

Table IV. Linkage test between *Rps1* and *Hm* loci in crosses among three soybean cultivars

Entry	Phenotypic classes				df	χ^2 (9:3:3:1)	P	Recombination ± SE (%)
	<i>Rps1 Hm</i>	<i>Rps1 hm</i>	<i>rps1 Hm</i>	<i>rps1 hm</i>				
Reciprocals of P ₁ and P ₃ *								
Totals	436	26	16	146	6	479.37	<0.001	6 ± 0.98
Pooled χ^2					1	472.11	<0.001	
Homogeneity χ^2					5	7.26	>0.20	
Reciprocals of P ₂ and P ₃ *								
Totals	223	9	6	62	6	201.88	<0.001	5 ± 1.2
Pooled χ^2					1	201.78	<0.001	
Homogeneity χ^2					5	0.10	>0.70	

* P₁ = Tracy-M; P₂ = Douglas; P₃ = D55-1492

linked alleles would need to be made initially. If selection were for *Hm*, at least two screening options would be available to the soybean breeder. Screening could be effectively accomplished in a hydroponic system in a greenhouse, and the selected *Hm Hm* F₃ lines planted in a field for seed increase. A second option would be to plant seed from all F₂ plants from a cross in a progeny row field nursery, using metribuzin as part of a weed control system. Because 25 percent of the lines having the genotype *hm hm* would be discarded during the F₃ generation, screening efficiency would increase. Screening for the linked allele giving resistance to phytophthora rot would be conducted on the agronomically desirable advanced lines the winter before conducting replicated yield trials.

References

1. ATHOW, K. L., F. A. LAVIOLETTE, and J. R. WILCOX. Genetics of resistance to physiologic races of *Phytophthora megasperma* var. *sojae* in the soybean cultivar Tracy. *Phytopathology* 69:641-642. 1979.
2. BARRENTINE, W. L., C. J. EDWARDS, JR., and E. E. HARTWIG. Screening soybeans for tolerance to metribuzin. *Agron. J.* 68:351-353. 1976.
3. BERNARD, R. L. and M. G. WEISS. Qualitative genetics. In *Soybeans: Improvement, Production, and Uses*. B. E. Caldwell, Ed., Am. Soc. Agron., Madison, Wisconsin. p. 117-154. 1973.
4. BUZZELL, R. I., B. R. BUTTERY, and R. L. BERNARD. Inheritance and linkage of a magenta flower gene in soybeans. *Can. J. Genet. Cytol.* 19:749-751. 1977.

5. DEVINE, T. E., R. G. PALMER, and R. I. BUZZELL. Analysis of genetic linkage in soybeans. *J. Hered.* 74:457-460. 1983.
6. HARTWIG, E. E. Registration of Tracy soybeans. *Crop Sci.* 14:777. 1974.
7. ———, W. L. BARRENTINE, and C. J. EDWARDS, JR. Registration of Tracy-M soybeans. *Crop Sci.* 20:825. 1980.
8. HILDEBRAND, D. F., J. H. ORF, and T. HYMOWITZ. Inheritance of an acid phosphatase and its linkage with the Kunitz trypsin inhibitor in seed protein of soybeans. *Crop Sci.* 20:83-85. 1980.
9. IMMER, F. R. and M. T. HENDERSON. Linkage studies in barley. *Genetics* 28:419-440. 1943.
10. KIANG, Y. T., M. B. GORMAN, and Y. C. CHIANG. Genetic and linkage analysis of a leucine aminopeptidase in wild and cultivated soybeans. *Crop Sci.* 25:319-321. 1985.
11. KILEN, T. C. and W. L. BARRENTINE. Linkage relationships in soybean between genes controlling reactions to phytophthora rot and metribuzin. *Crop Sci.* 23:894-896. 1983.
12. MORGAN, F. L. and E. E. HARTWIG. Physiologic specialization in *Phytophthora megasperma* var. *sojae*. *Phytopathology* 55:1277-1279. 1965.
13. PALMER, R. G. Soybean cytogenetics. In *World Soybean Res. Conf.-III: Proc.*, R. Shibles, Ed. Westview Press, Boulder, Colorado. 1985.
14. ———, S. L. BROICH, and X. DELANNAY. Linkage group 12. *Soybean Genet. Newsl.* 11:97-99. 1984.
15. ——— and M. L. H. KAUL. Genetics, cytology, and linkage studies of a desynaptic soybean mutant. *J. Hered.* 74:260-264. 1983.
16. ROANE, C. W., S. A. TOLIN, and G. R. BUSS. Inheritance of reaction to two viruses in the soybean cross 'York' × 'Lee 68'. *J. Hered.* 74:289-291. 1983.
17. SADANAGA, K. Locating *wm* on linkage group 8. *Soybean Genet. Newsl.* 10:39-41. 1983.

The Journal of Heredity 77:277-278. 1986.

Mutant allele frequencies in domestic cats of Taiwan

Kevin Chu

ABSTRACT: Preliminary data for Taiwanese cats generally agree with previous findings in far eastern populations, especially Vladivostok. However, surveys are still too few in number to achieve any detailed perspective for this vast region.

MUTANT ALLELE frequency data for domestic cat populations are now available for much of the world, especially Europe^{3,11,15,19,22}, the Mediterranean^{12,21,23}, the Middle East^{6,17}, USSR^{4,16}, the Indian subcontinent^{1,20}, North America^{2,13}, South America²⁶, Australia^{5,9}, and elsewhere^{8,23,24,25}. However, few studies have been conducted in the far east. In fact, apart from some fragmentary data from Japan¹⁰, the only surveys that are available are from Vladivostok^{4,14}, Hong Kong and Macao⁷, Singapore¹⁸, and Thailand⁷. The latter, owing to special historical and geographic circumstances does not appear to be representative of the region. Given the foregoing considerations, it is of more than casual interest to present new data, even if of a preliminary nature.

Materials and Methods

During February 1984, it was possible to record a sample of 177 cats from three cities, T'aipei, Kaohsiung, and Hengch'un, on the island of Taiwan. All animals seen were free roaming in streets, alleys, yards, etc. Mutant

phenotypes at six loci and the phenotype frequency of the trait kinky-tail were scored. The mutant alleles included sex-linked orange (*O*) and the autosomal factors nonagouti (*a*); the tabbies Abyssinian (*T^a*) and blotched (*b^b*); dilute (*d*); piebald spotting (*S*) and dominant white (*W*). No long-haired (*l*) or polydactyl (*Pd*) phenotypes were observed.

Results and Discussion

Animals were not individually sexed, so estimates for *qO* are based on a maximum likelihood method. The phenotypes observed conform to the expectation for Hardy-Weinberg equilibrium ($\chi^2 = 3.56$; 1 df) presuming a 1:1 sex ratio. All autosomal allele estimates are based on the assumption of panmixia. For these coat color and pattern mutants there are no significant differences between the three cities studied. For the kinky-tail trait, however, some strong differences appear. Hence, although the three samples have been pooled, it would be imprudent to conclude that all Taiwanese cats belong to a single, homogeneous population. These data are summarized in Table I.

The author is affiliated with the Department of Biology, Boston University, Boston, MA 02215, and the Ocean Research and Education Society, Inc., Gloucester, MA 01930. He wishes to thank Dr. N. B. Todd for assistance in the preparation of this manuscript.

© 1986, American Genetic Association.

Table I. Phenotypes observed in three samples of Taiwanese cats and mutant allele estimates for the pooled samples

	T'aipei	Kaohsiung	Hengch'un	Total	Mutant allele frequency
+/?	32	48	17	97	0.339 ± 0.036
+/O	9	14	5	28	
O/?	14	24	5	43	
+-	20	36	11	67	0.543 ± 0.043
aa	13	12	3	28	
+-	14	28	11	53	0.699
t ^b b	3	2	0	5	0.289 ± 0.062
T ^a -	0	2	0	2	0.012 ± 0.010
+-	52	84	24	160	0.253 ± 0.037
dd	2	5	4	11	
S-	40	63	21	124	0.468 ± 0.032
++	14	23	9	49	
W-	1	0	0	1	0.003 ± 0.003
++	56	90	30	176	
Kinky	7	28	13		
Normal	50	61	13		

Table II. Mutant allele frequency estimates and observed incidence of kinky-tail trait for several cat populations of the far east

	O	a	T ^a	t ^b	d	S	W	Kinky %	Reference
Vladivostok	0.11	0.53	0	0.31	0.20	0.41	0.01	12.8	4, 15, 16
Japan	0.35	0.81	?	?	?	?	0.02	present	11
Taiwan	0.34	0.54	0.01	0.29	0.25	0.47	0.003	12-50	Table I
Hong Kong	0.39	0.44	0.15	0.48	0	0.46	0	24	8
Macao	0.36	0.44	0.23	0.39	0	0.46	0.005	19	8
Singapore	0.31	0.60	0.24	0.11	0.13	0.44	0.01	65	18

In Table II are presented the data currently available for those far eastern populations to which it may be informative to compare with Taiwan. The first thing to be noted is the general agreement between the profiles of Taiwan and Vladivostok, these two differing significantly only in the frequency of sex-linked O. There also are obvious similarities between Taiwan and Singapore and, in some respects, they are more similar to one another than Taiwan is to either Hong Kong or Macao, which are geographically much closer. The Japanese data are not especially helpful in that they indicate a very high level of one mutant (a), which only adds to the complexity of the regional pattern. In fact, the present data points are hundreds, even thousands of miles apart and far too sparse to justify any detailed discussion. What is ur-

gently needed are many more studies, especially in Japan, China, and The Philippines.

References

1. AHMAD, M., B. BLUMENBERG, and M. F. CHAUDHARY. Mutant allele frequencies and genetic distance in cat populations of Pakistan and Asia. *J. Hered.* 71:323-330. 1980.
2. ANDERSON, M. M. and S. H. JENKINS. Gene frequencies in the domestic cats of Reno, Nevada: confirmation of a recent hypothesis. *J. Hered.* 70:267-269. 1979.
3. BLUMENBERG, B. and A. T. LLOYD. Mutant allele frequencies in the domestic cat: a preliminary discussion of selection with particular reference to the United Kingdom and Eire. *Genetica* 54:17-28. 1980.

4. BORODIN, P. M., G. P. MANCHENKO, R. ROBINSON, and N. B. TODD. New studies of mutant allele frequencies in U.S.S.R. cat populations. *Carnivore Genet. Newsl.* 4:153-167. 1980.
5. DARTNALL, J. A. and N. B. TODD. A study of population genetics in the domestic cats of Hobart. *Australian J. Zool.* 23:405-409. 1975.
6. DAVIS, B. K. and M. AHMAD. Allele frequencies in Saudi Arabian cat populations. *Carnivore Genet. Newsl.* 4:224-229. 1983.
7. FAGEN, R. and K. MEESWAT. Population genetics and demography of the domestic cat in Thailand. *Nat. Hist. Bull. Siam Soc.* 29:137-150. 1981.
8. JAFFE, W. P. Cat gene frequencies in Seychelles. *Carnivore Genet. Newsl.* 3(9):339-345. 1978.
9. KINNEAR, J. F. Mutant allele frequencies in domestic cats of Melbourne, Australia. *Carnivore Genet. Newsl.* 3:408-417. 1979.
10. KOMAI, T. Incidence of the genes for coat colors in Japanese cats. *Annot. Zool. Japon.* 25:209-211. 1952.
11. LLOYD, A. T. Mutant allele frequencies in domestic cat populations in the Netherlands. *Genetica* 58:223-228. 1982.
12. ———. Towards a comprehensive picture of the Mediterranean: Population genetics of the cats of Rome. *Carnivore Genet. Newsl.* 4:235-241. 1983.
13. ———. Geographic distribution of mutant alleles in domestic cat populations of New England and the Canadian Maritimes. *J. Biogeog.* 12:319-322. 1985.
14. MANCHENKO, G. P. Frequencies of "orange" and "kinky-tail" phenotypes as evidence of a complex origin of the Vladivostok cat population. *Carnivore Genet. Newsl.* 4:133-137. 1981.
15. POINTIER, D. Fréquences géniques chez le chat domestique, *Felis catus*, dans quatre communes rurales françaises. *Genetica* 62:69-73. 1983.
16. ROBINSON, R. and G. P. MANCHENKO. Cat gene frequencies in cities of the U.S.S.R. *Genetica* 54:41-46. 1981.
17. SALITERNIK, R. and N. B. TODD. Population genetics of domestic cats in Iran. *Carnivore Genet. Newsl.* 3:148-154. 1977.
18. SEARLE, A. G. A study of variation in Singapore cats. *J. Genet.* 56:1-17. 1959.
19. TODD, N. B. Cats and commerce. *Sci. Amer.* 237(5):100-107. 1977.
20. ———. Cat population genetics on the littoral of the Indian Ocean and South China Sea: a preliminary assessment. *Carnivore Genet. Newsl.* 4:248-262. 1983.
21. ——— and B. BLUMENBERG. Mutant allele frequencies and genetic distance relationships in domestic cat populations of Lower Egypt and the eastern Mediterranean. *TAG* 52:257-262. 1978.
22. ——— and A. T. LLOYD. Mutant allele frequencies in domestic cats of Portugal and the Azores. *J. Hered.* 75:495-497. 1984.
23. ——— and L. M. TODD. Mutant allele frequencies in the domestic cats of Turkey and Greece. *Genetica* 46:183-192. 1976.
24. VAN AARDE, R. J., B. J. ERASMUS, and B. BLUMENBERG. Frequencies of mutant alleles in the cat populations of Cape Town and Pretoria, South Africa. *So. Afr. J. Sci.* 77:168-171. 1981.
25. VUILLEUMIER, B. R. J. and F. VUILLEUMIER. Mutant allele frequencies in the domestic cats of New Caledonia. *Carnivore Genet. Newsl.* 3:350-355. 1978.
26. WATANABE, M. A. Estudo Populacional da Cor de Pelagem de Gato Doméstico (*Felis catus*, L.) em Dezesesseis Localidades do Brasil. Ph.D. thesis, Univ. de São Paulo. 1984.