6.12

Immunogenetic relationships of erythrocytic antigens of goats and cattle. K. A. STILLE and W. J. MILLER. Iowa State University, Ames, Iowa.

Until DNA sequencing comparisons in studies of relationships of species is applied to blood group systems, the older immunogenetic methods of Irwin and associates are still pertinent. Indeed, these methods should be cross compared and show much agreement in the conclusions.

Erythrocytic antigenic comparisons were made on ten cattle blood grouping systems with goat red cells. One hundred one cattle blood typing reagents as well as many normal sera of cattle were placed in hemolytic tests with goat erythroyctes. A selection of 31 reagents exhibiting positive reactions was made for absorption tests with goat cells. This should distinguish naturally occurring antibodies from immune specificities, if the absorptions are complete or significantly reduce the titer for cattle cells.

Seven classes of results were noted according to the total or partial removal of reactions for all or some goat and cattle cells by the absorptions. Cells of some of the goats possess identical or fully cross-reactive antigens to those of cattle: B, P, Q, D'-like, and E'_1 of the B system, R_2 and W of the C system, (A_2), V, R', S' and new factor 33. Some goats possess similar antigens that are partially cross-reactive with those of cattle: G, Y_2, L, F, M_1, J, Z, and H factors. These absorptions demonstrate variations in specificities between some cattle reagents. For example, anti-J of one reagent failed to react with goats, but that of another reacted. It's specificities were completely removed by cells of some goats. Other goats do not possess antigens cross-reactive with named immune specificities of cattle, since the cross-reactions may be attributed to naturally occurring antibodies.

There were 18 successful alloimmunizations of goats. In reciprocal tests to those above, surprisingly, all these reagents failed to show cross-reaction with red cells of cattle.

6.13

Characterization of class I genes in the marsupial Monodelphis domestica. R. C. STONG, K. KOCHAN, E. KRAIG and W. H. STONE. So. West Fdtn. Biomed. Res., Trinity U. and U. Texas Health Sci. Ctr. San Antonio, TX.

The major histocompatibility complex (MHC) has been defined in several mammalian species but has not been studied in a marsupial. Because marsupial (metatherian) mammals separated from placental (eutherian) mammals more than 100 million years ago, comparison of the MHC in these widely separated species will contribute to our basic understanding of the evolution of this important genetic system.

We used Southern blot analysis to determine the extent of hybridization of a murine class I probe to Monodelphis genomic DNA. Because of the wide species difference, we used pH2IIa, a cDNA probe derived from the more conserved 3' region of the mRNA. A 1-week exposure revealed several EcoRl fragments which hybridized with moderate strigency, suggesting that mouse and Monodelphis DNAs share at least 70% homology. We have constructed a genomic library from Monodelphis liver DNA, using gtWesB cloning vector. Screening revealed many clones which hybridize to pH2IIa. Those which appear to contain marsupial class I genes will be further characterized by restriction mapping. One of the lambda clones will be used to screen a cosmid genomic library which is near completion. Supported by NSF Grant DCB 8408233 RUI.

6.14

Temperature-dependent differences in polygene expression in Drosophila melanogaster. J.N. THOMPSON, JR. and R.R. TUCKER. Zoology Department, University of Oklahoma, Norman, Oklahoma.

In a recent study of the role of polygenic variation in developmental homeostasis, Schnee and Thompson (1984, Genetics 108: 409-424) found that certain polygenic loci had a significant stabilizing effect upon the number of sternopleural bristles in D. melanogaster. The polygenic alleles that are favored by selection for increased bristle number at 18°C alter total bristle number much less than those that are favored by selection at 29°C. Temperature alone has the opposite effect; bristle number tends to be larger at lower temperatures. This implies that a different set of alleles or different polygenic loci are active under alternate environmental conditions. We have tested this hypothesis by carrying out artificial selection for increased bristle number at 25°C until a plateau in response had been reached. We then transferred a subculture to 29°C and continued to select. While the original 25° culture remained at its plateau, the 29° culture began to respond again to artificial selection. Polygenic contributions to these selection responses were quantified by whole chromosome mapping. In a complementary set of experiments, isolated whole chromosomes from wild-caught isofemale strains were compared at stable (18, 21, 25, and 29°) temperatures and diurnally cycling (5° to 32°) temperatures. Mean bristle numbers, variation, asymmetry, and sex differences were compared across these conditions. The results support the hypothesis that polygenic loci can help buffer development against shifts in critical environmental variables. (Supported by NSF grant BSR-8300025).