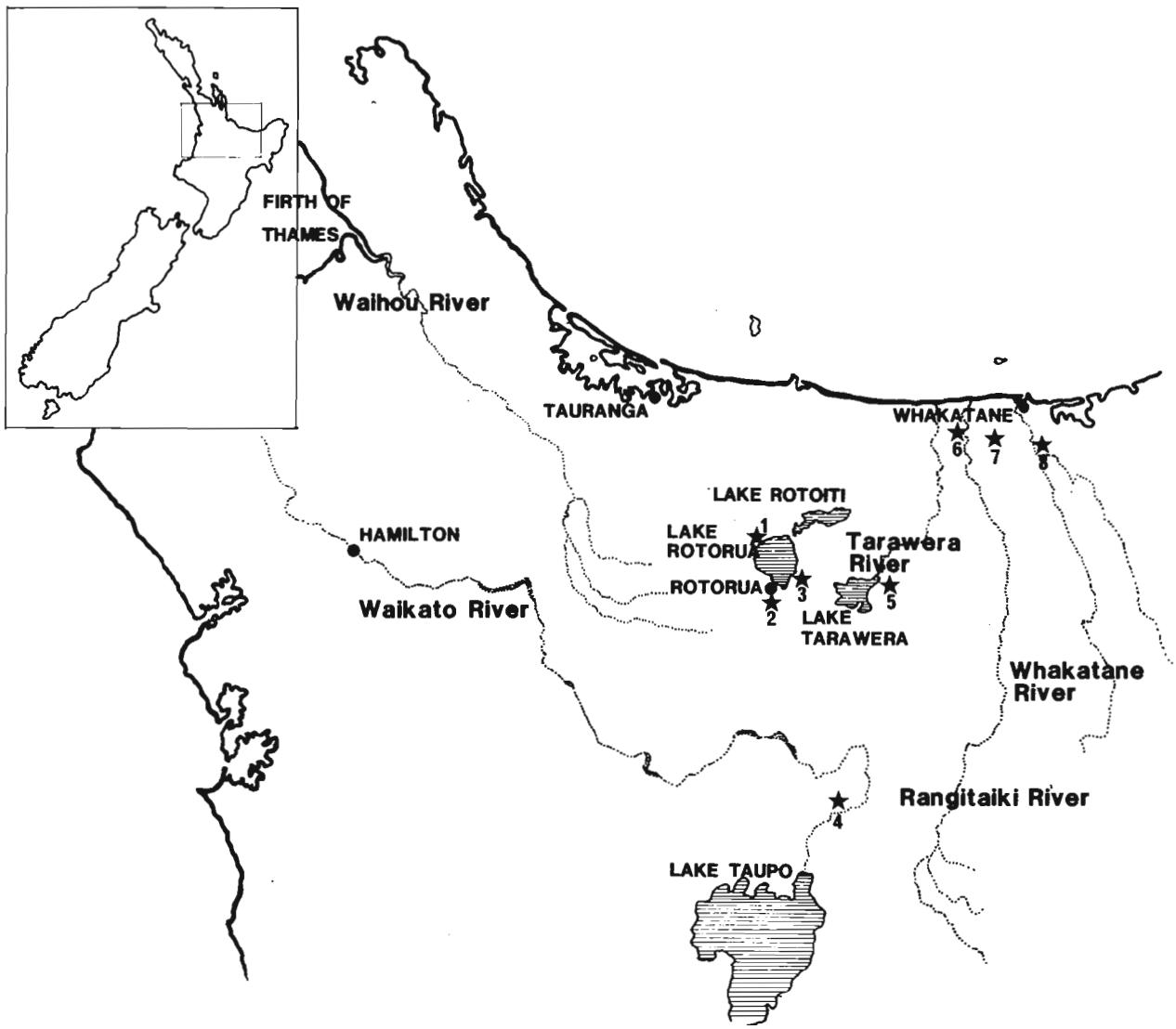
ontogenesis, as was proposed previously (Altukhov 1980). The data of some authors on the viability of null-alleles in a homozygote or a heterozygote with a deletion for a majority of enzymic loci in which they are discovered do not reflect the dynamics of their formation and concern nulls which probably passed already the selection at early stages of ontogenesis. The conducted work indicates it is necessary to take into account this fact in estimating the mutation tempo, studying the correlation between the molecular weight of protein subunits and mutation frequency for corresponding genes, as well as in elucidating the role of selection in maintaining biochemical polymorphism.

References: Lewis, E. and F. Backer 1968, DIS 43:193; Traut, H. 1981, DIS 56:140-141; Altukhov 1980, Proc. XIV Intl.Genet.Congr. 1(1):238-256(Moscow).

Lambert, D.M. & M.C. McLea. University of Auckland, New Zealand. Drosophila pseudoobscura in New Zealand.

We report here the existence of populations of Drosophila pseudoobscura from a number of localities in the North Island of New Zealand. Individuals have been captured from 8 localities in the Bay of Plenty/Rotorua area (see Fig. 1).

Fig. 1. Sites in North Island, New Zealand, where individuals of D. pseudoobscura have been collected. (1) Apple Valley Orchard, 5 km from Ngongotaha; (2) Suburban Rotorua; (3) Fairbank Orchard, opposite Rotorua Airport; (4) On Highway 5 near Rainbow Mountain; (5) at outlet of Tarawera River; (6) Edgecumbe; (7) MacDonnel Road off Highway 30; (8) Suburban Taneatua.



Parsons (1982) has recently reported collecting D. pseudoobscura from Te Kaha in the East Cape. On two trips to this locality we have not been able to collect any specimens despite finding a number of other Drosophila species. Apart from the New Zealand population, D. pseudoobscura is known from North America and from areas around Bogota in Colombia. We are studying New Zealand populations in order to ascertain whether they have diverged genetically from those found in North and South America. In particular we are interested in any possible divergence in their mate recognition systems. We are also analysing the third chromosome arrangements present in populations with a view to first estimating the possible geographic origin of the New Zealand population. Secondly, we are interested to see if there is any seasonal fluctuation in the frequency of arrangements from a single locality.

Individuals have been found to be in low numbers at most collecting sites. Only site 3 near Rotorua has consistently yielded more the usual 1-5 females found at other localities. Even here we have not been able to collect individuals during winter months. We have found the best catches came from banana baits laid near citrus trees, while baids laid in native bush and commercial pine forests have never resulted in any pseudoobscura.

References: Parsons, P.A. 1982, Evol. Biol. 14:297-350.

Latorre, A., L. Pascual & R. deFrutos. University of Valencia, Spain. Loci active in two strains of Drosophila subobscura.

The puffing patterns of two strains of Drosophila subobscura were studied. The strains were Ral21 from Las Raices, Canary Islands (Spain) and H271 from the South of Finland, near Helsinky. The following arrangements: A_2, J_1, U_{1+2}, $E_{1+2+9+12}$ and O_{3+4} in Ral21 and A_{st}, J_{st}, U_{st}, E_{st} and O_{st} in H271 were fixed by us in homozygous.

This study was carried out in 5 moments around the beginning of prepupation (late 3rd instar, 0 h, 1½h and 2½h prepupa), and 2 moments of late prepupation (before 14h and 17h prepupa). In each chromosome, except in the sex chromosome 50 preparations per stage and 5 nuclei per preparation were analyzed. In sexual chromosomes, only female were analyzed. All larvae were dissected in Ringer solution (pH 7.2). Salivary glands were fixed in ethyl alcohol: acetic origin (3:1) for approx. 3 min, and were stained in lacto-acetic-orcein 60%, lactic acid 40%). All experiments were carried out at 19°±1°C.

The active loci have been classified in three groups, according to maximum frequency of appearance in any of the seven stages analyzed (see Table 1):

-- loci active in less thant 25% of the preparations studied. We consider the puffs of this group as occasional puffs.

-- loci with a frequency between 25% and 75%. They generally reach a medium development.

-- loci with a frequency higher than 75%. We have considered the puffs in this group to be "developmentally specific" (Clever 1962) and they define the pattern characteristic of each chromosome.

Table 1: Active loci in Ral21 and H271 strains.

Chromosomes		< 25%	25-75%	> 75%	Total
A	Ral21	7	9	6	22
	H271	7	9	6	22
J	Ral21	19	7	5	31
	H271	13	10	6	29
U	Ral21	9	7	14	30
	H271	12	7	13	32
E	Ral21	14	8	13	35
	H271	11	9	14	34
O	Ral21	21	10	12	43
	H271	15	13	14	42
Total:					
	Ral21	70	41	50	161
	H271	58	48	53	159

As can be seen, there are differences between the two strains, and they vary depending on the chromosomes. Thus, the activity of the A chromosome in relation to the number of active loci is the same in the two strains. This chromosome was the one found to be least active, except in the late third instar. Of the other chromosomes, the U chromosome is that which shows the greatest similarity between the two strains in relation to the puffs of medium or maximum development. This is also the chromosome that proportionally has the greatest number of developmentally specific puffs. In the J, E and O chromosomes, the strain with the greatest number of active loci is always H271, when the occasional puffs are not taken into consideration. Finally, it is the E chromosome