

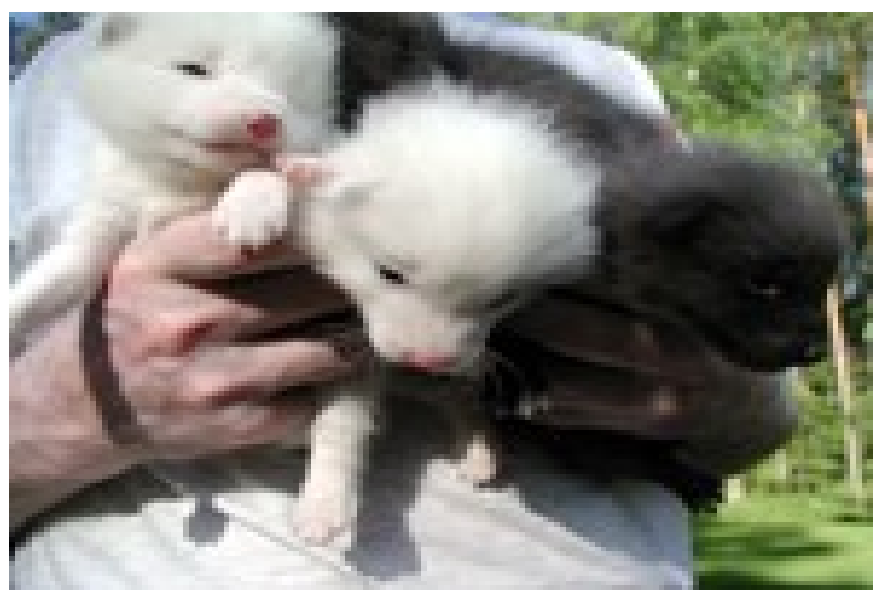
The sequencing of genomes of several domestic animals together with the novel information about genes associated with economical traits has created interesting opportunities for studies with close relatives of domestic animals. Comparative approach can be utilized e.g. in evolutionary studies and in analyses of candidate genes for economically important traits. Recent studies have demonstrated that rather high percentage of canine microsatellites have worked with silver fox and blue fox DNA. In this study, molecular genetic markers were selected from published linkage maps of domestic dog.

The main aim of this study was to construct first genetic linkage map for the blue fox (*Alopex lagopus*). This linkage map will be utilized in quantitative trait mapping efforts in blue fox. In addition, the map will facilitate comparative mapping between dog and blue fox as well as increase our understanding of the evolution of their genomes.

# A genetic linkage map of the blue fox (*Alopex lagopus*)

Table 1. Number of animals by sex.

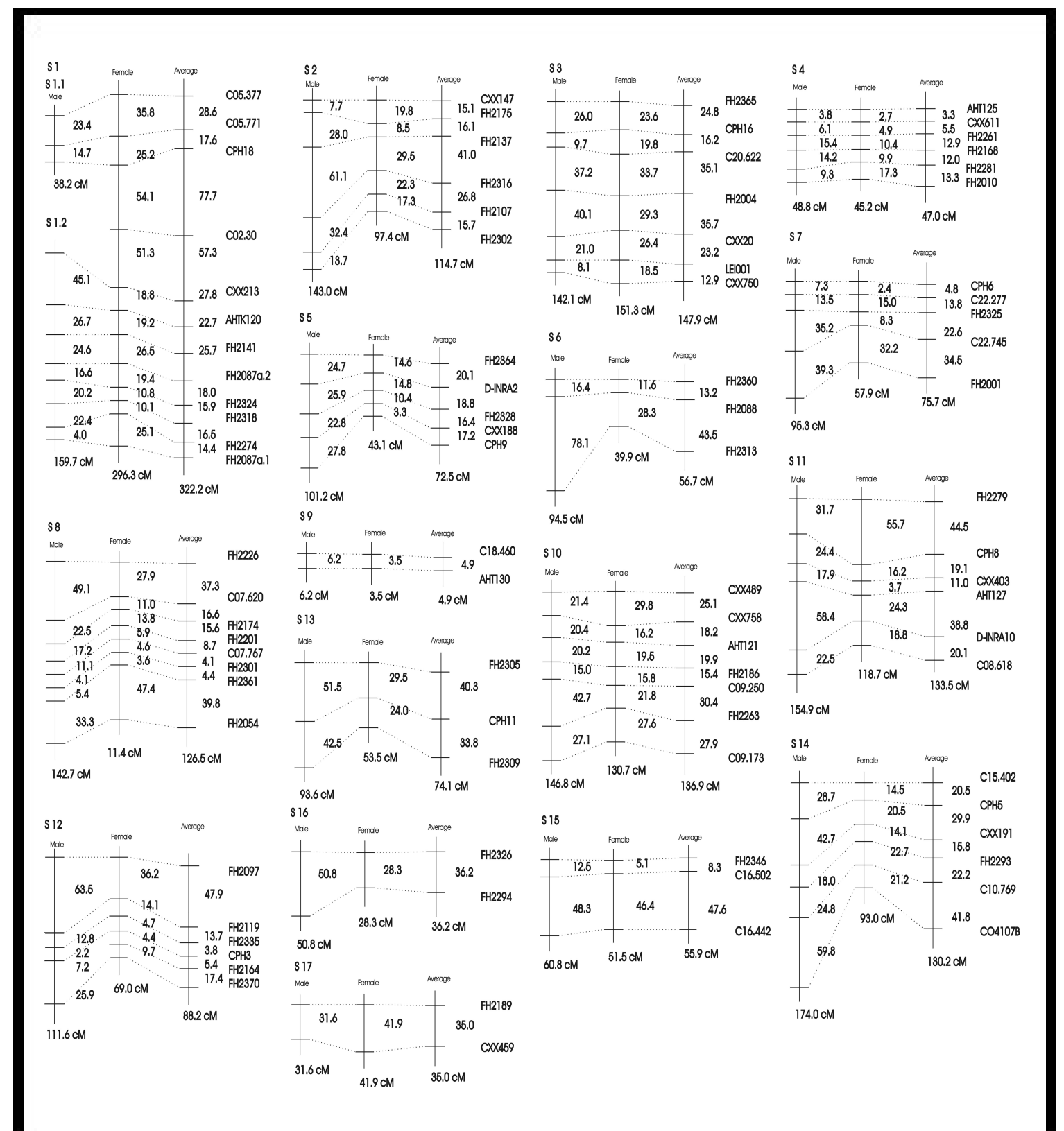
Generation	Females	Males	Total
Parental animals (P)	16	4	20
F1	33	10	43
F2	170	222	392
Total	219	236	455



Photos: Finnish Fur Breeders' Association



Figure 1. Male, female and sex-averaged linkage maps for blue fox.



## Material and methods

A linkage map was constructed for the blue fox using a three-generation mapping population. Numbers of animals in mapping population are given in Table 1. We tested 130 previously published canine microsatellite markers to find highly informative markers for the blue fox. Genetic linkage map was constructed using the CRI-MAP program. Microsatellites were assigned to linkage groups based on LOD score 3.

## Results and discussion

We were able to genotype 102 markers in mapping population, 28 primer pairs tested were either monomorphic or did not amplify DNA fragments with interpretable banding patterns. Percentage of informative meioses per marker varied from 30 to 99 % (mean 71%). The sex-averaged map consisted of 89 markers assigned to 17 linkage groups and the total length of the map was 1658 cM (Figure 1). Lengths of sex-averaged linkage groups ranged from 4.9 cM to 322.2 cM. Thirteen markers remained unlinked with any other marker. Our study suggests that many linkage groups are conserved between dog and blue fox. For instance, blue fox linkage groups S4, S5, S8, S10 and S12 are thought to be largely conserved with canine chromosomes CFA24, CFA29, CFA7, CFA9 and CFA6.

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