

Litter Analysis

Litter Summary

PARENTS

Information	Parent One	Parent Two
Name	Harmony Mt Acer Vom Pawpaw	Harmony Mtn High Caliber
Breed	Poodle - Standard	Poodle - Standard
VGL Case Number	DR100207	DR100814
DLA Haplotype 1	1002 2001	1002 2001
DLA Haplotype 2	1008 2005	1004 2002

This litter analysis is based on 1000 simulated puppies.

DLA HAPLOTYPES

Probability for Each Puppy to Inherit	DLA Extended Haplotype 1	DLA Extended Haplotype 2
Combination 1 - 25%	1002 / 2001	1002 / 2001
Combination 2 - 25%	1002 / 2001	1004 / 2002
Combination 3 - 25%	1008 / 2005	1002 / 2001
Combination 4 - 25%	1008 / 2005	1004 / 2002

INBREEDING

These are measures of inbreeding in each parent and the litter average. Two inbred dogs, when unrelated, can make very outbred pups, and two outbred dogs, when genetically similar, can make very inbred pups. IR and HL are estimates of genome wide inbreeding and better correlate with fitness. Percent homozygosity shows the percentage of loci where an identical allele was inherited from each parent.

Dog or Dogs of This Breed	Internal Relatedness (IR)	Homozygosity by Loci (HL)	Percent Homozygosity
HARMONY MT ACER VOM PAWPAW	0.02	0.30	30.3%
HARMONY MTN HIGH CALIBER	0.19	0.44	45.5%
Breed Averages	0.03	0.31	32.3%

Potential Litter Statistics	Internal Relatedness (IR)	Homozygosity by Loci (HL)	Percent Homozygosity
Averages	0.03	0.32	33.1%
Minimums	-0.23	0.13	15.2%
Maximums	0.32	0.52	54.6%

GENETIC RELATEDNESS

Average GR shows how similar to its breed a dog is on average. Below 0 means the dogs are unrelated, and the farther below zero, the less alike the dogs are. Parents and full siblings have GR figures of about

0.50, while grandparent, grandchild, aunt, uncle or half-sibling have GRs of about 0.25. First cousins and great grandparents have GRs of approximately 0.125. If a pair of dogs is unrelated by pedigree, but receives a higher GR when paired with another dog, they most likely have many common ancestors and should be considered related in breeding decisions. If dogs are related based on pedigree but have lower than expected GRs when compared, they can be considered less related in breeding decisions.

Dog or Dogs of This Breed	Average GR to Others	Percent of Breed Unrelated to This Dog	This Pair's GR
HARMONY MT ACER VOM PAWPAW	-0.03	62.2%	0.03
HARMONY MTN HIGH CALIBER	0.00	49.5%	0.03
Breed Averages	-0.01	54.4%	-0.01

ALLELES

The Outlier Index uses ratios of infrequent, neutral and highly frequent alleles to measure how unusual a particular dog is or estimate how unusual a litter will be compared to its breed. All purebred dogs have a certain percentage of "typical" alleles, but inbred breeds have higher average typical alleles. Breeders should aim for a higher OI than the breed average to preserve the diversity in the breed.

Dog or Dogs of This Breed	Infrequent Alleles	Neutral Alleles	Highly Frequent Alleles	Outlier Index
HARMONY MT ACER VOM PAWPAW	7	8	51	0.26

HARMONY MTN HIGH CALIBER	4	8	54	0.20
Breed Averages	8	5	53	0.23

Potential Litter Statistics	Infrequent Alleles	Neutral Alleles	Highly Frequent Alleles	Outlier Index
Averages	5	8	53	0.23
Minimums	0	3	45	0.11
Maximums	11	13	59	0.39

ANCESTRY

By assessing frequencies of alleles at each locus, we can estimate the percentage of typical, neutral, unusual or admixed ancestry each dog has, and each litter will have on average.

"Admixed" ancestry is when a dog inherits a very infrequent allele from one parent and a highly frequent one from the other. The more admixed percentage there is, the more likely the dog inherited genes from an unusual dog who was a recent ancestor.

Dog or Dogs	Unusual Ancestry	Neutral Ancestry	Typical Ancestry	Combined Ancestry
HARMONY MT ACER VOM PAWPAW	3.0%	3.0%	75.8%	18.2%
HARMONY MTN HIGH CALIBER	3.0%	3.0%	84.8%	9.1%
Breed Averages	4.0%	1.5%	77.5%	17.1%

Potential Litter Statistics	Unusual Ancestry	Neutral Ancestry	Typical Ancestry	Mixed Ancestry
Averages	2.3%	3.7%	79.6%	14.4%
Minimums	0.0%	0.0%	60.6%	0.0%
Maximums	6.1%	12.1%	97.0%	30.3%

ALLELE COMPARISON

Locus	Dog 1	Dog 1	Dog 1	Dog 1	Dog 2	Dog 2	Dog 2	Dog 2	Dog 1	Dog 1	Dog 2	Dog 2
	STR A	STR B	Freq. of A	Freq. of B	STR A	STR B	Freq. of A	Freq. of B	Type of A	Type of B	Type of A	Type of B
1	98	100	0.3352	0.0888	100	108	0.0888	0.1986	Hfrq	Nt	Nt	Hfrq
2	141	141	0.3974	0.3974	137	141	0.1643	0.3974	Hfrq	Hfrq	Hfrq	Hfrq
3	123	123	0.0928	0.0928	119	123	0.3917	0.0928	Nt	Nt	Hfrq	Nt
4	225	225	0.1851	0.1851	219	219	0.3552	0.3552	Hfrq	Hfrq	Hfrq	Hfrq
5	238	246	0.5837	0.2113	246	248	0.2113	0.0587	Hfrq	Hfrq	Hfrq	Infr
6	91	95	0.6707	0.1288	91	91	0.6707	0.6707	Hfrq	Infr	Hfrq	Hfrq
7	286	288	0.0986	0.3935	284	284	0.1265	0.1265	Infr	Hfrq	Nt	Nt
8	116	118	0.0832	0.4168	116	118	0.0832	0.4168	Nt	Hfrq	Nt	Hfrq
9	132	144	0.4459	0.2618	144	144	0.2618	0.2618	Hfrq	Hfrq	Hfrq	Hfrq
10	164	172	0.0023	0.0849	156	156	0.5597	0.5597	Infr	Nt	Hfrq	Hfrq

11	240	242	0.7185	0.0814	240	240	0.7185	0.7185	Hfrq	Infr	Hfrq	Hfrq
12	91	91	0.3666	0.3666	91	91	0.3666	0.3666	Hfrq	Hfrq	Hfrq	Hfrq
13	124	124	0.5170	0.5170	124	126	0.5170	0.4436	Hfrq	Hfrq	Hfrq	Hfrq
14	152	152	0.3922	0.3922	144	152	0.3185	0.3922	Hfrq	Hfrq	Hfrq	Hfrq
15	210	216	0.2077	0.3794	214	220	0.3014	0.0128	Hfrq	Hfrq	Hfrq	Infr
16	85	85	0.6645	0.6645	95	107	0.1065	0.1923	Hfrq	Hfrq	Infr	Nt
17	241	241	0.5193	0.5193	241	241	0.5193	0.5193	Hfrq	Hfrq	Hfrq	Hfrq
18	206	208	0.5570	0.0777	206	206	0.5570	0.5570	Hfrq	Infr	Hfrq	Hfrq
19	216	218	0.4260	0.2682	216	218	0.4260	0.2682	Hfrq	Hfrq	Hfrq	Hfrq
20	162	164	0.5938	0.3000	162	164	0.5938	0.3000	Hfrq	Hfrq	Hfrq	Hfrq
21	268	272	0.4977	0.2164	268	268	0.4977	0.4977	Hfrq	Hfrq	Hfrq	Hfrq
22	226	228	0.2353	0.1999	232	232	0.3398	0.3398	Hfrq	Hfrq	Hfrq	Hfrq
23	153	153	0.2529	0.2529	147	147	0.2579	0.2579	Hfrq	Hfrq	Hfrq	Hfrq
24	12	12	0.3002	0.3002	12	20	0.3002	0.0341	Hfrq	Hfrq	Hfrq	Infr
25	17.1	18.1	0.1174	0.2751	18.1	21.1	0.2751	0.2787	Hfrq	Hfrq	Hfrq	Hfrq
26	14	19	0.1344	0.3220	13	13	0.1692	0.1692	Hfrq	Hfrq	Hfrq	Hfrq
27	28	29	0.1098	0.0026	16	26	0.0462	0.4757	Hfrq	Infr	Nt	Hfrq
28	17	19	0.0220	0.4410	19	19	0.4410	0.4410	Infr	Hfrq	Hfrq	Hfrq
29	13	14	0.2485	0.2338	9	14	0.4000	0.2338	Hfrq	Hfrq	Hfrq	Hfrq
30	17	18	0.1947	0.1356	15	18	0.2219	0.1356	Hfrq	Nt	Hfrq	Nt
31	13	20.3	0.1157	0.1213	15	19.3	0.1711	0.1170	Hfrq	Hfrq	Hfrq	Hfrq

32	15	19	0.2305	0.1128	15	17	0.2305	0.5390	Hfrq	Nt	Hfrq	Hfrq
33	12	16	0.1528	0.3298	16	16	0.3298	0.3298	Nt	Hfrq	Hfrq	Hfrq

