in lightweight heifers may adversely affect the relationship between marbling and external fatness.

Table 1. Effects Rev200 vs IHFH on Performance and Carcass Traits

Trt	ADG, kg	G:F	HCW, kg	YG	MarbScore[1]	%Ch
IHFH	1.36	0.187	330	2.85	417[a]	48[a]
R200	1.39	0.187	333	2.87	407[b]	40[b]

[1] 400=Small[0]; 500=Modest[0]; [a,b] Columns without common superscripts differ ($P = 0.07$).

Key Words: Anabolic implants, Trenbolone acetate, Feedlot

Breeding and Genetics: Phylogenetics and Genetic Diversity

544 An overview of phylogenetics. M. Cronin*, *University of Alaska, School of Natural Resources and Agricultural Sciences*, *Fairbanks*.

Phylogeny generally refers to the genealogy of a group of organisms. For example, the phylogeny of the ruminants would include all of the ancestors, including the common ancestor, of the extant species of cattle, sheep, goats, deer, etc. In this paper, I present basic concepts of phylogenetics, and give examples of phylogenies of domestic and wild species above and below the species level. Taxonomic classifications are based on phylogenetic relationships, which can be inferred from paleontology, morphology, or genetics. Phylogeny can also be inferred for genes, as the genealogy of genes derived from a common ancestral gene. Gene phylogenies and species phylogenies are not always concordant for a variety of reasons. It is also important to recognize that phylogenetics is an historical science, and phylogenetic relationships can only be inferred. Nevertheless, phylogenetic inference has become a rigorous science, with important empirical and theoretical advances in the last few decades. The phylogeny of the horse, including ancestors with progressively decreasing numbers of toes over time, is an example of classical phylogenetic inference from fossils and morphology. The advances of molecular genetics have greatly enhanced and expanded phylogenetic inference from DNA sequences. In general, DNA sequences are assumed to evolve as a function of time, and similarity of sequences indicates recent common ancestry. However, is important to understand the factors affecting molecular sequences that may invalidate this assumption, including linkage, selection, modes of inheritance, lineage sorting of ancestral alleles, and gene duplication. The importance of distinguishing molecular sequence data from gene frequency data is also discussed. Examples are given of mitochondrial DNA (mtDNA) and nuclear DNA sequences that have been used to infer relationships of taxa at the levels of family, genus, species, and intra-species. At the level of higher taxa, the phylogeny of artiodactyls (even toed ungulates) has been inferred from molecular sequences for several genes. This includes the relationships among artiodactyls including non-ruminants (e.g. pig), ruminants (e.g., cattle sheep, deer), and more distantly related groups (e.g. whales). At the level of species, subspecies, and breeds, examples of cattle, bison, and several deer species are described. This includes groups in which molecular phylogenies are discordant with classical understanding of relationships from morphology, distribution, and natural history. The phylogenies of some domestic and wild ruminants are compared, and the concepts of wild subspecies and domestic breeds are discussed.

Key Words: Phylogenetics, Genealogy

545 Measuring diversity among breeds and populations. P. W. Hedrick*, *Arizona State University*.

There are a number of new genetic markers and approaches that can be used to measure and evaluate genetic diversity among different breeds and among populations of a breed. I will first evaluate the relative merits of different types of markers for these purposes, including microsatellite loci, mtDNA variants, SNPs, and QTLs. I will then discuss various approaches to measure the pattern of diversity among and within breeds, including FST, genetic distance, assignment, and clustering. The comments about these markers and approaches will be illustrated with data from recent studies in various cattle breeds.

Key Words: Microsatellite loci, FST, Clustering

546 Applications of phylogenetic inference to livestock science. A. R. Freeman*, *Smurfit Institute, Trinity College Dublin*, *Dublin, Ireland*.

The phylogenetics of domestic animals are profoundly influenced by domestication. The gene pools which these species possess today are the result of episodes of capture and taming of the wild progenitors which were restricted both spatially and temporally. In this presentation I will outline some of the wide-ranging applications of phylogenetics with reference to livestock science. More specifically, I will show how well-constructed phylogenies can be use to test varying hypotheses about the history of a population. Firstly, livestock species are not genetically homogenous, but rather are usually the result of two or several separate episodes of domestication. These scenarios have been confirmed by mitochondrial DNA phylogenetic analysis in many species. Secondly, phylogenies describe patterns of diversity which reflect both the history and biology of a species. In the case of a domesticated species, the number of original wild founders that created the population, the diversity levels in the wild ancestral populations, continual introgression from wild relatives and hybridization can affect the diversity levels in the modern population. Thirdly, the relationship between different breeds within a species may be clarified with careful interpretation of phylogenetic data. Finally, and perhaps most interestingly, different selection pressures acting in the two populations can also result in divergence at particular genetic loci which can be detected using phylogenetics. These loci are likely to relate to traits that have been selected in particular breeds, but also to the historical disease challenge that a species has faced. Thus, identification of these loci that show signatures of natural selection

is likely to be critical in understanding differences between breeds in terms of productivity and disease resistance.

547 Current efforts in conservation of animal genetic diversity. H. Blackburn*[1] and D. Bixby[2], [1]*ARS-National Animal Germplasm Program, Ft. Collins, CO*, [2]*American Livestock Breeds Conservancy, Pittsboro, NC*.

Changing consumer demand, threat of disease, and contraction of genetic diversity drive the need to establish vibrant livestock conservation activities. For effective in-situ and ex-situ conservation strategies to function, dialog and synergetic action between public and private sectors must occur. This type of interaction exists and provides a basis for the operation of the National Animal Germplasm Program (NAGP), the American Livestock Breeds Conservancy (ALBC), other non-governmental organizations, and livestock breeders. Both NAGP and ALBC have increased the security of genetic diversity for a number of rare, minor and major livestock breeds in the US. In-situ security has improved with ALBC efforts to increase breed population size for 21% of the breeds in Critical/Threatened/Watch conditions between 1977 and 2005. These 16 breeds are now in the Recovering category. Since 1999, NAGP has developed an ex-situ collection of germplasm of approximately 250,000 units of semen, embryos and blood from 104 major, minor and rare breeds of cattle, sheep, goats and pigs. A key element in the public-private sector dialog is the collection, evaluation and utilization of information. Information such as, population census data, pedigrees, and number of breeders raising a breed have been collected and utilized to varying degrees. This information can serve as a basis for dialog and actions by the public and private sector. While some information is available for some breeds, the US has not fully engaged its capacity to measure genetic diversity by using molecular information. Such information would greatly add to the ability to assess diversity levels and contribute to decisions concerning conservation strategies. Additionally phenotypic assessments of many US rare and minor breeds are out of date and not relevant to populations today. This information void could dampen consumer demand for niche products as well as the effort to explore for unique genes and gene combinations. While conservation activities to date have strengthened genetic security, there are still significant knowledge, information and collection voids.

Key Words: Genetic diversity, Livestock conservation

Dairy Foods: Cheese II

548 Effect of mountain and sea level pasture on monoterpene composition in milk, curd and Ragusano cheese at 4 and 7 months of aging. S. Carpino*[1], T. Rapisarda[1], and G. Licitra[1,2], [1]*CoRFiLaC, Regione Siciliana, Ragusa, Italy*, [2]*D.A.C.P.A. Catania University, Catania, Italy*.

Dynamic headspace extraction (P&T) (Tekmar 3100) in combination with GC/MS using chiral stationary phase was employed to analyze the monoterpene composition of milk, curd (during cheese making), and cheese at 4 and 7 months aged from a farm of the Hyblean region sited on mountain level (ML) in Spring 2004. In farm ML we had three groups of Holstein cows (10 per group): group 1 fed TMR (ML0) no pasture; group 2 fed TMR supplemented with 30% DM of pasture (ML30), and group 3 fed TMR supplemented with 70% DM of pasture (ML70). Another farm sited on sea level (SL) was also tested. In this farm we selected only one group of Holstein cows, at similar lactation days and milk production level to the ML farm, fed TMR supplemented with 30% DM of pasture(SL30). The aim of this work was to study the impact of different level of pasture in the diet and the farm location on monoterpenes profile. A total of 16 milk and curd samples and 32 cheeses were analyzed. The general monoterpenes compostion detected in ML0 showed significant lower level compared with the ML30 and ML70 samples. The general terpene composition of samples obtained from mountain level (ML) farm was more abundant than the samples from sea level (SL). The monoterpene composition showed compounds like (-)-β-pinene, (+)-d-limonene, (+)-α-pinene in common between the ML30 and SL30 samples. It is important to note that some exclusive compounds were detected in ML samples: β-myrcene, (+)-sabinene, (-)-d-limonene, (+) δ-3-carene (ML), (+)-β-pinene, (+)-α-terpinolene, α-terpinene instead (-) Camphene was exclusively detected in the SL samples. These results indicate that the altitude may influence the type of pasture and the terpene profile that are transferred directly to the dairy products. The terpene composition, in fact, in dairy products depends on the type of pasture and therefore on the territory and its relative macroclimate. These compounds might be useful and used as valuable biomarkers for dairy products with Protected Designation of Origin.

Key Words: Ragusano cheese, Pasture, Monoterpene composition

549 Characterization of calcium lactate crystal growth on Cheddar cheese. P. Rajbhandari* and P. S. Kindstedt, *University of Vermont, Burlington*.

Previous research demonstrated that the total area collectively occupied by calcium lactate crystals on Cheddar cheese surfaces increased during storage in approximately linear manners but at different rates for different cheese samples. Evidence of substantial migration of calcium and lactate ions from cheese interior to surface during surface crystal growth was also observed. The objective of the present study was to characterize the growth of individual calcium lactate crystals on the surface of Cheddar cheese during refrigerated storage. A random weight (ca. 300g) retail sample of naturally smoked Cheddar cheese exhibiting white surface crystals was obtained from a commercial source. The sample was stored at 4°C for 30 weeks and a digital photograph was taken of one of the surfaces (ca. 55x120mm) at 3 wk intervals. The total area occupied by crystals on the photographed surface was measured at 3 wk intervals using image analysis. In addition, five small (ca. 0.3 mm radius) individual crystals on the first photographed surface were chosen for observation over the 30 wk period. The crystals were evaluated for area, radius and shape factor (circularity) every 3rd week using image analysis. The area collectively occupied by crystals on the photographed surface increased in a linear manner (R^2=0.95) from about 0.44% to 7.42% of the total surface area over the 30 wk period. Throughout this period, the shapes of the five individual crystals closely approximated perfect circles, and the area occupied by each of the five crystals increased in a near linear manner (R^2=0.85-0.96). The radii of each of the 5 crystals increased in a non-linear manner that conformed most closely to a second order