The Case for Selection at CCR5-Δ32

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The C-C chemokine receptor 5, 32 base-pair deletion (CCR5-Δ32) allele confers strong resistance to infection by the AIDS virus HIV. Previous studies have suggested that CCR5-Δ32 arose within the past 1,000 y and rose to its present high frequency (5%–14%) in Europe as a result of strong positive selection, perhaps by such selective agents as the bubonic plague or smallpox during the Middle Ages. This hypothesis was based on several lines of evidence, including the absence of the allele outside of Europe and long-range linkage disequilibrium at the locus. We reevaluated this evidence with the benefit of much denser genetic maps and extensive control data. We find that the pattern of genetic variation at CCR5-Δ32 does not stand out as exceptional relative to other loci across the genome. Moreover using newer genetic maps, we estimated that the CCR5-Δ32 allele is likely to have arisen more than 5,000 y ago. While such results can not rule out the possibility that some selection may have occurred at C-C chemokine receptor 5 (CCR5), they imply that the pattern of genetic variation seen at CCR5-Δ32 is consistent with neutral evolution. More broadly, the results have general implications for the design of future studies to detect the signs of positive selection in the human genome.

Introduction

The impact of evolutionary selection on the human population is of central interest and, with increasing information about genetic variation, has become a subject of intense examination [1–6]. Knowledge of selective events and selected loci provide insight into the genetic etiology of human disease, past and present, and into the events that have shaped our species. As infectious diseases pose a major selective force, selected variants may give insight into immunological defense mechanisms—highlighting important pathways in pathogen resistance.

Evolutionary pressure generates a number of potentially detectable signals at a locus under selection as compared to the neutrally evolving genome. Because different populations are subject to distinct selective environments, selection may produce population-specific alleles and greater population differentiation at an affected gene, which can be measured with the FST statistic [7]. Positive selection may also cause a rapid rise in an allele’s frequency, creating a disparity in the age of an allele estimated from its high frequency in the population (characteristic of an old allele) and its long-range linkage disequilibrium (LD, characteristic of a young allele). LD-based methods such as the Long-Range Haplotype test have been developed to detect this signal [3,8–10].

C-C chemokine receptor 5 (CCR5) is one of the most prominent reported cases of recent natural selection in the human genome. First identified as encoding a principal entry receptor for HIV-1 infection of CD4-bearing T lymphocytes, CCR5 has been the subject of intense focus by geneticists [8,11–14]. A well-established association exists between a 32 base-pair deletion variant in CCR5 (CCR5-Δ32) and protection from HIV infection, demonstrating that CCR5 plays an important biological role in HIV entry into cells.

The first suggestion that CCR5 may have been subject to positive selection was a high proportion of nonsynonymous mutations at CCR5, suggesting selective pressure for amino acid divergence [12]. More compelling evidence for selection on CCR5-Δ32 came from work by Stephens et al. [8]. This study found that Δ32 occurs at high frequency in European Caucasians (5%–14%, with north-south and east-west clines) but is absent among African, Native American, and East Asian populations, suggesting that the Δ32 mutation occurred after the separation of the ancestral founders of these populations. Moreover, Stephens et al. [8] reported strong LD between CCR5-Δ32 and two microsatellite markers, suggesting an estimated age for the allele of only ~700 y (range 275–1,875 y). The apparent rapid rise in frequency implied strong positive selection, and the specific age raised intriguing possibilities for the selective agent, such as the bubonic plague in Medieval Europe.

With the recent availability of comprehensive information

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Abbreviations: cM, centimorgan; DAF, derived allele frequency; EHH, extended haplotype homozygosity; EHL, extended haplotype length; LD, linkage disequilibrium; REHH, relative extended haplotype homozygosity; SNP, single-nucleotide polymorphism

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about patterns of allelic diversity in the human genome, we can now reexamine the case for selection at CCR5 by comparison with extensive empirical data and more sophisticated predicted distributions. We carried out high-density single-nucleotide polymorphism (SNP) genotyping around CCR5 in multiple populations, and analyzed the data with the benefit of large genomic comparison datasets and revised physical and genetic maps. Our results show that CCR5-Δ32 does not clearly stand out in terms of genetic diversity or long-range haplotypes relative to other variants at the locus or throughout the human genome.

Results/Discussion

We genotyped CCR5-Δ32, two microsatellites, and 70 SNPs (dbSNP data release 120, www.ncbi.nlm.nih.gov/SNP) extending 837 kbp centromere-distal and 430 kbp centromere-proximal to the CCR5 locus (Table S1). We studied 340 chromosomes from three populations: European-Americans, Chinese, and Yoruba from Nigeria. Eight of the European-American chromosomes bore the Δ32 mutation. In addition, we genotyped a subset of the SNPs in 12 Δ32/Δ32 individuals from the original study. This provided a total of 32 chromosomes bearing the Δ32 allele. We carried out all analyses on both datasets (Table S2).

We first examined the allele frequencies at SNPs around CCR5 in the European-American, Yoruba, and Chinese population samples for evidence of selection. As a genome-wide empirical comparison, we used two datasets. The first is 2,359 SNPs genotyped in the same 340 samples in the three populations. These SNPs are distributed in 168 immunologic genes from 64 loci across the genome; they were chosen according to the same methodology and have a similar physical distribution as for CCR5 [15] (see Materials and Methods). The second is data for 63,149 SNPs on Chromosome 3 from the International HapMap Map Project (HapMap, data release 16) genotyped in the same three populations.

CCR5 is not a significant outlier relative to the 168 genes or HapMap Chromosome 3 with respect to heterozygosity and FST (Table 1; Figure S1). The heterozygosity statistic assesses the genetic diversity in a population; a selective sweep can reduce genetic diversity and balancing selection can increase genetic diversity. The FST statistic [7] compares the frequency of an allele between populations; a population-specific selective pressure may produce greater population differentiation at an affected gene. We also looked at the derived allele frequency (DAF) distribution, which can detect the genetic hitchhiking of variation linked to an allele under positive selection, and found no evidence for selection [16] (Table 1; Figure S2). All of these tests have limited power, with genotyping data ascertained to favor common shared SNPs and using the chimpanzee sequence for comparison. Therefore, while the results provide no evidence for selection, it can not be ruled out; this could be further explored with sequencing of a large number of chromosomes.

We also assessed the significance of the observation that Δ32 is at moderately high frequency (8%) in the European-Americans but absent in the Chinese and Yoruba populations sampled. The observation is not exceptional in our available polymorphic data: of SNPs present at similar frequency (7%–9%) in European-Americans, ~7% are not found in the Chinese and Yoruba populations for the 168 genes, and 6% are not found for the same populations for the HapMap data. These estimates are likely to be conservative considering that the ascertainment of these studies favors shared polymorphisms. As more data become available, this analysis should be extended by larger sample sizes, more populations, and more closely matched data (including insertion/deletion polymorphisms and functional polymorphisms).

We next tested for signatures of selection by examining the extent of LD around CCR5-Δ32. For this purpose, we used the Long-Range Haplotype test for selection [3] (see Materials and Methods). Specifically, we calculated the relative extended haplotype homozygosity (REHH), which is sensitive to recent directional positive selection, and extended haplotype homozygosity (EHH), which is more sensitive to multiple selective sweeps at a locus. To estimate the recombination rate, we used two measures: the genetic distance from a family-based linkage study [17] and the number of observed historical recombination events [3] (Material and Methods).

We initially examined the centromere-distal side of CCR5 using the approach of Stephens et al. [8] (Figure 1A). Specifically, we sorted the chromosomes into two groups: Δ32-bearing and non-Δ32-bearing chromosomes. Consistent with the previous study [8], we found that the Δ32-bearing chromosomes have much longer LD than non-Δ32-bearing chromosomes: the EHH is 5.96 times greater than the average EHH of other variants at this locus (REHH = 5.96 at a distance of 500 kbp or 0.25 centimorgans [cM]) (Figure 1B).

We reasoned, however, that the apparent long-range LD might be a result of sorting the chromosome into only two

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### Table 1. Genetic Diversity at CCR5 in Comparison with Genetic Diversity for Regions from Two Large Empirical Datasets

| Measure | Population | CCR5 | Comparison Regions (64) | HapMap Chromosome 3 |
|---------|------------|------|------------------------|---------------------|
| Average heterozygosity | European-American | 0.34 | 0.27 (0.16–0.39) | 0.29 (0.14–0.44) |
| | Chinese | 0.26 | 0.24 (0.11–0.37) | 0.26 (0.09–0.43) |
| | Yoruba | 0.22 | 0.27 (0.17–0.37) | 0.3 (0.19–0.41) |
| Average FST | European-American versus Chinese | 0.11 | 0.14 (0.02–0.27) | 0.09 (0.03–0.15) |
| | European-American versus Yoruba | 0.12 | 0.16 (0.01–0.30) | 0.14 (0.07–0.21) |
| | Chinese versus Yoruba | 0.19 | 0.17 (0.02–0.31) | 0.16 (0.08–0.23) |
| Average DAF distribution | European-American | 0.34 | 0.35 (0.21–0.48) | 0.41 (0.24–0.58) |
| | Chinese | 0.26 | 0.35 (0.21–0.49) | 0.4 (0.23–0.58) |
| | Yoruba | 0.22 | 0.29 (0.19–0.40) | 0.34 (0.2–0.49) |

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classes based on their genotype at CCR5-Δ32, rather than dividing them according to the full variation seen at CCR5. Figure 2 shows how an apparent signal of long-range LD can readily arise in this fashion. Briefly, one class (for example, the non-Δ32) may contain multiple distinct haplotypes whose individual signals of long-range LD may be obscured when grouped together, with the result that the other class (for example, the Δ32) appears to have much longer relative LD.

In fact, this is precisely the case for CCR5. We fully delineated the variation at CCR5 by genotyping seven additional SNPs within the gene and defined haplotypes as previously described [18] (Figure S3). There are five distinct haplotypes, including the Δ32-bearing haplotype with frequency 8% (Table S3). The relative LD of the Δ32-bearing haplotype is significantly lower than for two other haplotypes (REHH = 1.92 versus 6.77 and 3.29 at distance 500 kbp or 0.25 cM; see Figure 1C), indicating that there is no significant evidence of long-range LD on the centromere-distal side of CCR5.

We next analyzed LD on the centromere-proximal side of CCR5. We first employed the approach used in the original study and again found the Δ32-bearing chromosomes had much longer LD than non-Δ32-bearing chromosomes (REHH = 20.22 at a distance of 250 kbp or 0.25 cM; see Figure 1B). We then reanalyzed the data by disaggregating the chromosomes into the five haplotypes described above. The relative long-range LD for Δ32-bearing chromosomes is much lower (REHH = 7.26), although it is still the highest among the five haplotypes.

We sought to assess whether the extent of LD in the centromere-proximal direction on Δ32-bearing chromosomes is unusual relative to that seen across the human genome. We first compared the results to the genome-wide distribution of REHH scores for the HapMap (Release 16, www.hapmap.org), and found that Δ32-bearing chromosomes do not clearly stand out from other haplotypes of similar frequency (6%–10%) (Figures 3A and S4). Because the 120 European-American chromosomes genotyped in the HapMap project have limited power for studying low-frequency haplotypes (P. V., B. F., E. S. L., and P. C. S., unpublished data), we augmented the analysis by comparing all 32 Δ32-bearing chromosomes to simulations with larger sample size [19] (see Materials and Methods). We simulated 1,000 1-mbp regions in 400 European-American chromosomes under a neutral model, generating 5,915 haplotypes matched with a frequency similar to the Δ32-bearing haplotype (6%–10%). The level of EHH for the Δ32-bearing haplotype was not unusually high on either the centromere-distal (ρ = 0.49) or centromere-proximal (ρ = 0.15) side of CCR5 when compared to the level seen at an equivalent recombination distance for the simulated regions. The REHH (we used the EHH of the two common haplotypes for a relative value) was also not unusually high (Figure 3B).

We further examined the extent of the Δ32-bearing haplotype in comparison to other haplotypes of similar frequency. For this purpose, we defined the extended haplotype length (EHL) on each side of a haplotype to be the genetic distance at which the EHH score falls to 0.5. The EHL for the Δ32-bearing haplotype is 0.212 cM on the centromere-distal side, corresponding to a total of 0.470 cM (Figures 3 and S5). We then determined the EHL for haplotypes of comparable frequency (6%–10%) for both the HapMap data (average EHL is 0.354; CCR5-Δ32 is the 88th percentile) and for the simulated data (average EHL is 0.453; CCR5-Δ32 is the 64th percentile). The distribution is presented in Figure 3. Long-range LD around rare alleles is a prevalent feature in the genome, and the EHL for CCR5-Δ32 therefore does not stand out in comparison to either the HapMap or simulation.
The EHL for CCR5-D32 would only be significant if the recombination rate in this region were several-fold higher than that measured by the current recombinational maps or by counting of historical recombination events (Protocol S1).

Given that long-range LD is a common feature of rare alleles in European-Americans, we wanted to test if our method would have the power to detect selection of an 8% allele over the time scale previously proposed [8]. We simulated 500 regions of 1 mbp length in 400 and 120 European-American chromosomes that had undergone a partial selective sweep beginning either 700 or 2,000 y ago for both groups of chromosomes, carrying the selected allele to a frequency of 8%. We were able to detect recent selection in the 400 chromosomes; 69% of selected alleles originating 700 y ago and 39% of selected alleles originating 2,000 y ago have EHL values above the 95th percentile when compared to the neutral distribution. There is far less power in the 120 chromosomes (30% and 10% of selected alleles originating 700 y ago and 39% of selected alleles originating 2,000 y ago have EHL values above the 95th percentile when compared to the neutral distribution). With improvements in the genetic map over the past 7 y [17], the microsatellites were shown to be on opposite sides of CCR5 and at a much shorter genetic distance (0.18 cM, Figure S6). Using the methodology and data employed by Stephens et al. [20] (Table S5), but with the revised genetic map, the estimated age rises from 688 y (275–1,875 y, 95% confidence interval) to 7,000 y (2,900–15,750 y, 95% confidence interval). When we expanded the analysis to include 32 genetic markers that have been genotyped in the D32-bearing chromosomes, the estimated age also rises, to a similar value of 5,075 y (3,150–7,800 y, 95% confidence interval). The SNP-based estimate of the age differs and has tighter error bars because the denser map holds more information about historical recombination events than the two microsatellites, whose genetic diversity is roughly equivalent to two SNPs (Figure S7). The older age estimate is consistent with unpublished work on DNA extracted from 3,000-y-old burial sites in central Germany showing that the CCR5-D32 was present at an appreciable frequency several millennia ago, at least in central Germany [21].

Finally, we revisited the estimated date of origin for the CCR5-D32 mutation. The original estimate [8] was based on the analysis of two microsatellites that were in strong LD despite apparently being at a considerable genetic distance away (0.91-cM interval and both centromere-distal, according to the genetic maps that were current at the time). With improvements in the genetic map over the past 7 y [17], the microsatellites were shown to be on opposite sides of CCR5 and at a much shorter genetic distance (0.18 cM, Figure S6). Using the methodology and data employed by Stephens et al. [20] (Table S5), but with the revised genetic map, the estimated age rises from 688 y (275–1,875 y, 95% confidence interval) to 7,000 y (2,900–15,750 y, 95% confidence interval).

Figure 2. Model of Haplotype-Based Selection Approach

The image compares this approach, where the variants at the gene being studied are fully elaborated, to a model where the variants are not fully elaborated. At the top, multiple SNPs are genotyped to fully define the variants that exist in the gene. The resultant observed haplotype structure is shown in both bifurcation diagram and EHH plot formats (see Materials and Methods). At the bottom, only one SNP is genotyped, collapsing all other variants into a seemingly diverse super-haplotype and creating an impression of extension for the remaining haplotype.

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selective event within the past millennium. If selection did play a role in the high frequency of the allele, the initial selection pressure must have occurred before the period calculated in the previous estimate [8]. It should be noted that the data do not rule out some additional selection occurring within the past millennia, but none that would be detected by the methodology used in Stephens et al. or in the current paper.

Our reanalysis of CCR5 shows that CCR5-D32 does not clearly stand out from the rest of the genome in terms of allele frequency distribution, population differentiation, or long-range LD (Figure S8). The high population differentiation and long-range LD found for CCR5-D32 are, in fact, far more common in the genome than previously believed, and therefore do not provide support for the hypothesis of strong selection for CCR5-D32. Using methods described both in the previous study [8] and in the current study, and by examining currently available data, there is no detectable evidence for recent selection for CCR5-D32. Of course, the lack of support does not exclude the possibility of selection for the allele or the locus. Given the biology of the gene, it is certainly possible that it has been subject to some selection despite the lack of clear evidence. We note that small-scale studies of the distribution of mutations [12–14,22] have provided suggestive evidence for selection, but these results may be less convincing in comparison to recently available genome-wide distributions [23].

Beyond the specific results for CCR5, our results have important implications for studies of selection in the human genome. First, accurate assessment of LD benefits from fully delineating the core haplotypes at a locus; it may not be sufficient to compare a haplotype of interest to the set of all other haplotypes. Second, long-range LD around specific alleles is a prevalent feature in the genome; the significance of LD results should therefore be assessed relative to empirical distributions observed in genome-wide studies with larger numbers of samples. Third, accurate estimates of an allele’s age require accurate genetic maps.

With the growing availability of genome-wide datasets, it should soon be possible to search the genome for signs of strong selective events [3] by studying the pattern of variation at every gene relative to a comprehensive genome-wide distribution. The results should shed light on important factors that have shaped our species and may provide valuable information about natural mechanisms of disease resistance.

Materials and Methods

Samples. DNA samples for 93 individuals from 12 multigenerational pedigrees of European-American ancestry were obtained from Coriell Repositories (http://locus.umdnj.edu/ccr). DNA samples from 93 healthy individuals (31 mother–father–child clusters) from the Yoruba in Nigeria were obtained as part of the International Collaborative Study of Hypertension in Blacks. DNA samples from 30 Han Chinese trios from Guanchi were included. DNA samples
from a chimpanzee, gorilla, and orangutan were obtained from Coriell Repositories.

Genotype data. We genotyped 71 SNPs in and around the CCR5-Δ32 using the mass spectrometry-based MassArray platform provided by Sequenom (San Diego, California, United States), implemented as previously described [18]. The names, locations, alleles, and flanks for all SNPs used are shown in Table S1. Microsatellite genotyping was conducted at the McGill University and Genome Quebec Innovation Center (Quebec, Canada), by use of MultiProbe and MiniTrak Liquid Handling Systems (Perkin-Elmer, Wellesley, California, United States) and 3730 DNA sequencers (Advanced Biosystems, Foster City, California, United States). PCR was performed with fluorescently labeled markers in standard conditions (annealing temperature of 54 °C).

We also used genotypes of 2,359 SNPs, distributed in 168 immunologic genes from 64 loci throughout the genome in the same three populations [15]. SNPs were selected from public databases in our ascertainment of haplotype structure and may reduce the representation of rare and population-specific variation; we comment in the paper where this bias might affect our observations.

We used publicly available data from the International Haplotype Map Project as a comparative distribution of variance in the genome with which to compare our results (http://www.hapmap.org).

Phasing. We prepared these files using Genehunter (http://www.broad.mit.edu/distribution/software/genehunter/) to uncover unambiguous phasing using family data [25]. The child chromosomes broad.mit.edu/ftp/distribution/software/genehunter/) to uncover unambiguous phasing using family data [25]. The child chromosomes were then discarded, and we kept only the independent parent chromosomes. We then used PHASE (http://www.stat.washington.edu/stephens/software.html [26-27]) to obtain complete phased data.

Simulations. We used a computer program that simulates gene history with recombination based on a neutral model of evolution described elsewhere [19,28]. The program was modified to generate data comparable with that collected from the three populations—Chinese, European-American, and Yoruba. The simulations were calibrated to provide data consistent with the HapMap with respect to various genetic measures (including $F_{ST}$, heterozygosity, and minor-allele frequency distribution) and used model parameters (including demographic and recombination rate) consistent with current estimates [19]. We simulated a long region (1 mlp in length) of DNA and then mimicked the SNP selection strategy used by the SNP Consortium [29], which was the source of most of the SNPs in our study. We modified the program to generate simulations of a partial selective sweep in 400 European-American chromosomes, where 32 chromosomes had a common ancestor 2000 y ago. We also tested where the 32 chromosomes had a common ancestor 700 y ago as per Stephens et al. [8]. We also tested where the 32 chromosomes had a common ancestor 2000 y ago.

$F_{ST}$. Mean pairwise distance fixation index, $F_{ST}$, was used to calculate genetic differentiation between the three populations [30,31]. $F_{ST}$ partitions the total variance into within- and between-population components, quantifying the inbreeding effect of population substructure.

Heterozygosity. Nei’s measure of heterozygosity [32], the probability that any two randomly chosen samples from a population are the same, was used to calculate SNP diversity:

$$\pi = \frac{n}{n-1} \left(1 - \frac{p_i^2}{p_i}\right)$$

where $n$ is the number of alleles at a locus, and $p_i$ is the frequency of the $i$th allele.

DAF distribution. We calculated the DAF distribution for all SNPs where it was likely that the ancestral allele could be determined by genotyping a representative chimpanzee, gorilla, and orangutan. If there was consensus primate allele across all successfully genotyped primates, it was identified as the ancestral allele. Otherwise, no ancestral allele was defined.

EHH, EHH. EHH assesses the age of each haplotype at a gene by measuring the decay of the extended ancestral haplotype (i.e., SNPs far away from the gene), which occurs over time with recombination. For a population of individuals sharing core haplotype $X$, EHH is the probability that any two randomly chosen samples of core haplotype $X$ have the same extended haplotype [3]. It is a measure of the decay of LD across a region of the genome that has two advantages: first, it can be used with multi-allelic markers so a core haplotype model can be studied if desired, and second, it measures LD across a region with many loci and not just between a pair of loci. The EHH is calculated as:

$$EHH = \frac{\sum_{i=1}^{n} \left(\frac{f_i}{2}\right)}{\sum_{i=1}^{n} \left(\frac{f_i}{2}\right)^2}$$

$$EHH = \frac{\sum_{i=1}^{n} \left(\frac{f_i}{2}\right)}{\sum_{i=1}^{n} \left(\frac{f_i}{2}\right)^2}$$

where $i$ is the core haplotype tested, $e$ is the number of samples of a particular core haplotype, $e$ is the number of samples for a particular extended haplotype, and $s$ is the number of unique extended haplotypes.

The relative EHH (i.e., REHH) is simply $EHH/EHH$. EHH and REHH were calculated for all haplotypes in all haplotype blocks for CCR5, HapMap Release 16 Chromosome 3, and the 1,000 simulated regions (120-chromosome and 500-chromosome sample sets). Haplotypes were placed into 20 bins based on their frequency. $p$-Values were obtained by log-transforming the EHH and REHH in the bins to achieve normality, and calculating the mean and standard deviation. All analysis was carried out using the Sweep software program (P. V., B. F., E. S. L., and P. C. S., unpublished data).

Observed historical recombination (marker breakdown, all EHH). When comparing EHH/REHH values across regions, it is important to make sure that the value is being calculated at a similar genetic distance. This will soon be replaced with better CM values, but, where they are not known, this can be matched by the “marker breakdown,” that is the degree to which each added marker at a further distance causes the extended haplotypes to decay for all core haplotypes [3]. This gives an evaluation of how much historical recombination (observed recombinants) has occurred over a distance from the core, and therefore what generic distance is being looked at. This can be calculated as “all EHH.”

$$relEHH = \frac{\sum_{i=1}^{n} \left|\sum_{j=1}^{n} f_i f_j\right|}{\sum_{i=1}^{n} \left|\sum_{j=1}^{n} f_i f_j\right|}$$

where $n$ is the number of different core haplotypes, $e$ is the number of samples of a particular core haplotype, $s$ is the number of samples of a particular extended haplotype, and $s$ is the number of unique extended haplotypes.

Bifurcation diagram. To visualize the breakdown of LD on core haplotypes, we used bifurcation diagrams [3]. The root of each diagram is a core haplotype, identified by a dark-blue circle. The diagram is bidirectional, portraying both proximal and distal LD. Moving in one direction, each marker is an opportunity for a node; the diagram either divides or not, depending on whether both or only one allele is present. Thus, the breakdown of LD on the core haplotype background is portrayed at progressively longer distances. The thickness of the lines corresponds to the number of samples with the indicated long-distance haplotype.

Supporting Information

Figure S1. $F_{ST}$ and Heterozygosity for SNPs within 100 kb of CCR5 Genotyped to 100-kbp Sliding Windows for HapMap Release 16 for European-Americans

Found at DOI: 10.1371/journal.pbio.0030378.sg001 (54 KB DOC).

Figure S2. The DAF Distribution of CCR5 Compared to 100-kbp Sliding Windows for HapMap Release 16 for European-Americans

Found at DOI: 10.1371/journal.pbio.0030378.sg002 (62 KB DOC).
Figure S3. Haplotype Bifurcation Diagrams in European-Americans Found at DOI: 10.1371/journal.pbio.0030378.sg003 (231 KB DOC).

Figure S4. The REHH versus Frequency Distribution at Matched Genetic Distance [17] Found at DOI: 10.1371/journal.pbio.0030378.sg004 (99 KB DOC).

Figure S5. Estimating the Rate of Degradation of EHH Found at DOI: 10.1371/journal.pbio.0030378.sg005 (40 KB DOC).

Figure S6. Remapping of Microsatellite Markers from First Study Given the Improved Genomic Maps Found at DOI: 10.1371/journal.pbio.0030378.sg006 (45 KB DOC).

Figure S7. Microsatellite Genotyping Found at DOI: 10.1371/journal.pbio.0030378.sg007 (71 KB DOC).

Figure S8. Comparison of Overall Genetic Diversity and Specific Haplotype EHH in Different Populations Found at DOI: 10.1371/journal.pbio.0030378.sga08 (38 KB DOC).

Protocol S1. Recombination-Rate Estimates for CCR5 from Family-Based Linkage Studies (deCODE and Marshfield Maps), from Preliminary Sperm-Typing, and from Population Genetics (LDhat) Found at DOI: 10.1371/journal.pbio.0030378.sd001 (32 KB DOC).

Table S1. Information for Δ32 (rs333), 70 SNPs, and Two Microsatellites Used in the Study Found at DOI: 10.1371/journal.pbio.0030378.sd002 (30 KB XLS).

Table S2. CCR5-Δ32 EHH Values for Eight European-American Chromosomes versus the 32 Total Genotyped Chromosomes Found at DOI: 10.1371/journal.pbio.0030378.sd003 (25 KB DOC).

References
1. Olson S (2002) Population genetics. Seeking the signs of selection. Science 298: 1324–1325.
2. Bamshad M, Wooding SP (2003) Signatures of natural selection in the human genome. Nat Rev Genet 4: 99–111.
3. Sabeti PC, Reich DE, Higgins JM, Levine HZ, Richter DJ, et al. (2002) Detecting recent positive selection in the human genome from haplotype structure. Nature 419: 832–837.
4. Akey JM, Eberle MA, Rieder MJ, Carlson CS, Shriver MD, et al. (2004) Population history and natural selection shape patterns of genetic variation in 132 genes. PLoS Biol 2: e286. DOI: 10.1371/journal.pbio.0020286.
5. Walsh EC, Mathei KA, Schaffner SF, Farwell L, Daly MJ, et al. (2003) An integrated haplotype map of the human major histocompatibility complex. Am J Hum Genet 73: 580–590.
6. Rockman MV, Hahn MW, Soranzo N, Loisel DA, Goldstein DB, et al. (2004) Positive selection on MMP3 regulation has shaped heart disease risk. Curr Biol 14: 1531–1537.
7. Taylor MF, Shen Y, Kreitman ME (1995) A population genetic test of coalescence of haplotypes. Am J Hum Genet 62: 1507–1515.
8. Tishkoff SA, Varkonyi R, Cahinhinan N, Abbes S, Argyropoulos G, et al. (2001) Haplotype diversity and linkage disequilibrium at human GGP2: Recent origin of alleles that confer malaria resistance. Science 295: 455–462.
9. Toomajian C, Ajoka RS, Jorde LB, Kushner JP, Kreitman M (2003) A method for detecting recent selection in the human genome from allele frequency estimates. Genetics 163: 287–297.
10. Dean M, Carrington M, Winkler C, Huttley GA, Smith MW, et al. (1996) Genetic restriction of HIV-1 infection and progression to AIDS by a deletion allele of the CCR5 structural gene. Hemophilia Growth and Development Study, Multicenter AIDS Cohort Study, Multicenter Hemophilia Cohort Study, San Francisco City Cohort, ALIVE Study. Science 273: 1856–1862.
11. Carrington M, Kissner T, Gerrard B, Ivanov S, O’Brien SJ, et al. (1997) Novel alleles of the chemokine-receptor gene CCR5. Am J Hum Genet 61: 1261–1267.
12. Carrington M, Dean M, Martin MP, O’Brien SJ (1999) Genetics of HIV-1 infection: Chemokine receptor CCR5 polymorphism and its consequences. Hum Mol Genet 8: 1939–1945.
13. Bamshad MJ, Haldorsen H, Eriksen G, Eriksen G, et al. (2002) A strong signature of balancing selection in the 5’ cis-regulatory region of CCR5. Proc Natl Acad Sci U S A 99: 10539–10544.
14. Walsh EC, Sabeti P, Hutcheson HB, Fry B, Schaffner SE, et al. (2005) Searching for signals of evolutionary selection in 168 genes related to immune function. Hum Genet. In press.
15. Fay JC, Wu CI (2000) Hitchhiking under positive Darwinian selection. Genetics 155: 1405–1413.
16. Kong A, Gu, B., Saitou R, Tsuchida T, Gunji T, et al. (2002) High-resolution recombination map of the human genome. Nat Genet 31: 241–247.
17. Carrington M, Kissner T, Gerrard B, Ivanov S, O’Brien SJ, et al. (2002) Detecting recent positive selection in the human genome from haplotype structure. Nature 419: 832–837.
18. Gabriel SB, Schaffner SF, Nguyen H, Moore JM, Roy J, et al. (2002) The structure of haplotype blocks in the human genome. Science 23: 2225–2229.
19. Schaffner S, Fuso C, Gabriel SB, Reich D, Daly MJ, et al. (2005) Calibrating a coalescent simulation of human genome sequence variation. Genome Res. In press.
20. Reich DE, Goldstein DB (1999) Estimating the age of mutations using variation at linked markers. In: Goldstein DB, Schlötter C, editors. Microsatellites: Evolution and applications. Oxford: Oxford University Press. pp. 128–138.
21. Duncan SR, Scott S, Duncan CJ (2005) Reappraisal of the historical selective pressures for the CCR5-Δ32 mutation. J Med Genet 42: 205–208.
22. Wooding S, Stone AC, Dunn DM, Mummadri S, Jorde LB, et al. (2005) Contrasting effects of natural selection on human and chimpanzee C-C chemokine receptor 5. Am J Hum Genet 76: 291–301.
23. Nielsen R, Bustamante C, Clark AG, Glanowski S, Sackton TB, et al. (2005) A scan for positively selected genes in the genomes of humans and chimpanzees. PLoS Biol 3: e170. DOI: 10.1371/journal.pbio.0030170.
24. Reich DE, Gabriel SB, Altshuler D (2005) Quality and completeness of SNP databases. Nat Genet 35: 457–458.
25. Kruglyak L, Daly MJ, Reeve-Daly MP, Lander ES (1996) Parametric and nonparametric linkage analysis: A unified multipoint approach. Am J Hum Genet 58: 1347–1363.
26. Stephens M, Donnelly P (2000) A comparison of Bayesian methods for haplotype reconstruction from population genotype data. Am J Hum Genet 76: 1162–1169.
27. Stephens M, Smith NJ, Donnelly P (2001) A new statistical method for haplotype reconstruction from population data. Am J Hum Genet 68: 978–989.
28. Hudson RR (1996) Genealogies and the coalescent process. Oxford University Press. 7: 1–44.
29. Sachidanandam R, Weissman D, Schmidt SC, Kakol JM, Stein LD, et al. (2001) A map of human genome sequence variation containing 1.4 million single nucleotide polymorphisms. Nature 409: 928–933.
30. Nei M, VanDevanter RR (1983) Estimation of fixation indices and gene diversities. Ann Hum Genet 47: 253–259.
31. Akey JM, Zhang G, Zhang K, Jin L, Shriver MD (2002) Interrogating a high-density SNP map for signatures of natural selection. Genome Res 12: 1805–1814.
32. Nei M (1987) Molecular evolutionary genetics. New York: Columbia University Press. 512 p.