prepared so that the most viable in a particular natural setting can be selected.

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The Rhesus Syntenic Group in Man

THE two principal approaches to mapping human autosomes —the study of pedigrees and of cell hybrids—may sometimes complement each other.

Pedigree studies by Lawler and her co-workers[1] established a close linkage (0.03 morgans) between Rh, the rhesus set of blood group loci, and one of the loci, El_1, that can lead to elliptocytosis of the red cell. There seems to be, in addition, at least one isophenic, or mimicking, locus[2] which is not closely linked to Rh. Weitkamp, Guttormsen and Greendyke[3,4] have demonstrated that Rh is linked to $6PGD$, the polymorphic locus for 6-phosphogluconate dehydrogenase. The maximum-probability estimate of the map distance (taking no account of the sex difference uncovered by these authors) is about 0.24 morgans (0.13–0.36). The study of man/hamster cell hybrids has recently added PGM_1, the locus for one species of phosphoglucomutase molecules, to this syntenic group[5,6]. A high correlation was found in loss or retention of the human PGM_1 and human $6PGD$ isozymes as studied in clones derived at various stages during the progressive loss of whole chromosomes (preponderantly human) from the hybrid cells.

To determine the sequence of the PGM_1, Rh, $6PGD$ loci, thus shown to be on the same chromosome, I have estimated the map distances on a large section of the data tested during 1965–68 in my laboratory (then in Glasgow).

A set of aggregate lods (standardized likelihoods in logarithmic form) is given in Table 1 for the $Rh : PGM_1$ interval together with another set for the $PGM_1 : 6PGD$ interval. The lods of Weitkamp *et al.*[4] are used unmodified for the $Rh : 6PGD$ interval and no account has been taken here of a sex difference in the recombination fractions. From inspection alone, it would seem that Rh lies between the other two loci, and a full analysis, using the Bayesian methods of Renwick and Bolling[7], confirms this. The posterior odds on this ordering as opposed to any alternative, are $5 : 1$. (The relative position of El_1

is unresolved until more substantial data are available to indicate its distance from PGM_1 and $6PGD$.)

If this ordering with Rh near the centre of the group is correct, the $Rh : PGM_1$ interval is estimated as 0.27 M (95% probability limits are 0.16 and 0.43) and it is thus the longest map distance to be well estimated directly in man. As the data come from one laboratory, it is likely that direct estimations of longer intervals—up to 0.35 M or beyond—are within the limits of the method when data from several laboratories are combined. The simple addition of the lengths of the two component intervals gives a reasonable estimate of a still longer interval length—$PGM_1 : 6PGD$ (over 0.50 M), but this is indirect. Direct estimation of the corresponding recombination fraction may give some indication of the strengths of genetical interference in man but a good estimate would require an enormous body of high quality data.

Table 1 Lods for Various Values of Recombination Fractions

	Recombination fraction						
	0.5	0.45	0.4	0.3	0.2	0.1	0
$6PGD : Rh^4$	0	1.322	2.722	5.023	5.335	0.602	$-\infty$
$Rh : PGM_1$	0	0.704	1.409	2.947	2.290	-5.370	$-\infty$
$6PGD : PGM_1$	0	0.016	0.032	0.099	0.053	-0.367	$-\infty$

Lods are standard likelihoods in logarithmic form to base 10.
Pedigrees: CADDY, CAFFN, CALMS, CAOOD, CAPEA, CAPEB, CATTS, CAWWR, CDKGK, CD1LL, CD2BL, CLACL, CLAGE, EA1ME, EA1MR, EB1BR, EB1GS, EL1RS, JM1MY, JN1AN, MX1BK, MX1IE, NP1.W, NP1.X, NP1AB, NP1AC, NP1U1, NP1U2, NP1U3, PE1DY, PE1LK, PE1MD, PE1PD, PE1YY, SSEDL, SSEGE, SSEGR, SSEMD, SSESE, SY1MD, TY3VA, TY4BE, TY4PN, V21AN, WM1ME, WM1WE, 9J.GN, 9JATN, 9JCMY, 9JTF1, 9JTF2.

In summary, pedigree methods suggest that Rh and El_1 lie between PGM_1 and $6PGD$. The necessary analyses might have been long delayed but for the hybrid-cell demonstration of synteny of PGM_1 and $6PGD$. PeC, the locus for peptidase C, has recently been added to this syntenic group[8].

A different hybrid clone, one between human and mouse cells, was used by Conover and Hirschhorn[9] to assign tentatively this syntenic group or, more exactly, one of its members —the PGM_1 locus—to a C group chromosome. Fluorescence techniques from Caspersson's laboratory and other new staining procedures should allow this C group chromosome to be more precisely identified.

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