



## Genotypes in Ace Champion Racing Pigeons

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### Abstract:

Selection of racing pigeons for key races is currently more an art than science. With the development and commercial availability of genotyping, a more scientific approach may be feasible. Progress has been made in recent years, but it is unknown if this knowledge is sufficient to apply in selection and breeding. The relationship between variability in individual genes and race performance in racing pigeons has previously been suggested for *LDHA*, *DRD4* and *CRY1*. Such relationship has been hypothesized for other genes like *F-KER*, *MSTN*, *GSR* and *LRP8*. Recently a multivariate analysis showed a relationship between the combination of *DRD4 CCCT* and *F-KER TT* to be related to consistent race performance. This pattern was established in a closely bred family of racing pigeons and the general applicability was still to be proven. In a pilot experiment to seek confirmation in unrelated racing pigeons, a study was undertaken to compare the genotype profile of 7 Top National Ace Champion birds in the USA One Loft Races (OLRs) in 2023 with the profile of the general population of birds. Even with this small sample size, a clear trend was observed in favor of hens with at least one *Q* allele for *LRP8*, but the previously observed relation between *DRD4 CCCT* and *F-KER TT* to be related to consistent race performance was not confirmed. It is obvious that large prospective studies are needed involving unrelated birds, in addition to continued search to other genes and, in particular, genotype profiles to provide more clarity on the relationship between genetic makeup and race performance.

**Key Words:** pigeon racing; lactate dehydrogenase; dopamine receptor; cryptochrome; feather keratine; LDL receptor related protein 8; glutathione-disulfide reductase; myostatin

### Introduction

In recent years several studies have suggested suggestions for genotype linkage to race performance for one or more genes (Proskura *et al* 2015, Proskura *et al* 2017, Dybus *et al* 2018, 2021, Kolvenbag *et al* 2022). Initial reports associate single gene variability with race performance. More recently genotypes association has been reported (Kolvenbag *et al* 2022). For the genes explored in these studies there have been suggestions as possible related to race performance in racing pigeons and make biologically sense to impact the performance physiology.

Variability in *LDHA* may result in differences of lactate dehydrogenase functioning and hence energy metabolism during exercise (Dybus *et al* 2006, Proskura *et al* 2014, Proskura *et al* 2015, Proskura *et al* 2015a). *DRD4* codes for dopamine receptor 4, which function is associated with intelligence, personality traits influencing sport achievements and is

associated with variation in the level of exploratory/novelty-seeking behavior. A relationship to race performance was reported by Proskura *et al* (2015). The *F-KER* gene is coding for keratin is related to the quality of the feathers, which may influence flight. (Proskura *et al* 2017). A relation between variability in cryptochrome 1(*CRY1*) genotype and race performance has been suggested (Dybus *et al* 2021). *CRY1* is involved with magneto-reception (Du *et al* 2014) and therefore variability in genotypes could potentially have impact on special orientation. Other genes related to orientation include *LRP8* and *GSR* in which mutations were identified in racing pigeons (Shao *et al* 2020). *LRP8* and *GSR* may play a role in race performance. *LRP8* is a gene that encodes for the LDL receptor related protein 8 that is involved the spatial memory and learning ability. *GSR* (encoding glutathione-disulfide reductase) may be involved in magneto-reception and may be part of the biocompass pathway in the homing pigeon. The myostatin (*MSTN*) gene encodes a transforming growth factor that controls

the growth and development of muscle tissue. It has been hypothesized that variability in *MSTN* may be related to increases in muscle mass and superior racing performance (Dybus *et al* 2013, Małgorzata *et al* 2018).

While a favorable profile for race performance was reported previously (Kolvenbag *et al* 2022), this was with birds from a closely bred family. It is of interest to demonstrate or confirm such profile in unrelated racing pigeons. In 2023, the top 10 performing birds over 4 races in 8 of the largest one loft races were reported (Table 1); For example the number 1 bird in the USA won 4<sup>th</sup> place against 750 birds in the race over 150 mile, 17<sup>th</sup> against 695 birds (186 mile), 9<sup>th</sup> against 650 birds 238 miles and 5<sup>th</sup> against 518 birds (350 miles). Genetic profiles were obtained for 7 of the top 10 birds in the USA in 2023. This report presents the genetic profiles for 7 of the Top10 USA OLR birds against the general population background prevalence.

OVERALL RANK	PERCENTAGE	LOFT NAME	BIRD	COLOR	SEX	ONE LOFT RACE
1	1.332%	Da-Dong	AU 23 TENT 3050	BBWF	H	Orlando Classic Golden
2	2.889%	Royal Heir Loft	AU 23 AA 10303	BC	H	Crooked Challenge River
3	2.991%	Ignacio Family Loft	AU 23 HRPC 3512	BC	H	Orlando Classic Golden
4	3.221%	Los 4 Loft	AU 23 ARPU 5802	BC	C	Orlando Classic Golden
5	4.033%	99 Problems	AU 23 EMIL 36	BBWF	H	Hoosier Classic Million Dollar Race
6	4.538%	Nemelka Racing Pigeon Loft	AU 23 NRPL 3035	BB	H	Crooked Challenge River
7	4.626%	Yang Loft	AU 23 YANG 0136	BB	H	USA Pigeon Derby
8	4.840%	Linda Loft	IF 23 LIND 1004	BB	H	USA Pigeon Derby
9	5.180%	Denis Loft	AU 23 AA 6007	BB	H	USA Pigeon Derby
10	5.354%	003 loft	AU 23 ARPU 81205	BCWF	H	USA Pigeon Derby

Abbreviations: One Loft Race (OLR)

**Table 1:** Top 10 ace champion birds in the USA OLRs in 2023.

## Methods:

All 10 owners of the Top 10 Ace Champion birds in the USA OLRs in 2023 were invited to participate, 7 responded with donating feathers. Samples were obtained by the owner and shipped to the author. Feathers were sent for analysis at Feanix Biotechnologies, 39 Glendale Ave, Suite 102, Asheville, NC 28803, tel (530) 205-3588, email: info@feanixbio.com

General prevalence allele frequencies were provided by Feanix Biotechnologies from 100 random samples. Comparison of profiles of top 7 birds versus general prevalence was performed by

goodness of fit tests for each of the gene categories (Snedecor et al 1989). The general prevalence data was used as the control and assessed, whether or not the distribution of the genotypes from the 7 pigeons are marking the different from the general prevalence data. P value of the Chi-square goodness of fit test is provided.

## Results

The largest differences observed comparing the profiles of the 7 top race birds versus the expected profiles are in gender, *LDHA*, *LRP8* and *GSR*, while no or small differences were seen in the other genes (Table 2).

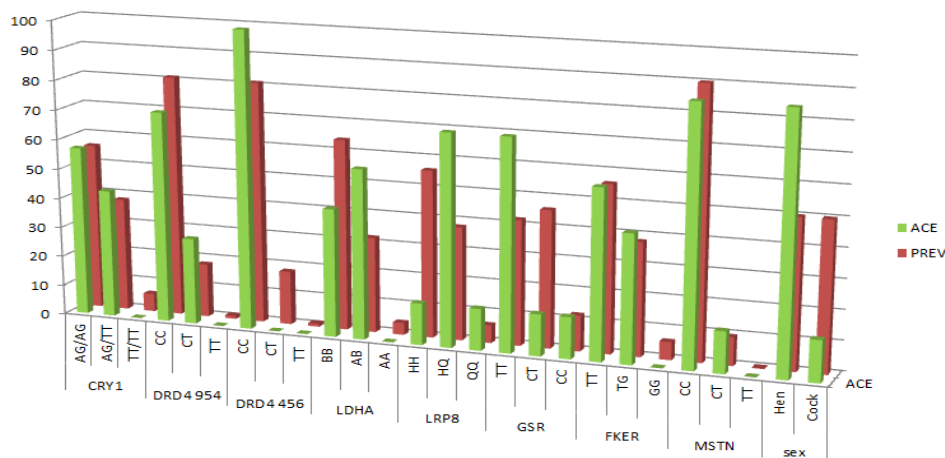
Gene	Genotype	ACE (n=7)	% of n	PREV (n=100)	Expected n	(O-E)^2/E	Chi-square	p-value
<i>CRY1</i>	<i>AG/AG</i>	4	57.1%	56%	3.92	0.002	0.465	0.793
	<i>AG/TT</i>	3	42.9%	38%	2.66	0.043		
	<i>TT/TT</i>	0	0.0%	6%	0.42	0.420		
<i>DRD4 954</i>	<i>CC</i>	5	71.4%	81%	5.67	0.079	0.584	0.747
	<i>CT</i>	2	28.6%	18%	1.26	0.435		
	<i>TT/TT</i>	0	0.0%	1%	0.07	0.070		
<i>DRD4 456</i>	<i>CC</i>	7	100.0%	81%	5.67	0.312	1.642	0.440
	<i>CT</i>	0	0.0%	18%	1.26	1.260		
	<i>TT</i>	0	0.0%	1%	0.07	0.070		
<i>LDHA</i>	<i>BB</i>	3	42.9%	64%	4.48	0.489	1.942	0.379
	<i>AB</i>	4	57.1%	32%	2.24	1.383		
	<i>AA</i>	0	0.0%	1%	0.07	0.070		
<i>LRP8</i>	<i>HH</i>	1	14.3%	58%	4.06	2.306	5.166	0.076
	<i>HQ</i>	5	71.4%	38%	2.66	2.058		
	<i>QQ</i>	1	14.3%	6%	0.42	0.801		
<i>GSR</i>	<i>TT</i>	5	71.4%	42%	2.94	1.443	3.004	0.223
	<i>CT</i>	1	14.3%	46%	3.22	1.531		
	<i>CC</i>	1	14.3%	12%	0.84	0.030		
<i>F-KER</i>	<i>TT</i>	4	57.1%	56%	3.92	0.002	0.465	0.793
	<i>TG</i>	3	42.9%	38%	2.66	0.043		
	<i>GG</i>	0	0.0%	6%	0.42	0.420		
<i>MSTN</i>	<i>CC</i>	6	85.7%	90%	6.3	0.014	0.233	0.890
	<i>CT</i>	1	14.3%	10%	0.665	0.169		
	<i>TT</i>	0	0.0%	0%	0.05	0.050		
SEX	Hen	6	85.7%	50%	3.5	1.786	3.571	0.059
	Cock	1	14.3%	50%	3.5	1.786		

Abbreviations: lactate dehydrogenase A (*LDHA*), dopamine receptor (*DRD*), myostatin (*MSTN*), feather keratin (*F-KER*), cryptochrome 1 (*CRY1*), LDL receptor related protein 8 (*LRP8*), encoding glutathione-disulfide reductase (*GSR*), Ace champion bird (ACE), general population prevalence (PREV)

**Table 2:** Genotype comparison of the 7 OLR ace champions versus expected prevalence.

No statistical significant differences were observed in the comparison of the genotypes of the 7 ace champions compared to the prevalence in the general population. Of interest are the trends towards a difference observed for gender and for *LRP8*. There was no suggestion for a difference in the other genes including *CRY1*,

*DRD4*, *LDHA*, *GSR*, *F-KER* and *MSTN*. There were 9 hens in the Top 10 (see Figure 1). Unfortunately from 3 no samples were received, hence the analysis and report is based on 7 birds. In the analysis of gender a 9:1 ratio would have been in favor of hens and statistically significant ( $p=0.001$ ).



Abbreviations: lactate dehydrogenase A (*LDHA*), dopamine receptor (*DRD*), myostatin (*MSTN*), feather keratin (*F-KER*), cryptochrome 1 (*CRY1*), LDL receptor related protein 8 (*LRP8*), encoding glutathione-disulfide reductase (*GSR*), Ace champion bird (ACE), general population prevalence (PREV)

**Figure 1:** Bar chart of genotype frequency of Ace Pigeon (ACE) population and general population (PREV)

## Discussion:

The hypothesis that race performance is determined by one or more genotypes still needs to be proven. Reports to date have created hypotheses (summarized by Kolvenbag et al 2022), but to date, no firm concluding evidence has been delivered. Partly because large prospective studies have not been performed and / or the actual genes causatively involved in race performance have not yet been identified.

Reports on individual genes have made suggestion about a gene to be associated with race performance, most often limited to a certain distance eg *LDHA* and *CRY1* on the short races (Proskura et al 2014, Dybus et al 2021), or for *F-KER* in long distance races

(Proskura et al 2017). Our previous study in a closely related family of racing pigeons generated a hypothesis for birds with the genotypes *DRD4 CCCT* and *F-KER TT* would relate to consistent race results (Kolvenbag et al 2022). This was subsequently observed in an individual bird from the same family with consistent race performance two years later (Kolvenbag 2024). However, the current study of the unrelated 7 top USA OLR birds, did not confirm this; with no observed difference in prevalence for variability in the *DRD4* and *F-KER* genotypes compared to the distribution in the general population. Thus this hypothesis is still to be confirmed or rejected in a large prospective study.

We recognize the limitations of our current study having a small sample size of  $n=7$ . However, these were 7 birds in the top 10 Ace Champion birds in the 2023 OLRs in the USA. A distinction from

the overall population, when existing, could be expected. It is striking that 6 of the 7 birds (or 9 out of 10) had the female gender. This contradicts our previous study in a close family of birds in which there was no difference in gender (Kolvenbag G and Scott M (2022)). This indicates that one has to be careful studying performance in a closely related family of birds as the results may not be applicable to the wider general population. The result of our study rejects the working hypothesis that *LRP8 HH* is related to better race performance than *LRP8 QQ*; it is surprising to see that all 6 hens had at least one *Q* allele for the *LRP8* gene, and the only male bird had *LRP8 HH*. It is unknown if there is a gender relationship with *LRP8* genotypes.

Another unknown is how close the reference allele frequencies used in this comparison are the real life numbers. Reference frequencies were provided by Feanix Biotechnologies from a random 100 birds from the USA sample size based on feathers submitted to their commercial laboratory for analysis. This could include a selection bias as one could expect that only feathers from good performing birds are submitted for analysis. Either way, the frequencies provided by Feanix Biotechnologies were largely consistent with the frequencies previously reported in our study (Kolvenbag et al 2022). Nevertheless, larger sample sizes need to be analyzed and reported to be able to reference the normal distribution of genotypes in racing pigeons.

The results in this report are not completely in line with the previous reported data and hypothesis on individual genes and genotype profiles related to race performance. This could be due to differences in pigeon population (eg related or not), the sample

size (most studies have a small sample size), and or results reported to-date are random findings as the true causative genes related to performance may still need to be identified.

In conclusion, this report showed that in the population of racing pigeons studied, there was a suggestion there may be a difference in profiles for USA OLR Ace Champion birds versus the general population; i.e. hens with at least one *Q* allele for the *LPR8* gene was typical of the Ace Champions. Given this observation and reports made to-date, the call should be made for large prospective studies involving birds that are not family related. In parallel, research should continue to identify other genes or gene profiles potentially related to race performance. In the meantime, selection of racing pigeons remains an art.

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**Ethics Statement:** Study was conducted by an independent scientist without institutional relationship. No human subjects were involved in this study. Ethics review was not available. Study was conducted following high standard and generally accepted practice to breed and race racing pigeons.

**Consent to participate:** N/A: no human subjects were involved in this study.

**Data availability:** N/A: All data are incorporated into the article.

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