*selection.*—Direct and correlated responses to selection were used to investigate the genetic relationship between growth rate, measured by 42-day body weight, and age (in days) of sexual maturity. Five lines were established from a single base population and selected according to one of the following criteria: high weight (HW), low weight (LW), early maturity (EM), late maturity (LM) or a random control (C). Males and females were randomly selected in the weight and maturity lines, respectively, because age at maturity could not be evaluated in females and males stop growing when they reach sexual maturity.—After five generations of single-sex selection, male age at maturity averaged 42.1, 43.2, 34.7, 59.6 and 37.3 days in the HW, LW, EM, LM, and C lines, respectively. Similarly, female body weight averaged 282, 236, 255, 233 and 264 mg in the HW, LW, EM, LM and C lines, respectively. The greatest direct response to selection occurred in the LM line which matured, on the average, 22.3 days later than the C line in generation 5 and 2.7 SD later than the mean for the base population.The apparent but small responses in body weight of the HW and LW lines were achieved almost entirely after the first generation of selection, suggesting strong maternal effects. Correlated responses to selection were inconsistent relative to the control line but slightly negative and consistent when measured only in the selection lines.—The high realized heritability observed for age of sexual maturity suggests a mode of inheritance similar to that for Xiphophorus, for which age at maturity has been shown to be controlled by a single locus with multiple alleles (Kallman and Borkoski, Genetics **89:** 79–119, 1978).

(*18.8*) **Miller, W. J., T. A. Olson and K. Stille,** Iowa State University, Ames, and University of Florida, Gainesville. *Blood types of Florida Scrub cattle and their comparison with other Iberian source stocks.*—Feral Spanish colonial cattle are represented by two remnant stocks in the United States, the Texas Longhorn and the Florida Scrub cattle (FSC). Both have admixtures of other cattle types, but the amount is thought to be low in longhorns. The scrub cattle are less well known. Ten blood-type systems of cattle were analyzed for 43 FSC. FSC were polymorphic in all systems and for a new factor.—Founder effect, genetic drift and small samplings make the degree of relationships difficult to estimate. Nevertheless, the FSC are reasonably like Texas Longhorn, Mexican Sonoran creole, Brazilian Caracu and Argentine criollo in most systems. FSC have higher frequencies than the other Iberian cattle sources of dash "–" (no detected factor) in the S system, and of D, J. L. and R′, in four more systems. All of these Iberian cattle sources have a closely similar frequency of Z, which is much higher than in other European source cattle, such as Ayrshire and Brown Swiss.—The B system is especially useful for breed phenogroup comparisons. We postulated in FSC 28 B phenogroups already established in other breeds and, additionally, eight not previously observed. There were 13 of 37 or 35% of the list of different B phenogroups estimated for FSC that were known to occur in Texas Longhorns or Argentine criollo. Or, 50% of the B phenogroups occupying the B system in these FSC were known to occur in Texas Longhorn or criollo, indicating a closer relationship than to, perhaps, the next closest breed by B system considerations, the Shorthorn.

(*18.9*) **Smith, J., H. Rytting, N. Samples, J. L. Vandeberg and W. H. Stone,** Trinity University and the Southwest Foundation for Biomedical Research, San Antonio, Texas. *The Monodelphis lymphocyte antigen system: a marsupial MHC.*—Marsupials occupy a unique position in the phylogeny of mammals, because of their separation from placental mammals between 100 and 150 million yr ago. Thus, the definition of the MHC of a marsupial should illuminate the evolution and the origin of this unique gene family. We have a colony of about 1000 pedigreed Monodelphis at the Southwest Foundation for Biomedical Research for our studies. A panel of 20 cytotoxic antisera were obtained following skin implantation (*i.e.*, a plug of skin was placed subcutaneously into a pocket cut on the back of each recipient). In general, reciprocal implants were made between individuals chosen by pedigree to be most distantly related based on a coefficient of kinship. Although the results are preliminary, we noted a considerable degree of polymorphism among the sera when screened against the lymphocytes of more than 50 randomly chosen donors. A cluster analysis by computer showed that the 20 sera fell into five distinct groups, each group presumably detecting a lymphocyte antigen coded by dominant genes. The results of limited family studies confirm that each cluster is detecting an antigen on the lymphocytes encoded by an autosomal dominant gene. At least three independent loci appear to be involved. We presume that some of these are class I antigens belonging to the Monodelphis lymphocyte antigen MHC because the antisera were engendered by skin implantation, but histocompatibility assays between matched and mismatched pairs are not yet completed. [Supported by NSF grant PCM-8408233 R.U.I. Programs (W.H.S.) and NIH grant RR 01602 (J.L.V.).]