2.4 Examples of application of gene frequencies

When the gene frequencies in a population are known, the genotype frequencies for each genotype under H-W conditions can be calculated. Correspondingly the mating type frequencies under random mating can be calculated by means of the multiplication rule for probabilities, results shown in the table below. Note that when the two genotypes are different, there has to be multiplied with 2, as the two types can be combined in reverse orders.

				Offspring segregation	
Mating type	Frequency		AA	Aa	aa
AA x AA	p^2 x p^2	= p^4	1		
AA x Aa	2 x p^2 x 2pq	= $4p^3$ x q	0.5	0.5	
Aa x Aa	2pq x 2pq	= $4p^2$ x q^2	0.25	0.5	0.25
AA x aa	2 x p^2 x q^2	= $2p^2$ x q^2		1	
Aa x aa	2 x 2pq x q^2	= $4pq^3$		0.5	0.5
aa x aa	q^2 x q^2	= q^4			1

Calculation of mating type frequencies is important in relation to control of monogenetic inherited diseases. This topic will be discussed more detailed in chapter 5, where the classical segregation in offspring will be

Mating type	Total Freq.	Offspring AA	Offspring Aa	Offspring aa
AAxAA	0.9801495	0.9801495	0	0
AAxAa	0.0197014	0.0098507	0.0098507	0
AaxAa	0.0000990	0.0000247	0.0000495	0.0000247 99.00 %
AAxaa	0.0000495	0	0.0000495	0
Aaxaa	0.0000004	0	0.0000002	0.0000002 0.99 %
aaxaa	0.0000000	0	0	0.0000000 0.00 %
Calculate		sum = 0.9900249	sum = 0.0099500	sum = 0.0000250
Freq. p 0.995				

Gene frequencies also have a large area of application within bred studies. The gene frequencies for closely related breeds have a tendency to lie closer each other than not so closely related breeds.

Table 1. Distribution of albumin types among pure dog breeds and mongrels arrang
according to the frequency of the slow allele.

Breed	Genotypes *SS*	*SF*	*FF*	Total	Frequency of *S*
Basset Hound	0	2	30	32	0.03
Beagle	3	14	52	69	0.14
Dachshund	2	8	26	36	0.17
Small Münsterländer	2	3	12	17	0.21
Sheepdog, Shetland	0	6	5	11	0.27
Dalmatian	2	3	10	15	0.30
Collie	2	21	18	41	0.33
Cocker Spaniel	7	24	20	51	0.37
Grey Hound	4	6	8	18	0.39
St. Bernhard	3	8	7	18	0.39
Labrador Retriever	8	10	10	28	0.46
German Shepherd	36	47	23	106	0.56
Old Danish Pointer	5	5	2	12	0.63
Terrier, Tibetanian	10	11	3	24	0.64
Terrier, Airedale	5	12	0	17	0.65
Poodle, Miniature	9	8	2	19	0.68
Newfoundland	25	33	3	61	0.68
Poodle	39	36	6	81	0.70
Boxer	54	14	1	69	0.88
Carelian Bear Dog	15	4	0	19	0.89
Golden Retriever	53	3	1	57	0.96
Great Dane	9	0	0	9	1.00
Rottweiler	10	0	0	10	1.00
Basenji	44	0	0	44	1.00
Other pure breeds	94	57	38	189	0.65
Mongrels	22	41	24	87	0.49
Total	463	376	301	1140	
Genotypic frequencies	0.406	0.330	0.264		
Expected genotypic frequencies	0.326	0.490	0.184		

The calculated gene frequencies were p(*S*) = 0.571

The above shown table gives the results from a study of the albumin types in Danish dog breeds. As mentioned in section 2.1 a fast and a slow albumin allele occur when serum is tested on an electrophoreses gel. These alleles have the designations F and S. The frequencies of the S allel varies from 0 to 1 in the dog breeds. The investigations have been carried out by K. et al. 1985; *Hereditas*, 102:219-223.

In the table below are the results from a study of some mikrosatellites in Danish dog breeds, as well as in the red and the blue foxes. Here are results from three loci each with several alleles, being named as the length of the DNA-string being amplified by the primers. The frequencies vary significantly between the dog breeds. The primers which are developed in the dog work equally well in both fox species. This indicates a large degree of genetic homology between dogs and foxes. H^e gives the information content of the loci. This depends on the percentage of heterozygotes in the population concerned. Genetically the heterozygotic animals are the most informative. In paternity tests or other genetic investigations the homozygotes give very little or no information about which of the parents' alleles an offspring has inherited. The investigations have been carried out by M. Fredholm et al. 1995; *Mamalian Genome*, 6:11-18.

Table 2. Allele sizes and allele frequencies of canine microsatellites.

Microsatellite locus	Core sequence	Allele	Flat-coated retriever[a]	Dachshund[b]	Arctic fox[c]	Red fox[d]
CPH1	$(TGG)_3$ - $TAG(TGG)_{11}$	125			1.00	
		132				0.30
		135		0.14		
		138				0.70
		141	0.83	0.56		
		144	0.17	0.30		
H[e]			**0.21**	**0.56**	**0.00**	**0.40**
CPH2	$(AC)_{15}$	95	0.20			
		97	0.36	0.36		
		99	0.20	0.06		
		103		0.06		
		107		0.52		
		109	0.24			
H[e]			**0.94**	**0.47**		
CPH3	$(GA)_2TA(GA)_{17}$	154			0.15	0.05
		158			0.10	0.25
		162	0.29		0.45	0.30
		164			0.15	0.40
		166			0.15	
		168	0.09	0.28		
		172	0.02	0.03		
		174		0.02		
		176	0.32	0.28		
		178	0.20	0.20		
		180	0.02	0.14		
		182	0.08	0.05		
H[e]			**0.67**	**0.63**	**0.80**	**0.90**