magnitude of the task for a "complete" human genetics. Even rough approximations are here relevant.

Estimates now available on the number of gene loci in man are based on argument by analogy from *Drosophila*. These arguments employ a single human datum, chromosome number. J. S. Huxley (*Evolution, the modern synthesis.* New York: Harper, 1943. P. 50), to cite a single case, suggests that man has 4–6 times the gene number of the fruit fly (where published estimates vary by a factor of about 6.5)—that is, a minimum of 8,000 to a maximum of 78,000. Sample sources of error in such arguments are the assumptions that human and *Drosophila* chromosomes contain the same mean number of genes and that they contain equal amounts of genetically inert material.

This note outlines two approaches to the problem of gene number using additional data specified on man. Individually, neither approach is fully satisfactory. Together they provide an interesting, but highly speculative, approximation.

(1) In *Drosophila* the total haploid chromosomal length with the X is about 6.85×10^{-4} cm (Gowen and Gay). Assume that the fruit fly has 5,000 genes (salivary chromosomal data; C. B. Bridges. *J. Heredity*, 1935, 26, 60–64); each gene would "occupy" an average of 13.7 units of this length. Evans and Swezy (*Mem. Univ. Calif.*, 1929, 9, 1–41) have measured the mean total length of all chromosomes in 10 late prophase nuclei from various tissues from 4 humans. Measurements by Andres and Navashin (*Proc. Maxim Gorky med.-genet. Res. Inst.*, 1936, 4, 506–524) provide nearly equivalent results for the 10 largest chromosomes from several individuals. These data suggest that the total haploid length in man, at a division stage roughly comparable to the *Drosophila* data, is about 58.46×10^{-4} cm. Letting human and *Drosophila* genes occupy the same mean chromosomal length, man would have a little over 42,000 gene loci.

(2) The notion of lethal mutation permits a second estimate. Assume that 22% of all conceptions terminate in nonviable offspring (A. H. Schultz. *Contr. Embryol.* (Carnegie Instn Wash. Publ. No. 275), 1921, 56, 177–191). This value is a little higher than the mean of 9 estimates by other workers ranging from 14% to 30.3% (A. S. Parkes. *Eugenics Rev.*, 1926, 17, 275–293). Of such abortus assume a sex ratio of 120.25 (Schultz)—a value somewhat lower than that (133.03) obtained by Ciocco (*Human Biol.*, 1938, 10, 36–64, 235–250) for stillbirths; in 27 estimates by various other workers this ratio ranges from 101 to 229 males for each 100 females (Parkes). Among these abortus, assume that the excess of males, E, amounting to 2.04% of all conceptions, is due to lethal mutations in the nonhomologous portion of the X—the chief chromosomal differential (together with the relatively small, nonhomologous region of the Y) between individual males and females. Statistical evidence strongly indicates the occurrence of such sex-linked lethals in man (C. C. Little and M. Gibbons. *Proc. Soc. exp. Biol. Med.*, 1921, 18, 111–115). If each locus in the nonhomologous part of the X mutates to lethal at a rate, r, of 1 in 50,000 conceptions (the approximate mutation rate for the normal sex-linked gene to its allele for hemophilia; J. B. S. Haldane. *J. Genetics*, 1935, 31, 317–326), then the number of loci, n, in the nonhomologous portion of the X, is given by $n = rE = 1{,}020$. It requires mention that small changes in the values of E and r will make for large differences in the value of n. More reliable data on aborted and stillborn fetuses in man (Ciocco; C. C. Little. *In* Mueller, Little, and Snyder's *Genetics, medicine, and man.* Ithaca: Cornell Univ. Press, 1947. P.71) and on mutation rates are much to be desired. On the assumption of a higher sex ratio for abortus, say 133.03 (Ciocco), the value of n becomes 1,560. An estimate of 1,000–1,500 sex-linked loci is in some accordance with indications from data for the sex-linked loci of myopic nightblindness and deuteranopia that the nonhomologous portion of the X is genetically "long"—that is, nearly 50 cross-over units in length (T. White. *J. Genetics*, 1940, 40, 403–438).

The cytological length of the X chromosome in man is about 4.5 μ; the nonhomologous segment is about 2/3 of the total length (P. C. Koller. *Proc. roy. Soc. Edinb.*, 1937, 57, 194–214). The ratio of the nonhomologous portion of the X to total haploid chromosomal length is of the order 1: 19.5. On the basis of these speculations there are then some 19,890–30,420 gene loci in man.

The above two independent approaches suggest that the number of gene loci in man is of the order 20,000–42,000.

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On the Solubility of Fibrin Clots

It is generally assumed that the fibrin clot formed by the action of thrombin in fibrinogen solutions or in oxalated plasma is the same as that formed during blood clotting or during the clotting of recalcinated plasma by its own thrombin. There are, however, marked differences between fibrin clots with respect to their solubilities. A clot obtained in purified fibrinogen solution or in oxalated plasma by the action of purified thrombin dissolves readily when an equal volume of 60% urea is added to the clot. The clot formed in recalcinated plasma by its own thrombin, however, does not dissolve in urea solution.

It was found that two factors together are responsible for rendering the clot insoluble in urea solution: one of them is the calcium ions and the other is some serum component which seems to be thermolabile. Adding these two factors in sufficient concentrations to purified fibrinogen prior to the addition of thrombin, the clot formed will be insoluble. Neither the calcium ions nor oxalated serum alone renders the clot insoluble. These observations are in accordance with the results of Kenneth C. Robbins (*Amer. J. Physiol.*, 1944, 142, 581), who studied the solubility of fibrin in weak acids and alkalies.

A detailed account of this work will appear shortly in *Acta Physiologica Hungarica.*

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