

Closing the Gap – the Time Path
By Dr. Carmen L. Battaglia

‘Talent wins but it takes team work and intelligence to produce championships’

Improving the conformation, health and temperament of purebred dogs should be the goal of every breeder. What makes this goal reachable began when the studbook for breeds closed. The result was the establishment of specific breeds. By definition, closing the stud book means that the diversity of the genes for a breed would be restricted to those already present. Thus, when a stud book closes, no new genes are allowed into the breeds that were not already present in the gene pool. The exception is the occurrence of a few infrequent mutations. By closing a gene pool, the pedigrees of each breed became dependable and reliable as a tool for improving breed type, health and temperament. Further refinements occurred as breeders began to use breed standards as their guide for breeding and selection. The result produced a large number (N=170) of desirable breeds with verifiable ancestries. Over time, these closely monitored populations have become especially suitable for the study of diseases. Most of the major advances have occurred during the past two decades. With the advancement of DNA tests more improvements became possible at a faster pace. Other notable advancements included those in the area of digital radiographs, laboratory tests, nutrition and better breeding methods. Today, breeders can use these protocols to breed by direction rather than by chance.

When the canine genome sequencing project was first undertaken, the **American Kennel Club, Canine Health Foundation (AKC/CHF)** became one of its largest non-profit supporters. Once it was completed, the canine genome joined four other completed sequences, including one for the human and another for the chimpanzee. Many benefits were quickly realized. The breakthrough discovery on Neuronal Ceroid Lipofuscinosis (Tibetan Terriers) led to landmark stem cell replacement therapy in a California boy who was suffering with a disorder called ‘Batten Disease’. Other useful advancements quickly followed. For example, a test was developed for copper toxicosis (CT) in Bedlington Terriers where 25% are affected, 50% are carriers and only 25% are clear (Bell). Other discoveries included a test for juvenile cataracts in Boston Terriers along with the mechanism involved in the transmission of the tick-borne disease, Rocky Mountain spotted fever (Brewer). Genetic markers for illnesses in Basenjis, Standard Poodles and English Cocker Spaniels followed. These technological advancements demonstrate what can be accomplished when breeders, clubs and research efforts are combined.

The key to this kind of success involves cooperation and sufficient funding. Perhaps the best example was the collaborative effort between the **AKC/CHF** and the **Orthopedic Foundation for Animals (OFA)** which resulted in the development of the **Canine Health Information Center (CHIC)** (www.caninehealthinfo.org). CHIC is an online registry that works with parent clubs to establish a panel of testable disorders for specific breeds. The CHIC concept is that dogs achieve a CHIC certification by completing the health-checks identified by their breed club. Passing each health test is not a requirement for certification. CHIC is about being health conscious, not about being faultless. For those not ready to share in an open database, CHIC offers a way to protect the privacy of their information. CHIC enters all test information into their database. Breeders who chose to restrict their test results participate in the aggregate because summary data is useful for research and statistical reporting.

CHIC functions not only as a tool for breeders and their clubs but as a resource for health information that can be shared in various ways. In this respect, every breeder can participate even if they are only willing to share limited amounts of information. Restricted data has value because it can be used for general searches about diseases and traits. This is often useful for research and the calculation of statistical averages. For example, summary data is useful to breeders who wish to compare their results to their breed’s average.

Since its inception, the AKC/CHF has funded more than 340 studies. Many of the top ten diseases found in purebred dogs are being studied at 74 veterinary schools and research institutions worldwide including those located in Argentina, Great Britain, France, Germany, Australia, and the Netherlands. Because of the many new methods and technological breakthroughs that have occurred, there are more than 60 DNA tests now available for screening breeding stock.

THE TIME PATH

One of the major obstacles in bringing new DNA tests forward is called the **time-path**. This is the amount of time and effort required to identify a problem, characterize it, call it by its proper name, and secure funding. If the researcher is successful and discovers a solution, a protocol is developed for use by veterinarians and breeders. Unfortunately, the time-path is often longer than most expect. For example, once a project has been identified and funded, blood samples and pedigrees must be collected. If the researcher is successful and a marker found, the next step is to make the information available in an easy to use and understandable manner. The time-path for the total process can be as short as a few years or as long as a decade. Each time a new test or new method is developed a new learning curve begins. Veterinarians and breeders must learn what laboratories can administer the test, how the results can be used and interpreted and what mechanism is available to identify and manage the carriers. With this kind of information and technology, the genes that took years to collect can be saved while diseases and disorders can be controlled and eliminated.

With DNA technology and new breeding protocols, the problems of the breeder can be addressed more directly. In the past the popular approach was to simply eliminate all of the carriers and affected dogs from a breeding program. Unfortunately, this approach quickly affected the diversity of a breed's gene pool. Others took a different approach and conducted test-matings to identify carriers, affected and normals. This did not prove to be a desirable method because the undesirable genes are either present or not and test breedings often produced affected dogs that had to be carefully placed or euthanized. More recently, better methods have become available that can reduce many of the problems of the past. For example, DNA testing can be used to eliminate problems because it allows breeders to manage carriers while saving the genes needed to maintain breed type and temperament. The screening of breeding stock, followed by the selection of quality offspring, offers a significant improvement over test-matings.

It has been well established that DNA tests will help breeders decrease the frequency of defective genes. If no test is available, carriers can be carefully bred. The approach recommended is to breed carriers to those that appear normal when evaluated. The assumption is that the breeder will follow-up on the offspring produced. Using this approach, breeders can select normal offspring for future breeding. This is a slower and less certain approach and it will not eliminate all of the carriers but it will reduce their frequency. Because of the increased awareness of diagnostic tests, better decisions can be made with positive results.

ABOUT THE AUTHOR

Carmen L Battaglia holds a Ph.D. and Masters Degree from Florida State University. He is an AKC judge, researcher and writer; he has been a leader in promoting better ways to breed dogs. An author of many articles and several books, he is also a popular guest on TV and radio talk shows including several appearances on Animal Planet. His seminars on breeding dogs, selecting sires and choosing puppies have been well-received by breed clubs. Those interested in learning more about his articles and seminars should visit the website <http://www.breedingbetterdogs.com>