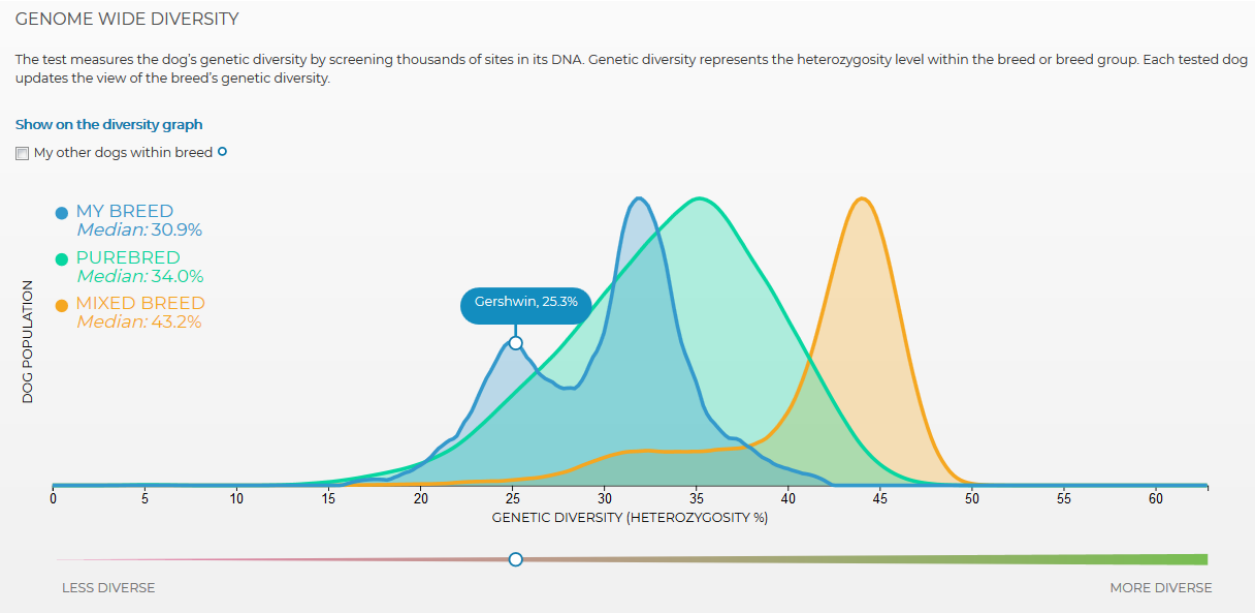
Coefficient of Inbreeding vs. Genetic Diversity Level in Greyhounds

It has been almost one and a half year since the last update[7] – in the meantime a lot has happened. 39 more Greyhounds have been tested with MyDogDNA, e.g. three F1 dogs from a racing x coursing line cross and one from a F2 racing x show line cross.
So it was high time for another review.

We introduced the MyDogDNA test in 2017[1], which has been used on some German-bred Greyhounds in the meantime. In addition, we gave an overview of the levels of inbreeding (COI) in Greyhounds born in Germany[2], which resulted in the recommendation to use tools to determine the real genetic diversity as well.

In this respect a comparison between the calculated COI and the measured genetic diversity would be interesting. So we will compare the following values:

- Coefficient of inbreeding for seven generations[3]
- Ancestor loss for seven generations [4]
- Genetic Diversity[5]: This is one aspect of the MyDogDNA test and is being analyzed by comparing more than 5000 SNP markers, which cover each of the 39 chromosome pairs in the dog genome with a defined intermarker distance. A particular emphasis was placed on marker selection in the chromosome 12, where genes of immunologic importance are located (DLA & MHC).
  With a screening like this we can determine the level of heterozygosity, which means the proportion of inherited similar or different alleles (genetic information) for one trait the respective dog has gotten from his dam and sire. If a dog inherited many similar (homozygous) alleles and only a few different one, it will get a low score for “Genetic Diversity”. If it has inherited a lot of different genes, it will score much higher for “Genetic Diversity”.
  A dog with a high share of homozygous genes does have a high congruence between outer appearance and inheritable traits, but may be less vital and adaptable. A (too) low level of genetic diversity is said to promote allergies and autoimmune diseases in dogs.
  In the MyDogDNA database the data of more than 20000 dogs is saved, whose levels of “Genetic Diversity” range from 4 – 50 %. The results of more than 100 tested Greyhounds cluster around a median of 30,9 % (1,5 years ago it was around 31,7 %).



Two of the tested dogs (blue circles) in comparison to all tested Greyhounds (blue line), to all purebred dogs in the database (green line, median of 34,0 %) and to all mixed-breed dogs in the database (orange line, median 43,2 %).

Listed below are the examined Greyhounds. These are 24 dogs from 13 German kennels, 10 from Ireland, six from Austria, five from France, three from the US, two each from Finland, Russia and Estonia and one each from Italy, Norway, Sweden and Hungary.

32 dogs are show-bred, 19 are out of Irish racing-lines, two coming from Irish coursing lines. Three dogs are F1 from racing x coursing line crosses and two show lines with some “racing blood”.
According to their own statements, there should be data of more than 100 Greyhounds recorded in the MyDogDNA database. Unfortunately they are not for public use.

Name	GD	IK	AV	Mutationen	GHI
Allaghaun	28,30%	5,73%	39,40%		95
Benghazis Enchanting Red Rose	26,80%	1,03%	30,30%		93
Branwen Grian Gryjandi	27,80%	2,19%	37,80%		94
Ceannloch Boa	32,20%	2,16%	17,70%		101
Christcile´s Oguenel	32,40%	0,00%	25,60%		102
Cool ahead‘s Amaze	31,80%	4,41%	27,60%		101
Deneview Snowfox	34,20%	0,36%	25,60%		102
Deneview Snowtoe	30,30%	2,08%	25,20%		95
Desecration Smile Carolina of Naifhounds Kingdom	26,00%	1,34%	36,20%		91
Epic Grandiose	20,20%	5,20%	46,90%		82
Estet Classic Dreamlike	28,10%	2,93%	40,20%		92
Estet Classic Milky Way	24,80%	9,90%	54,70%		86
Fortherinhays Beg your Pardon	23,10%	8,27%	55,50%		87
Harringay´s Quil´Dare	30,80%	5,81%	43,70%		99
Iceane Rose des Sables d‘Elodie	26,20%	3,88%	40,20%		92
I'll Never Leave You ad Honores	23,90%	1,58%	30,70%		88
Ina's Fashion Aristocrat	23,70%	7,15%	44,10%		88
Ina's Fashion Beloved	21,40%	5,76%	47,20%		84
Ina's Fashion Charming	20,70%	10,09%	48,00%		83
Jet's Love Me Or Leave Me	17,60%	19,23%	59,80%		78
Jupiter des Dames du Lac	22,40%	11,33%	51,20%		86
Katatjuta´s All Inclusive	29,30%	0,65%	16,10%		97
Katatjuta´s Anynamewilldo	28,90%	0,65%	16,10%		96
Katatjuta´s Behind Blue Eyes	30,80%	0,00%	18,90%		99
Katatjuta's Beir Bua	29,60%	0,00%	18,90%		97
Katatjuta´s Believe in Dreams	31,00%	0,00%	18,90%		100
Katatjuta‘s Zampino	32,20%	0,63%	13,80%		102
Kengyelfutó Elite Yankee	33,90%	0,01%	23,60%		104
Lochinvar Last Word	24,60%	16,76%	55,10%		89
Lochinvar Looks the Part	25,90%	16,76%	55,10%		91
Lochinvar Loves Rantalaukan	23,70%	16,76%	55,10%		88
Magnolia Des Dames Du Lac	28,20%	2,04%	41,70%		95
Mind Over Matter	25,60%	7,40%	46,90%		91
Rantalaukan Okalintu	24,80%	4,06%	39,00%		90
Rantalaukan Oma Puuma	26,80%	4,06%	39,00%		93
Razladzl Edgar	29,60%	4,86%	37,00%		97
Razldazl Lola	32,60%	2,84%	30,30%		102
Razldazl Oscar	30,70%	5,46%	34,60%		99

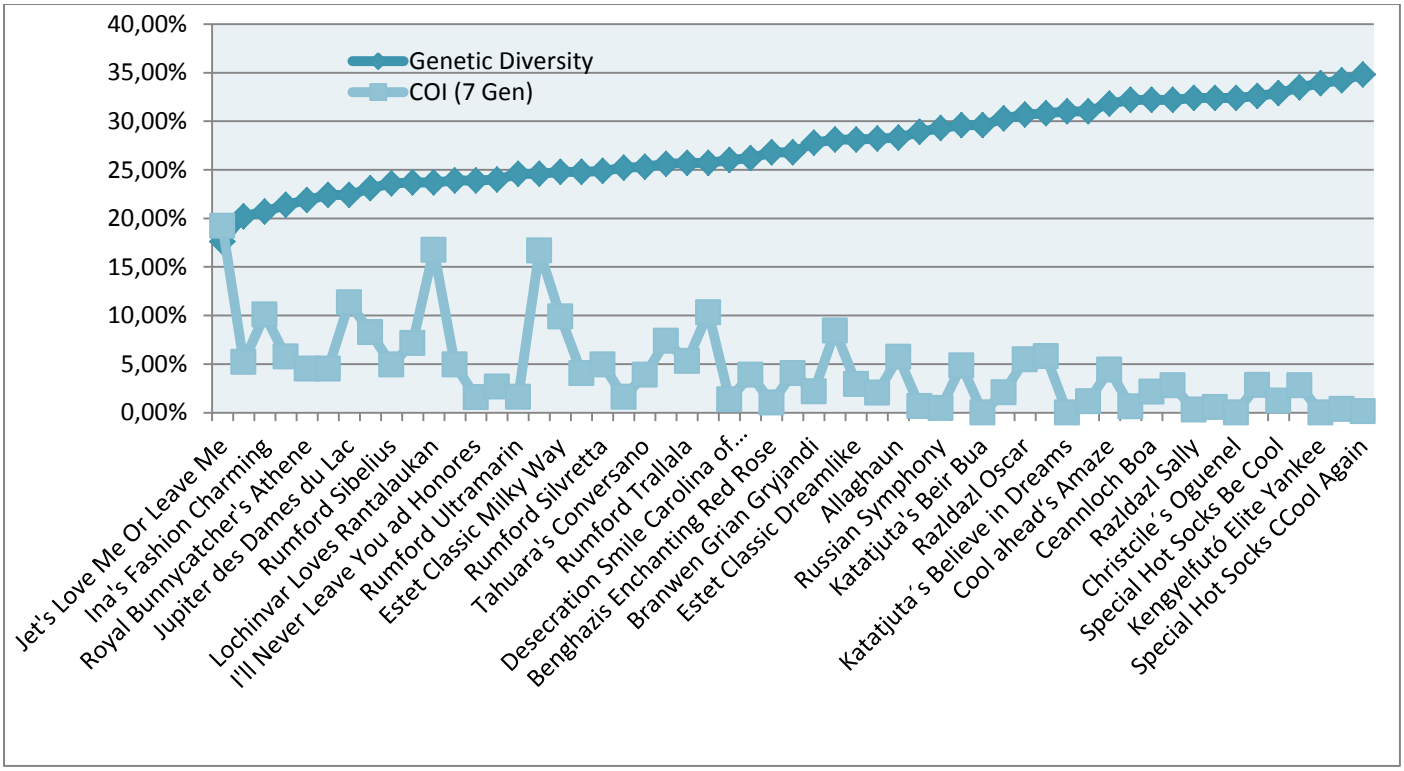
Razldazl Sally	32,40%	0,30%	16,50%		102
Royal Bunnycatcher's Aphrodite	22,40%	4,51%	39,80%		86
Royal Bunnycatcher's Athene	21,90%	4,51%	39,80%		85
Rumford Rollercoaster	24,00%	2,67%	37,40%		88
Rumford Sibelius	23,60%	4,93%	46,10%	-/del	88
Rumford Silvretta	24,90%	4,93%	46,10%	-/del	90
Rumford Sovereign	23,90%	4,93%	46,10%	-/del	88
Rumford Trallala	25,70%	5,30%	35,00%		91
Rumford Ultramarin	24,60%	1,61%	46,50%		89
Rumford Ustinov	25,20%	1,61%	46,50%		90
Russian Symphony	29,30%	0,46%	23,20%		94
Serene Angel	28,10%	8,45%	49,60%		95
Special Hot Socks Be Cool	32,90%	1,23%	24,00%		103
Special Hot Socks CCool Again	34,80%	0,13%	15,00%		106
Sun Storm	31,00%	1,17%	26,80%		97
Tahuara's Conversano	25,30%	3,88%	42,90%		90
Thurlesbeg Jo	32,40%	0,57%	23,60%		102
Vitruvians Beth	25,70%	10,32%	58,70%		91
Winsome Yankees Fantasy	33,50%	2,80%	31,90%		104
Winsome Yankees Faramir	32,20%	2,80%	31,90%		102

The relationship between Genetic Diversity and coefficient of inbreeding

If you compare the calculated COI with the measured levels of „Genetic Diversity“, you can – unsurprisingly – observe the following basic correlation:

The higher the COI is, the lower the level of „Genetic Diversity” will be.

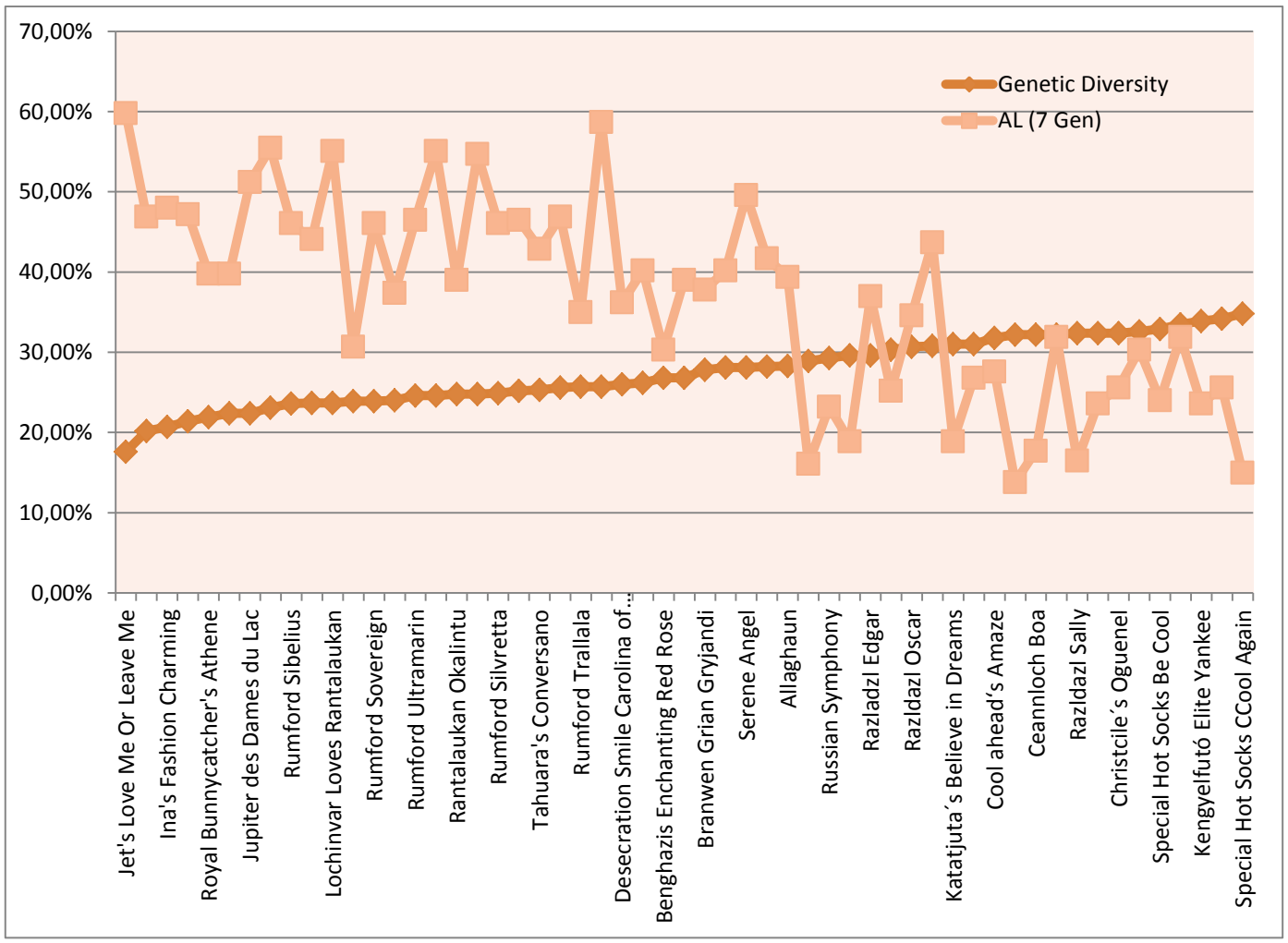
The dog of our group with the highest COI has also the lowest „Genetic Diversity” (“Jet's Love Me Or Leave Me”, COI 19.23 %, GD 17.60 %). On the other hand the dog with one of the lowest COI (“Special Hot Socks CCool Again”, COI 0.13 %) scores highest for “Genetic Diversity” (34.8 %).



But we also see that there are some distinct deviations:

In one bitch (“I'll Never Leave You ad Honores”) we find a “Genetic Diversity” of only 23.9 %, but with 1.58 % also a comparatively low COI. In comparison, “Lochinvar Loves Rantalaukan” shows almost the same “Genetic Diversity” (23.7 %), but his COI is more than tenfold as high at 16.76 %.

Maybe the ancestor loss is more reliable in predicting the genetic diversity?
At first glance we find another relation:
The higher the ancestor loss is, the lower the genetic diversity.
But there are exceptions from that rule as well. The bitch „Vitruvians Beth” shows a “Genetic Diversity” of 27.7 %, but also the highest ancestor loss of all tested dogs with 58.7 %. By contrast, “Rumford Trallala” scores similarly at 25.7 % for “Genetic Diversity”, but has a much lower ancestor loss with only 35.0 %.



Eventually we are only able to deduce from a sample of a size this small that calculated data like COI and ancestor loss can give us just a hint of a particular dog’s actual genetic diversity. Two more examples:

In order to take this important factor into account when making the breeding decisions for your kennel or even for whole populations, a much larger amount of data should be compared. Until then, we can only recommend to collect information about the actual genetic diversity with a test like MyDogDNA of so much breeding stock as possible.

Another thing is important in that respect: Littermates are not clones
Here the different “Genetic Diversity” results from tested siblings:

Lochinvar L-litter (COI 16,76%, AL 55,1%)

Last Word	24,60%
Looks The Part	25,00%
Loves Rantalaukan	23,70%

Rumford S-litter (COI 4,93%, AL 46,1%)

Sibelius	23,60%
Sovereign	23,90%
Silvretta	24,90%

Rumford U-litter (COI 1,61%, AL 46,5%)

Ultramarin	24,60%
Ustinov	25,90%

Katatjuata's A-litter (COI 0,65%, AL 16,1 %)

Anynamewilldo	28,90%
All Inclusive	29,30%

Katatjuata's B-litter (COI 0 %, AL 18,9 %)

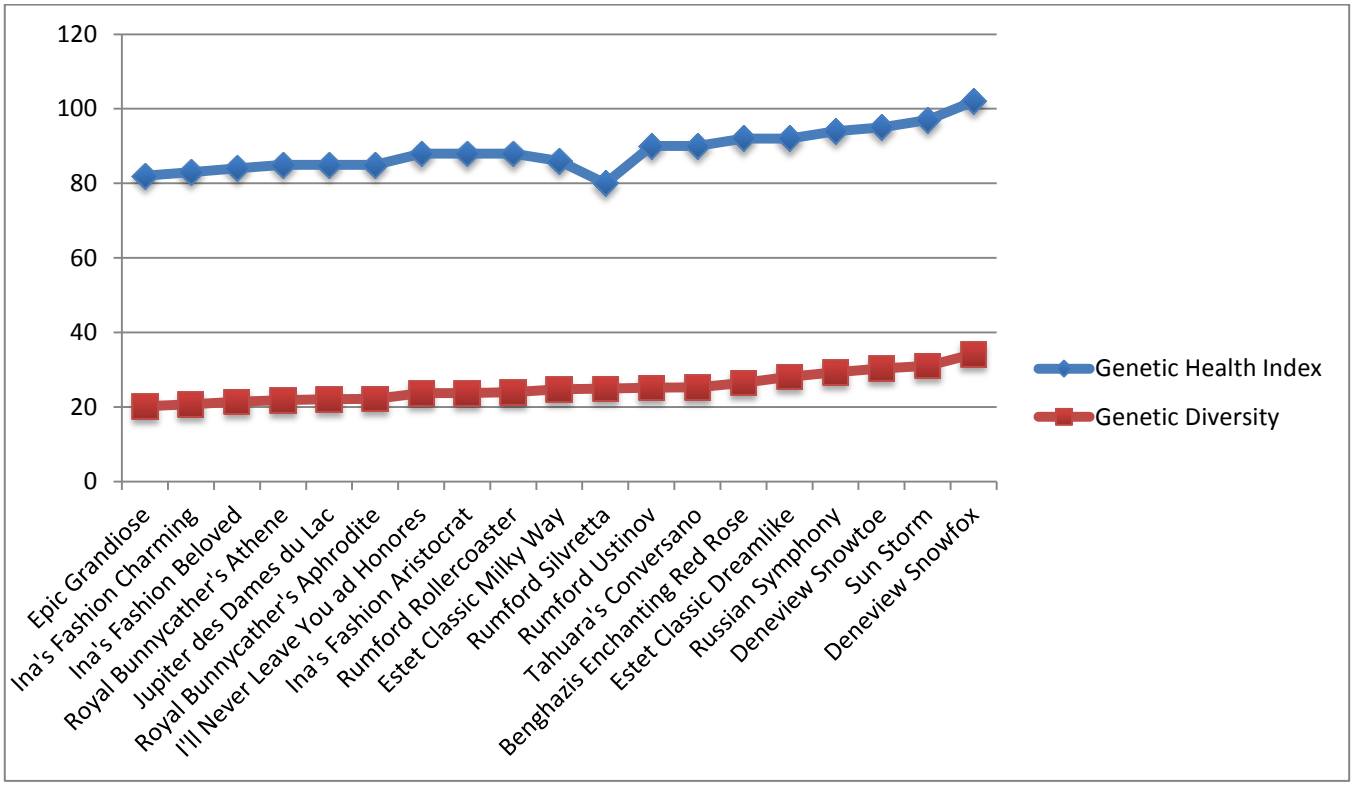
Behind Blue Eyes	30,80%
Beir Bua	29,60%
Believe in Dreams	31,00%

Winsome Yankees F-Wurf (COI 2,8 %, AL 31,9 %)

Faramir	32,20%
Fantasy	33,50%

Genetic Health Index[6]

As a summarizing test result, MyDogDNA gives a „Genetic Health Index“ for every tested dog.
This is composed from the results from the tests of genetic diseases and the level of “Genetic Diversity”. This index can change with time, as it is continuously compared to the scores of all tested dogs in the database.
“100” is the average value of all dogs in the database. If a dogs scores lower than 100, its level of “genetic health” is assumed to be lower than average, if he scores higher than 100, it is better than average.
As only one of the twelve dogs of our group had been positively tested for a genetic disease, we can say that the „Genetic Health Index“ of the other eleven dogs solely depends on their (invariably quite low!) results for „Genetic Diversity“.
One of the twelve is a carrier for Neuropathy, you should be able to spot it by yourselves:



The GHI is also used as the value issued for expected offspring for each combination. As almost a complete "Greyhound family" has been tested this year, we can check if the "forecast" is accurate:

Parents:	Mind Over Matter	GHI 91
	Katatjuta´s Anynamewilldo	GHI 96
"Forecast":	Breeder Tool	GHI 101
Offspring:	Behind Blue Eyes	GHI 99
	Beir Bua	GHI 97
	Believe in Dreams	GHI 100

As we can see, the actual values off the puppies differ slightly from the "forecast". Which is not very surprising, as every parent passes on only half of its genes to its' offspring – and in heterozygous alleles there is a 50/50 chance which one the offspring will inherit.
When we compare all Greyhounds with a public profile in the "Breeder Tool", we can make some quite enlightening observations. Interesting is e.g. that

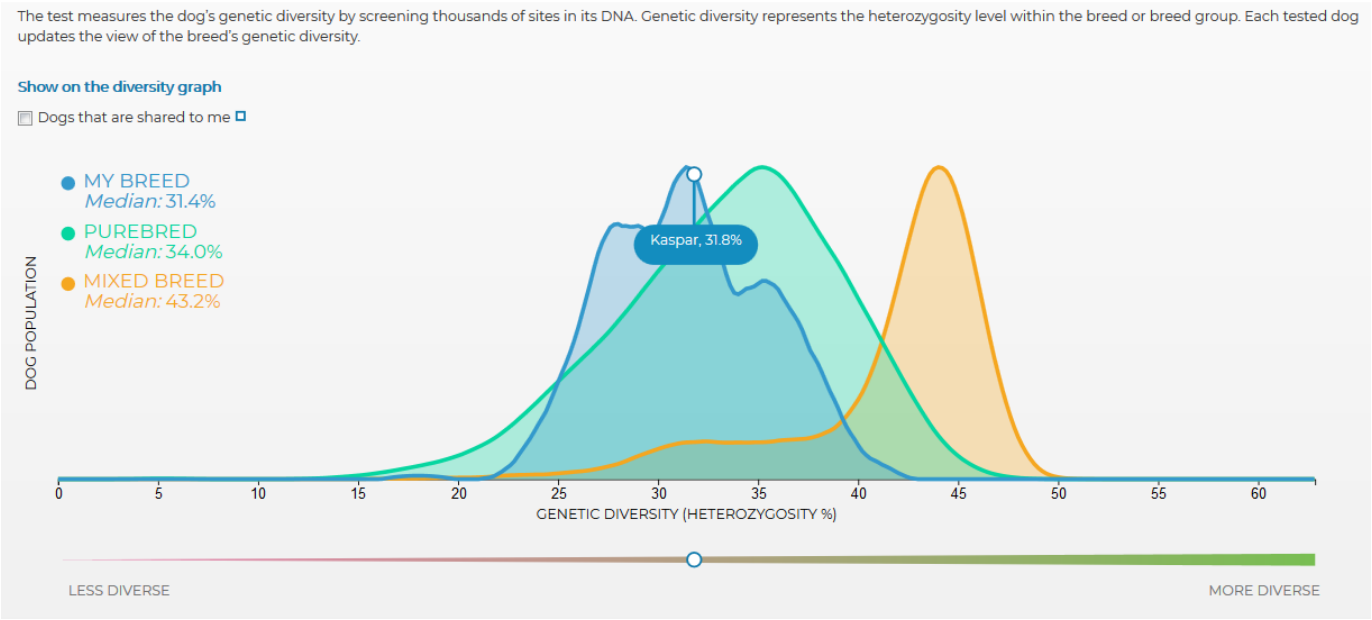
a) In crosses between racing dogs and show or coursing lines always a genetic diversity above average of the breed may be expected. Also matings between racing Greyhounds will result in a genetic diversity around the breed average (∅ GHI 100 = GD 31.0 %)*.
b) In crosses between coursing greyhounds and racing dogs – following the above-said – an above-average genetic diversity may be expected for the resulting offspring; in crosses with show-bred Greyhounds a below-average genetic diversity. Matings between two coursing dogs will likely result in a slightly below-average genetic diversity, too (∅ GHI 94 = GD 27.8 %)*.
c) Pure show-bred matings give reason to expect a below-average genetic diversity in any case (∅ GHI 91 = GD 25.7 %)**. It is amazing how a brief pedigree analysis may mislead in some cases. Examples:

- Tahuara's Conversano x Branwen Grian Gryjandi
  GHI: **86** (= GD 22.4 %), COI 7 generations: 14.64 %.
  In the first three generations two ancestors each are doubled. This is not surprising, as „Conversano" is „Branwen's" uncle.
- Ina's Fashion Beloved x Fortheringhay's Beg Your Pardon
  GHI: **86** (= GD 22.4 %), COI 7 generations: 5,9 %.
  There is no common ancestor in that pedigree up to the fourth generation! The grandparents of this hypothetic litter originate from Germany, the UK, Russia and Sweden – nevertheless the expected relatedness is that of an uncle-niece-mating.

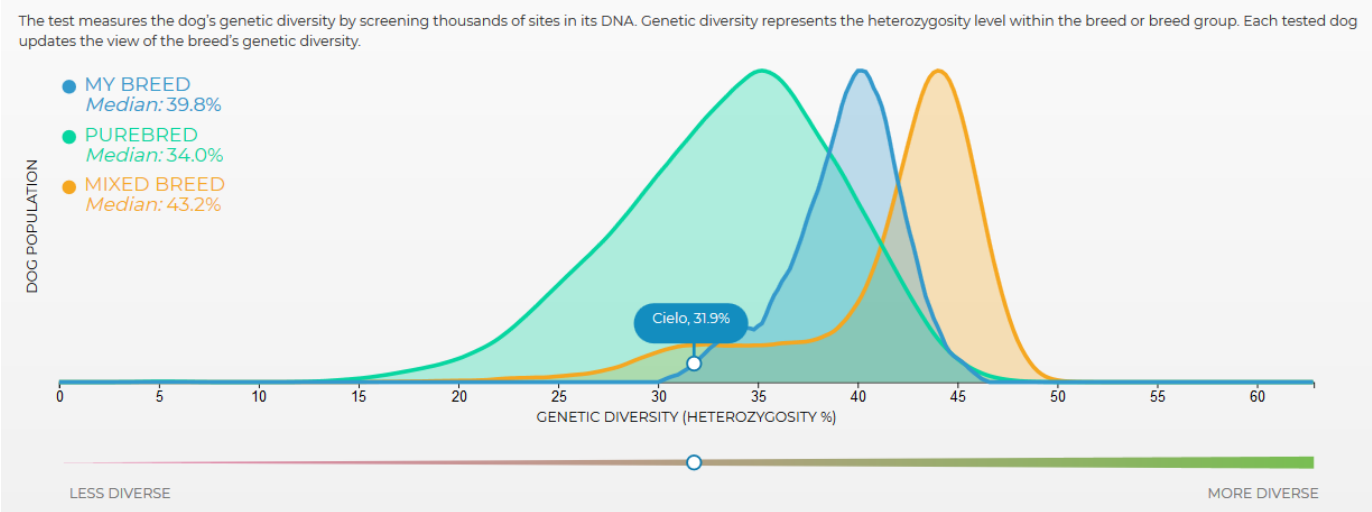
  Or:
- Winsome Yankees Faramir x Razldazl Lola
  GHI: **88** (= GD 24 %), COI 7 generations: 26,83 %. In the first four generations seven ancestors each are doubled. This is not surprising as well, as „Lola" is „Faramir's" dam.
- Rumford Ustinov x Vitruvians Beth
  GHI: **88** (= GD 24 %), COI 7 generations 3,33 %. No common ancestor in that pedigree up to the fifth generation! Here we also have dogs which are "unrelated" at first glance, but in the end as closely related as mother and son.

)* Adjusted for direct matings of relatives
)** Adjusted for direct matings of relatives and carriers

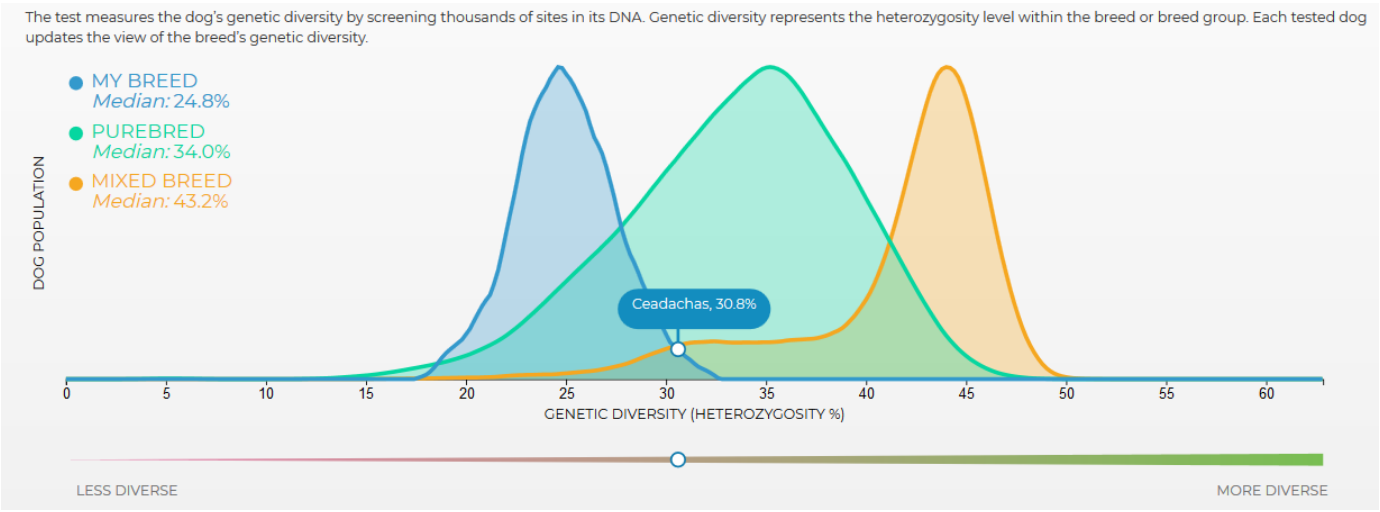
In summary it can be said, that the genetic diversity of Greyhounds on average is way below that of other purebred populations (median of 30,9 % compared to 34 % as the median of all tested purebred dogs). Here some other, closely related Sighthound breeds for comparison:



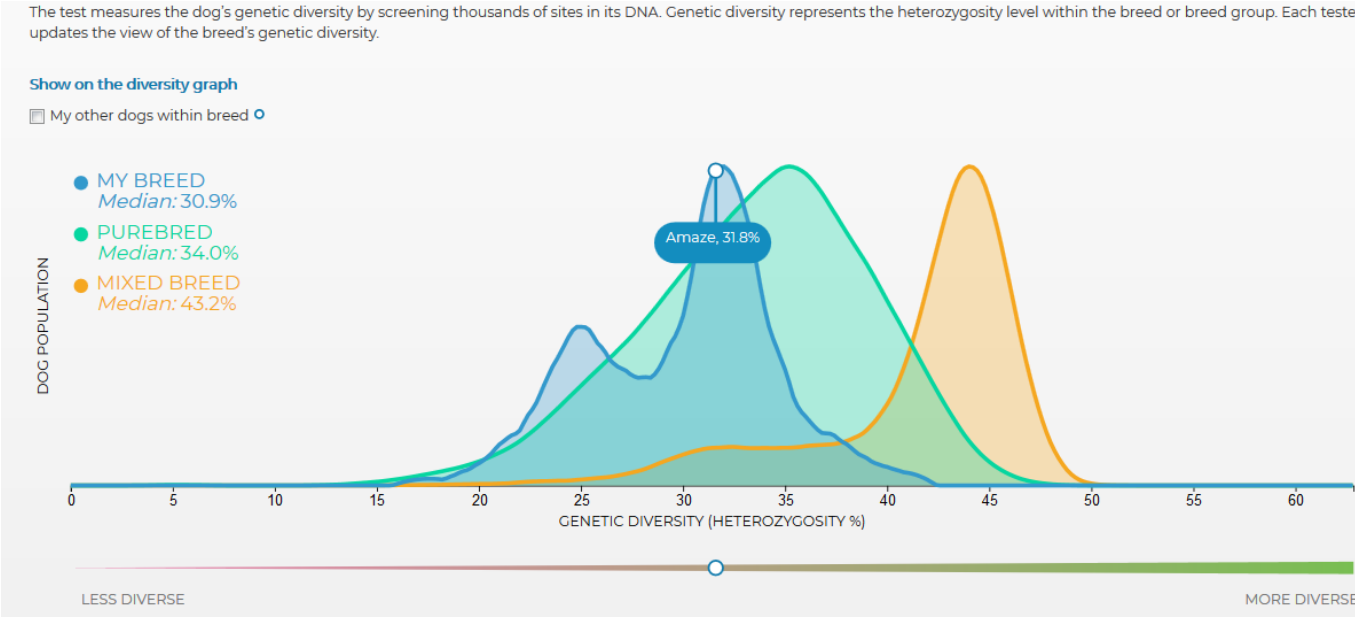
Whippets (blue line), median 31.4%, GD of the indicated dog: 31.8 %



Galgos Españoles (blue line), median 39.8 %, GD of the indicated dog: 31.9 %



Deerhounds (blue line), Median 24.8 %, GD of the indicated dog: 30.8 %



And again Greyhounds (blue line), median 30.9 %, GD of the indicated dog: 31.8 %

The tested dogs from **racing lines** still do quite well – the median of their "subpopulation" is around 32.2 %, which delivers an above-average GHI for the breed of 102.

More critical is the situation in coursing Greyhounds, of which only three specimens were tested. They group around a median GD of 28.1 %, which corresponds to a slightly below-average GHI median of 95.

The results of the Show-Greyhounds should give cause for concern:
Here we have a genetic diversity median of only 24.6 %, which corresponds to a GHI of 89. Not a single "Show Grey" has an above-average genetic diversity, the highest value in this subpopulation for GHI is therefore only 95.

But there is a way out, which can be seen in the "cross breeding products" (racing x coursing and show x racing). In those dogs the median for genetic diversity is 31 % and therefore exactly the breed average (GHI 100). In this group, the bitch out of a F2 line-cross (3/4 show line, ¼ racing line) scored highest for genetic diversity at 32.4 %.

So a first step has been made in order to investigate the aspect of „Genetic Diversity" in our Greyhounds and to maybe include it also into our breeding decisions. It is much to be hoped that more breeders and owners of stud dogs realize the value of those tools and make good use of them in the future.

Side note: Of course "Genetic Diversity" is not the only thing you should consider when striving to breed healthier dogs. The dog with the highest genetic diversity in this sample died (fully health tested!) at three years of age from a heart attack. Breeding healthy, long lived dogs is a very complex task, and genetic diversity is only one building block. Used skilfully, this test can contribute to increasing the genetic variability whilst maintaining type and soundness in our wonderful breed.

Footnotes:

1) „Deutsche Greyhounds bei MyDogDNA“: http://katrin-und-joachim.de/2017/06/20/deutsche-greyhounds-bei-mydogdna/
2) „Greyhound Breeding in Germany 2012 – 2016“: http://katrin-und-joachim.de/2017/10/13/greyhound-breeding-in-germany-2012-2016/
3) Calculated with the Tabular Method for seven generations. Source: https://greyhound.breedarchive.com
4) Calculated with formula $2^{(\text{Anzahl der Generationen} + 1)}$-2 for seven generations. Source: https://greyhound.breedarchive.com
5) „MyDogDNA®Technical Data Sheet”: http://www.mydogdna.com/sites/default/files/mdd-os-technical-sheet-2017.pdf
6) “Introducing MyDogDNA Pass and its reports - Part I: What is the Genetic Health Index (GHI) given by the MyDogDNA Pass?”: http://www.mydogdna.com/blog/introducing-mydogdna-pass-and-its-reports-part-i-what-genetic-health-index-ghi-given-mydogdna
7) “Update: Coefficient of Inbreeding vs. Genetic Diversity Level inGreyhound“: http://katrin-und-joachim.de/2018/06/12/update-inzucht-koeffizient-vs-genetische-diversitaet-beim-greyhound/