SENDING INFORMATION AND SAMPLES*
Chinook Cryptorchidism Research , Washington State University, Pullman

THANK YOU for participating in this important research project! The samples you provide will allow researchers to find the genes causing cryptorchidism in Chinooks, and dogs in general. As the canine genome is mapped, breeders will have an unprecedented opportunity to identify and avoid producing disease, and concentrate on positive advances in their breeding programs.

It is important that the information you provide with the samples is as complete and accurate as possible. In addition to cryptorchidism, please tell us presence of any other disease, unusual, or "undesirable" characteristics in your dog. Information on specific, individual dogs will not be revealed - results of the research will identify what markers have been found, but not the names of those who submitted the samples where a characteristic was located, nor which individual dogs show affected or carrier status for cryptorchidism. Information provided will be kept strictly confidential. As the research produces results, participants may request information on the genetic status of their dog(s).

Complete families are critical to locating specific genes and markers. Wherever possible, submit samples from all siblings, both parents, and all available grandparents.

Begin by gathering the pedigree, litter information, and litter list(s) for each family you plan to submit. You will need a correctly formatted (sire on top, dam on the bottom), typed or computer-generated pedigree (3- to 5-generation) of the litter where an affected appeared. The pedigree will connect each sample you submit to the family it comes from, so make copies for each individual dog that will be sampled. The breeder of the litter, or other person familiar with the litter should make a "Litter Packet" for each litter - this consists of the *Litter Information* sheet, *Litter List*, and the *Pedigree*. For the Litter ID code use the kennel name or breeder name, plus the date of birth of the litter, so if Pat Doe had a litter born May 15, 2001, the code would be "Doe 05-15-01". We have a different system of coding in the lab to anonymously identify samples, but the Litter ID code is a way to tie your information together and place individuals in the families where they belong as samples are submitted. This ID code should be on each form sent in. Keep a copy of the packet for your own records, and send a copy to the following address. This family information may be sent with the blood samples, or separately.

Next, begin collecting and submitting samples. See the *Sample Handling* sheet for procedures. The *Individual Dog* submission form should accompany each sample, along with the marked *Pedigree* copy that will tie in with the family information sent. Make copies of the *Sample Handling* and *Individual Dog* forms as needed for all samples to be submitted. If several dogs' samples are being sent together, number the forms and samples to be certain there is no confusion (Sample #1, #2, etc). On a spare copy of the pedigree you may want to mark (for yourself) who is alive and sampled, not sampled, and those no longer living, to keep track of who you need to get samples from. As stated before, entire families will give the best chance at finding specific genes - do your best to include all living family members.

Send samples and information at this address:

Chinook Cryptorchidism Research
Jennifer Michal, Department of Animal Sciences
Washington State University, Pullman, WA 99164-6351

If you any questions, please contact Jennifer Michal at email Jennifer_Michal@wsu.edu, phone: 509-335-1002. Jennifer is a technician on the project. You may contact Dr. Memon memon@vetmed.wsu.edu, if you have questions about the research project. Once again, thank you for participating in this important research - you are contributing to the betterment of canine health, especially the Chinook breed.

* *The form is adopted from Canine Epilepsy network* < http://www.canine-epilepsy.net/>