The phenotypes and their possible genotypes (assuming a Gm^{ab} allele) for the Gm^a and Gm^b factors in Negroes are shown in Table 4. From this table it may be seen that the Gm(a + b −) and the Gm(a − b +) individuals are homozygotes, hence the square roots of their frequencies provide estimates of the frequency of the alleles Gm^a and Gm^b, respectively, in American Negroes. These values (from the combined samples) are 0·150 ± 0·020 for Gm^a, and 0·160 ± 0·020 for Gm^b.

Table 4. PHENOTYPES AND POSSIBLE GENOTYPES FOR GM^a AND GM^b IN NEGROES

Phenotypes	Possible genotypes
Gm(a+ b+)	Gm^{ab}/Gm^{ab} ; Gm^{ab}/Gm^a ; Gm^{ab}/Gm^b ; Gm^a/Gm^b
Gm(a+ b−)	Gm^a/Gm^a
Gm(a− b+)	Gm^b/Gm^b

If we make the reasonable assumptions that the Negro ancestors of the American Negro were homozygous for Gm^{ab}, and that the alleles Gm^a and Gm^b in American Negroes were derived from White ancestors, the sum of their frequencies (0·310) is a measure of the proportion of the genotype of American Negroes which has been derived from these White ancestors. This value agrees with the value derived by Glass and Li[7] (0·306) on the basis of the R^0 allele of the Rh groups and thus reinforces their conclusion that White ancestors have contributed some 30 per cent of the genotype of American Negroes.

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Chromosome Number in the Blue Fox (*Alopex lagopus* (L.))

THE materials examined consisted of testes from five farm-bred blue foxes (*Alopex lagopus* (L.)) which were killed by electrocution during the breeding season. The testes were immediately removed, teased in distilled water where they remained for about 10 min. and then the pieces were put in either aceto-orcein or 50 per cent acetic acid. From the aceto-orcein coloured preparations, temporary slides were made by the usual squash methods. The preparations fixed in 50 per cent acetic acid were squashed in the same manner and coloured by the Feulgen method[1].

The testicular material under observation contained numerous spermatogonial cells undergoing division. Careful counts of only those metaphase plates which seemed to be intact gave 50 chromosomes as the diploid number (Fig. 1*a*). The diploid complex was remarkable for its comparatively small chromosomes.

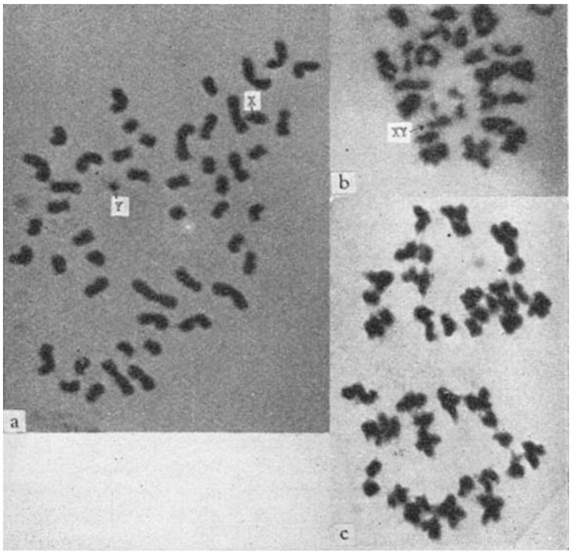

Fig. 1. Chromosomes of the blue fox (*Alopex lagopus*). *a*, Mitotic metaphase with 50 chromosomes. The *X* and *Y* chromosomes are indicated; *b*, first meiotic metaphase with 25 bivalents. The *X*—*Y* complex is indicated; *c*, the second meiotic division. (× *c*. 950)

Because of this the identification of the different chromosomes presented some difficulties. It was found, however, that the diploid complex consisted of 38 meta-centric or sub-metacentric, 11 teleocentric and one dot-like chromosome where the centromere could not be identified. This dot-like chromosome was remarkably smaller than the other ones and apparently has no counterpart. It seems justifiable to consider this to be one of the sex-chromosomes. The other element of the sex-chromosomes seemed to be a rod-shaped chromosome of medium size.

Counts from both the first and the second meiotic division confirmed the number given. The metaphase of the first meiotic division showed 25 bivalents (Fig. 1*b*). Here it was difficult to distinguish the *X*—*Y* complex. It seems that more than one pair of chromosomes have precocious condensation. The second meiotic division was in most cases difficult to count as the chromosomes were small and often lumped together and were diffuse in appearance; but also here 25 chromosomes were found (Fig. 1*c*).

The results obtained in this investigation show that the diploid number of chromosomes in the male blue fox (*Alopex lagopus*) is 50. This is not in agreement with results described earlier. Andes[2] has reported that the number of chromosomes in the blue fox (*Vulpes lagopus*) is approximately between 50 and 60 diploid. He found also 26 tetrads in the first meiotic division. He was, however, unable to distinguish the sex-chromosomes. Wipf and Shackelford[3] agreed with the counts of Andes. They found 52 chromosomes diploid. Neither could these authors find sex-chromosomes on the basis of heteropycnosis, differences in size or other morphological characters.

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