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## New technologies offer new opportunities for Nordic dog breeds

A joint Nordic project initiated by NordGen will contribute to sustainable breeding of Nordic dog breeds. Collaboration between researchers in Denmark, Norway, Finland, Iceland and NordGen on genetic characterization of a large number of dog breeds in the Nordic countries will provide information on the breeds' 'genetic health'. This information is important for planning sustainable dog breeding in the future.

Breeds are often developed in a defined geographical area and in many cases this region / country is also the area where the breed is widespread. Dog breeds often have characteristics that are uniquely customized to the area and the use they have or have had in the past. The Nordic countries are home to approximately 26 dog breeds, defined as national breeds (see table), and the Nordic countries have a key responsibility in relation to ensuring sustainable breeding and conservation of these breeds. 16 of these breeds are included in the joint Nordic project and we hope to include more breeds over time.

Many dog breeds, including the Nordic, have gone through population bottlenecks. A population bottleneck is a phenomenon where a population experiences a sharp decline in population size, after which it increases again. The current breeds have typically undergone a drastic reduction in population size in the domestication process, which is believed to have occurred approximately 15,000 years ago, and in connection with the establishment of individual breeds. In addition many breeds have been intensively selected for breed specific properties and only few individuals have been used for breeding. These factors, bottlenecks and intensive selection, have contributed to the low effective population size of many Nordic dog breeds. The effective population size is defined as the size of an idealized population with equal number of males and females, no selection, and random mating, which would



*The Norwegian Lundehund is an example of a Nordic dog breed with extremely low genetic variation and high level of inbreeding. The breed has relatively high mortality due to the disease intestinal lymphangiectasis (IL). Norwegian Lundehund Club is in the process of designing a new breeding strategy for the breed, as part of the joint Nordic cooperation described in this article. The strategy will be to cross individuals from other closely related Nordic dog breeds into the Lundehund. This will increase the genetic variation and reduce inbreeding, which is expected to reduce the problem of IL. The results from the SNP analysis are an important tool to assess which breeds will be relevant to use for crossing. Photo: Arild Espelien.*



*The Icelandic Sheepdog is a Nordic breed which has been through severe genetic bottlenecks. Studies show a correlation between the incidence of hip dysplasia and the degree of inbreeding in this breed - the more inbred an individual is the greater the risk of hip dysplasia. Photo: The Icelandic Sheepdog Club.*

result in the same increase in inbreeding as in the population of interest. In other words, the fewer individuals that contributes to the next generation the lower the effective population size.

A low effective population size is a problem because it increases the likelihood of 1) losing genetic variation (Figure 1) and 2) for mating related individuals, leading to inbreeding (Figure 2). In fact, many Nordic dog breeds have effective population sizes lower than 50-500 individuals that is proposed as the lower limit of what is sustainable. These two factors, high rates of inbreeding and loss of genetic variation, can and must be dealt with.

NordGen coordinates a project with researchers from Denmark, Finland, Iceland and Norway, where DNA collected from Nordic dog breeds is analyzed on a so-called SNP chip. Results from SNP chips can be used to identify and quantify genetic variation between individuals and breeds. The novelty of the SNP chip technology compared to previous methods is that 170,000 genetic markers may be examined simultaneously. Some of these will be neutral whereas others are of great importance to the traits of interest (including disease characteristics). Molecular studies of dogs traditionally used a small number of neutral markers (typically <30). This joint Nordic cooperation provides extremely useful information in terms of finding areas of the genome causing certain genetic diseases and quantifying the degree of inbreeding and genetic variation within and between breeds. These results can be used to plan breeding of the Nordic dog breeds so that both the loss of genetic variation and the increase in inbreeding are reduced. The results will be used to answer questions such as 1) in which breeds should focus be on increasing the effective population size, 2) in which breeds should crossbreeding with individuals from other breeds be considered, and 3) which breeds should be used for crossing. In the long term, data can be used for selection against harmful alleles and for the maintenance of adaptive variation.

Category	Breed name	'Home country'	Included in the current project
<b>Nordic Sledge Dogs</b>	Greenland Dog	Denmark	Yes
<b>Nordic Hunting dogs</b>	Norwegian Elkhound Grey	Norway	Yes
	Norwegian Elkhound Black	Norway	Yes
	Norwegian Lundehund	Norway	Yes
	Jömthund	Sweden	
	Norrbottnenspit	Sweden	Yes
	Karelian Bear Dog	Finland	Yes
	Finnish Spitz	Finland	Yes
<b>Nordic Watchdogs and Herders</b>	Icelandic Sheepdog	Iceland	Yes
	Norwegian Buhund	Norway	
	Swedish Lapphund	Sweden	Yes
	Swedish Vallhund	Sweden	
	Finnish Lapphund	Finland	Yes
	Lapponian Herder	Finland	Yes
	Finnish Spitz	Finland	Yes
<b>Continental Pointing dogs</b>	Old Danish Pointing Dog	Denmark	Yes
<b>Molossoid breeds</b>	Broholmer	Denmark	Yes
<b>Medium and small sized hounds</b>	Norwegian Hounds	Norway	Yes
	Halden Hound	Norway	
	Hygen Hound	Norway	
	Finnish Hound	Finland	
	Hamiltonstövare	Sweden	
	Schillerstövare	Sweden	
	Smålandsstövare	Sweden	
	Drever	Sweden	
	Danish/Swedish Farm Dog	Denmark/Sweden	Yes

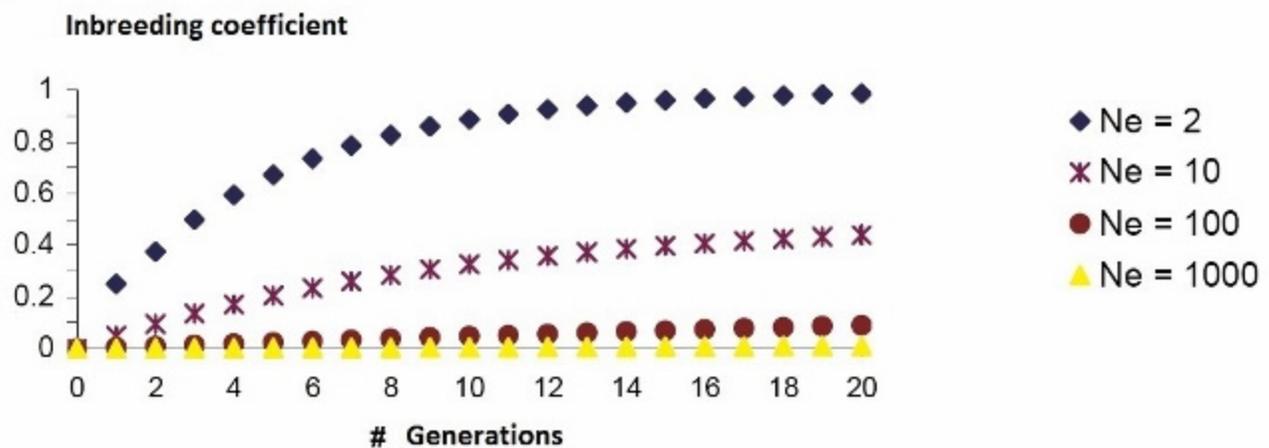


Figure 1: Inbreeding coefficient as a function of the number of generations for different effective population sizes (Ne).

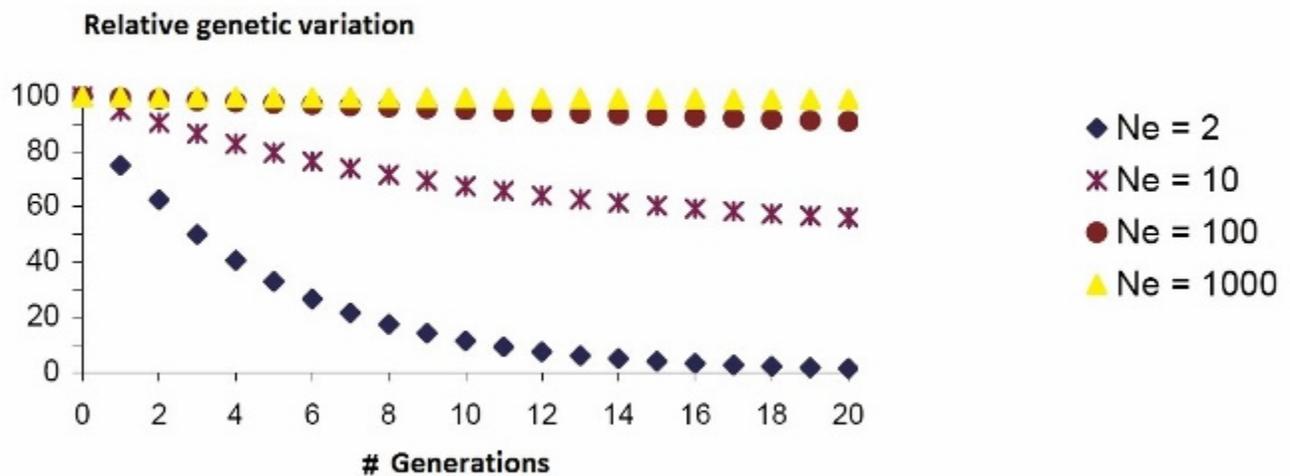


Figure 2: Relative amount of genetic variation in a population as a function of number of generations for different effective population sizes (Ne).

### For more information:

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