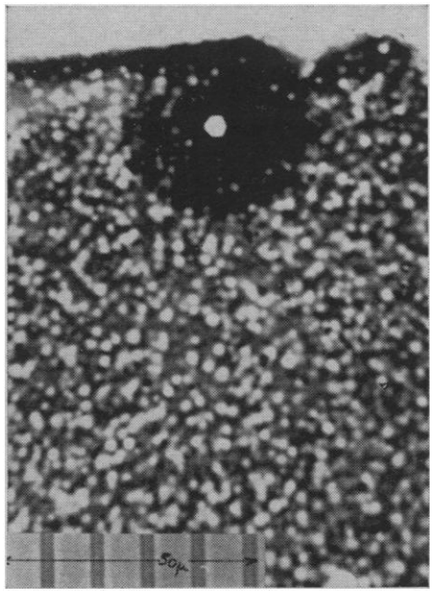

Fig. 2. Fossil α-recoil centers in the vicinity of a ^{210}Po halo (phase contrast).

halo types. The background fossil α-recoil density was measured before a count was made in the mica cleavage plane about 5 to 10 μ directly above the halo nucleus. The mica was then cleaved until the central inclusion appeared on the surface; the mica was etched again and another count was made to enable a density comparison of three separate regions.

The mean fossil α-recoil densities were 12.7×10^6 and 11.6×10^6 α/cm^2 for the Canadian and Irish micas, respectively, regardless of where the α-recoil count was taken. For a given etch period these results are reproducible within $\pm$ 10 percent. The fission-track density exhibited a random distribution in each piece of mica except (as expected) near the ^{238}U halos. The α-recoil:fission-track ratios were about 2.5×10^3 and 3.0×10^3, respectively, for the Canadian and Irish micas. Huang and Walker (*16*) have shown that the background α-recoil density in micas is due to both uranium and thorium α-decay; by using 100 Å and 10 μ for the alpha-recoil and fission-track ranges, respectively, one can determine that uranium alone contributes an α-recoil:fission-track ratio of about 2.2×10^3, any excess being due to thorium. Figure 2 portrays a ^{210}Po halo (Irish mica) showing the distribution of α-radioactivity (fossil α-recoil centers) in the vicinity.

As far as the experimental analysis is concerned, there is no detectable difference in the microscopic distribution of α-radioactivity (with respect to background density) near either the uranium or the polonium halos. [I note that thin clefts, which usually result near the edges of the mica from weathering (but not within the bulk of the mica), are easily detected by an acid etch since α-recoil tracks appear throughout the extent of the cleft area.] This finding seems to imply that there was no gross transport of α-radioactivity to the polonium-halo inclusions (i) by way of laminar flow of solutions (through thin clefts) disequilibrated as to uranium daughter-product activity, or (ii) by diffusion of radon, since an increased α-recoil density, higher than background by several orders of magnitude, should be evident within a 10-μ radius of the halo inclusions in either case. This last value is a conservative estimate, for I have considered only the decay of ^{218}Po atoms en route to an inclusion. Furthermore, autoradiographic experiments on the samples of Canadian mica containing ^{238}U, ^{232}Th, and polonium halos showed only the normal background distribution of α-tracks, indicating that if excess activity now exists it is below the detection level of the method.

Thus, as far as the experimental analysis is concerned, I cannot confirm Henderson's model for the secondary origin of the polonium halos. To the question of what mode of origin is consistent with the relatively short half-lives of the polonium isotopes (or their β-decaying precursors), I can say only that other mechanisms are under study.

Whatever hypothesis is invoked, to explain the origin of the polonium halos, must also explain both the one found by Henderson (*19*) [due to a combination of isotopes from both the thorium series (^{212}Po and ^{212}Bi) and the uranium series (^{210}Po)] and a halo presumably due to ^{211}Bi (*12*) from the ^{235}U series. Perhaps most interesting of all is the occurrence of 20,000 to 30,000 ^{218}Po and ^{210}Po halos per cubic centimeter in a Norwegian mica—without the ^{214}Po halos.

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20. I thank Paul Ramdohr, University of Heidelberg, for this particular specimen. Also I thank R. R. Gorbatschev (Uppsala), B. Loberg (Stockholm), D. E. Kerr-Lawson (Swastika, Ontario), J. H. J. Poole (Trinity College), and J. A. Mandarino (Royal Ontario Museum) for other mica specimens containing halos. I also thank H. L. Price for assisting in the α-recoil analysis and John Boyle, Oak Ridge National Laboratory, for the α-recoil experiments. For more extensive investigation I would appreciate contributions of samples of biotite from as many Precambrian localities as possible.

26 April 1968

Haptoglobin and Catalase Loci in Man: Possible Genetic Linkage

Abstract. *Slow- and fast-migrating electrophoretic variants of human erythrocyte catalase were encountered in four of approximately 200 families. Tests for nine genetic polymorphisms provided evidence suggesting linkage only in the case of the haptoglobin system.*

During a genetic study of blood specimens from a Brazilian population sample (*1*), four families were encountered in which electrophoretic variants of erythrocyte catalase were segregating (*2*). One variant, observed in three families, had an electrophoretic mobility that was about 7-percent faster than that of the usual enzyme type; the second had a mobility about 4-percent slower than normal (Fig. 1). The slow variant may be identical with Baur's Ct

Table 1. Segregation of catalase variants.

Mating type		Families (No.)	Offspring (No.)			Total
Father	Mother		Ct AB_2	Ct A	Ct AC_1	
Ct A	Ct AC_1	2	0	9	6	15
Ct AC_1	Ct A	1	0	4	6	10
Ct AB_2	Ct A	1	2	3	0	5
				Totals		
		4	2	16	12	30

Table 2. *Z*-Scores for haptoglobin-catalase linkage.

Family (No.)	Catalase alleles	*Z*-Scores for six recombination frequencies (θ)					
		0.05	0.10	0.15	0.20	0.30	0.40
407	Ct^A, Ct^{B2}	0.814	0.720	0.621	0.517	0.298	0.094
852	Ct^A, Ct^{C1}	− 0.628	− 0.167	.036	.129	.146	.058
227	Ct^A, Ct^{C1}	0.929	1.042	1.020	.934	.647	.260
				Totals			
		1.115	1.595	1.677	1.580	1.091	0.412

AB (*3*), although differences in technique make comparison difficult. The variant phenotypes were transmitted by parents of both sexes to approximately half their offspring of both sexes (Table 1). These findings suggest that the three phenotypes observed in this study correspond to the homozygous expression of a common allele, Ct^A, and heterozygosity for two rare alleles, Ct^{C1} and Ct^{B2}, an interpretation that accords with the observation that acatalasemia also is caused by an autosomal gene (*4*). Fresh blood samples were not available for quantitative comparison of the enzyme activity in the Ct A, Ct AB_2, and Ct AC_1 phenotypes, but no suggestion of difference was apparent from comparison of the phenotypes on starch gels.

One or more affected parents were also heterozygous at nine other loci. Linkage studies, with the Lod-score (*Z*-score) method (*5*), showed no evidence of even loose linkage with the *Rh, Gm, Inv, MNS, P, Fy, Se,* or *Le* loci. In all three families that provided information about linkage to the haptoglobin locus, however, *Z*-scores were positive (Table 2). A maximum-likelihood estimate of 14.3 percent for the recombination fraction was determined by iteration of the *Z*-scores for the three informative families. The *Z*-score at this maximum-likelihood value corresponds to a probability ratio of 47.7:1 favoring linkage (*6*).

Baur (*3*) discussed the possibility that the broad zone of human-erythrocyte catalase activity observed on starch gels may result from the presence of isozymes. This is an attractive hypothesis since structural studies indicate that the catalase molecule is composed of six subunits of at least two types (*7*). Our data suggest that the Ct^{B2} and Ct^{C1} genes are allelic, since both variants provided evidence of linkage to the *Hp* locus. Whether all acatalasemia mutations (*4*) are also allelic, involve loci determining other subunits, or result from changes in a genetic control element (*8*) is not known. Confirmation of our evidence of linkage could lead toward choice among these possibilities.

The chromosomal location of *Hp* and *Ct* in man is unknown. Bloom *et al.* (*9*) suggested that *Hp* may be located on the D_1 chromosome; this conclusion was based on observation of unusual haptoglobin phenotypes in the families of two probands having ring D_1 chromosomes. Although Bias and Migeon (*10*) could not confirm this tentative localization, our results suggest that measurement of catalase activity in individuals having D_1 deletions or D_1 trisomy could provide an independent test of the hypothesis, since effects of gene dosage on catalase may reasonably be expected in deletion hemizygotes and trisomic individuals if *Ct* is in fact linked to *Hp*, and if both are located on the D_1 chromosome.

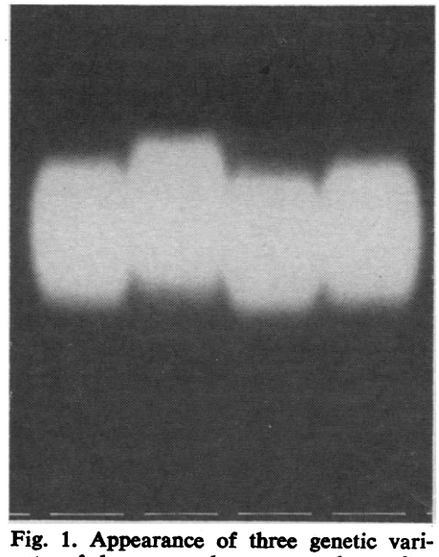

Fig. 1. Appearance of three genetic variants of human-erythrocyte catalase after starch-gel electrophoresis (*2*). The dark band above the broad light zone of catalase activity is hemoglobin. From left, the samples are Ct A, Ct AC_1, Ct AB_2, and Ct A.

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1. The population sample, mixed in ethnic origin, was estimated to be 30 percent Negro, 11 percent Indian, and 59 percent Caucasian; see N. E. Morton, *Cold Spring Harbor Symp. Quant. Biol.* **29**, 69 (1964).
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