochrome b gene sequence and structure of Pyrenophora teres and P. tritici-repentis and implications for QoI resistance. Pest Manag Sci. 2007 63(3):225-33.

1: Karlin S. 2005. Statistical signals in bioinformatics. Proc Natl Acad Sci USA. 102(38):13355-62.

2: Sierotzki H, Frey R, Wullschleger J et al. 2007. Cytochrome b gene sequence and structure of Pyrenophora teres and P. tritici-repentis and implications for QoI resistance. Pest Manag Sci. 63(3): 225-33.

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Cytochrome b gene sequence and structure of Pyrenophora teres and P. tritici-repentis and implications for QoI resistance.

Sierotzki H, Frey R, Wullschleger J, et al.

Sierotzki H, Frey R, Wullschleger J, Palermo S, et al. Cytochrome b gene sequence and structure of Pyrenophora teres and P. tritici-repentis and implications for QoI resistance. Pest Manag Sci. 2007. 63(3):225-33.

nature

http://www.nature.com/nature/authors/gta/index.html#a5.4

J. D. *Nature* **461,** 987-991 (2009).
2. Wyatt, T. D. *Pheromones and Animal Behaviour: Communication by Smell and Taste* (Cambridge Univ. Press, 2003).
3. Dickson, B. J. *Science* **322,** 904-909 (2008).
4. Jallon, J.-M. *Behav. Genet.* **14,** 441-478 (1984).
5. Shirangi, T. R., Dufour, H. D., Williams, T. M. & Carroll, S. B. *PLoS Biol.* **7,** e1000168 (2009).
6. Yew, J. Y. *et al. Curr. Biol.* **19,** 1245-1254 (2009).
7. Ejima, A. *et al. Curr. Biol.* **17,** 599-605 (2007).
8. Kurtovic, A., Widmer, A. & Dickson, B. J. *Nature* **446,** 542-546 (2007).
9. Ha, T. S. & Smith, D. P. *J. Neurosci.* **26,** 8727-8733 (2006).
10. Datta, S. R. *et al. Nature* **452,** 473-477 (2008).

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References

1. Parkin DM, Bray F, Ferlay J, Pisani P. Global cancer statistics, 2002. CA Cancer J Clin 2005;55:74–108.
2. Kmet J, Mahboubi E. Esophageal cancer in the Caspian littoral of Iran: initial studies. Science 1972;175:846–53.
3. Saidi F, Sepehr A, Fahimi S, et al. Oesophageal cancer among the Turkomans of northeast Iran. Br J Cancer 2000;83:1249–54.
4. Semnani S, Sadjadi A, Fahimi S, et al. Declining incidence of esophageal cancer in the Turkmen Plain, eastern part of the Caspian littoral of Iran: a retrospective cancer surveillance. Cancer Detect Prev 2006;30:14–9.
5. Islami F, Kamangar F, Aghcheli K, et al. Epidemiologic features of upper gastrointestinal tract cancers in northeastern Iran. Br J Cancer 2004;90:1402–6.
6. Akbari MR, Malekzadeh R, Nasrollahzadeh D, et al. Familial risks of esophageal cancer among the Turkmen population of the Caspian littoral of Iran. Int J Cancer 2006;119:1047–51.

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Oral Surg Oral Med Oral Pathol. 1978; 46(5):717-20.

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Zucchi I., Dulbecco R. 2002. Proteomic dissection of dome formation in a mammary cell line. J. Mammary Gland Biol. Neoplasia. 7(4):373-84.