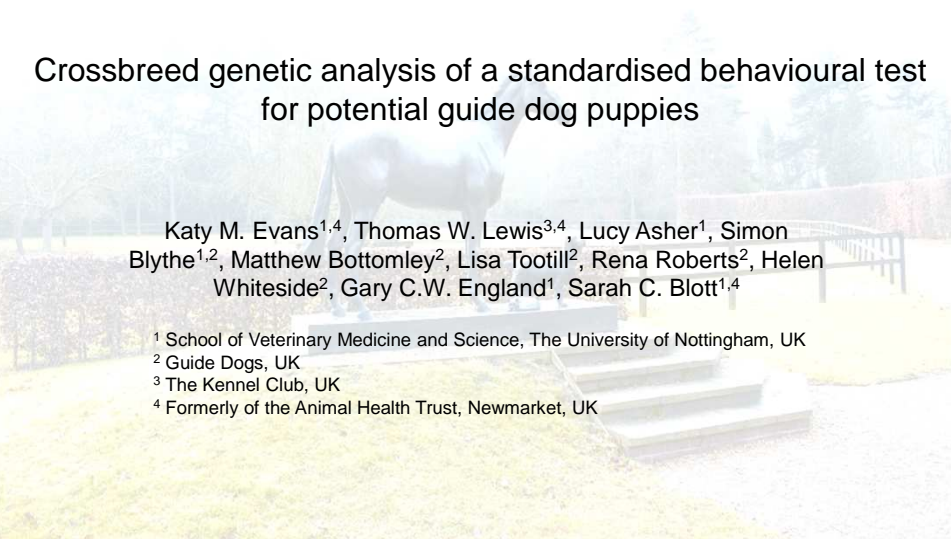


## Crossbreed genetic analysis of a standardised behavioural test for potential guide dog puppies

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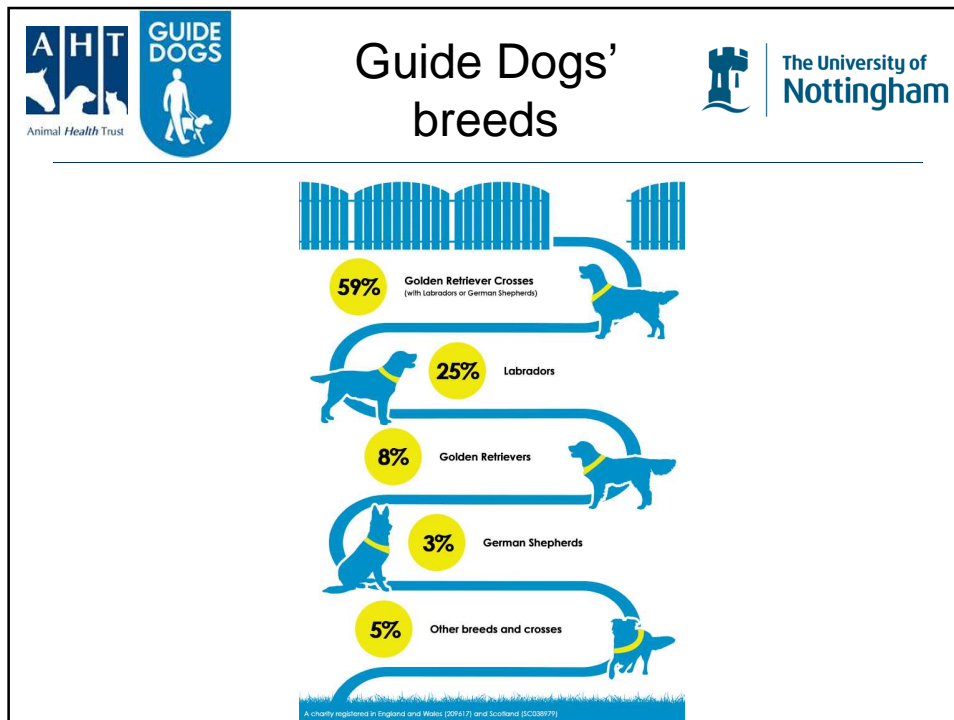


## Introduction



- Guide Dogs are the largest breeder and trainer of working dogs in the world.
- Guide Dogs are currently responsible for nearly 8,000 dogs including breeding stock and retired animals.
- More than 4,700 guide dog owners in the UK.








## Breeding



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- The organisation breeds the majority of its own dogs.
- Around 80 stud dogs and 275 brood bitches.
- New, purpose-built National Breeding Centre (NBC) opened in 2011 giving capacity to breed 1500 puppies a year.





## National Breeding Centre

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## Success rate

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- 70% of puppies bred by Guide Dogs successfully become working guide dogs or breeding stock.
- Hoping to increase this proportion further using quantitative genetic techniques.





## Early puppy management



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- Most brood bitches whelp in the homes of their volunteer Brood Bitch Holders.
- A small number will whelp in the National Breeding Centre.
- All puppies return to the National Breeding Centre at 6 weeks of age.
- Puppies then go to volunteer Puppy Walkers' homes at 7 weeks of age.



## Entering NBC at 6 weeks



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## Settled in

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## Puppies at NBC



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- Veterinary checks and vaccinations.
- Intensive socialisation programme.
- Puppy Profiling Assessment (PPA).






## Puppy Profiling Assessment (PPA)





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- A puppy test developed by Guide Dogs.
- Used to assess the behaviour of puppies prior to placement with Puppy Walkers.
- Developed to be feasible and standardised.
- Criterion validity has been assessed
- Came into routine use in April 2012.




## Puppy Profiling Assessment (PPA)



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**Research**

**A standardized behavior test for potential guide dog puppies: Methods and association with subsequent success in guide dog training**

Lucy Asher<sup>a,\*</sup>, Simon Blythe<sup>a,b</sup>, Rena Roberts<sup>b</sup>, Lisa Toothill<sup>b</sup>, Peter J. Craigon<sup>a,b</sup>, Katy M. Evans<sup>c</sup>, Martin J. Green<sup>a</sup>, Gary C.W. England<sup>a</sup>

<sup>a</sup>School of Veterinary Medicine and Science, University of Nottingham, Sutton Bonington Campus, Loughborough, Leicestershire, UK  
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## PPA description 1



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- PPA consists of 11 components, each scored on a 7-point scale.
- Components measure responsiveness, willingness and confidence.





## PPA description 2




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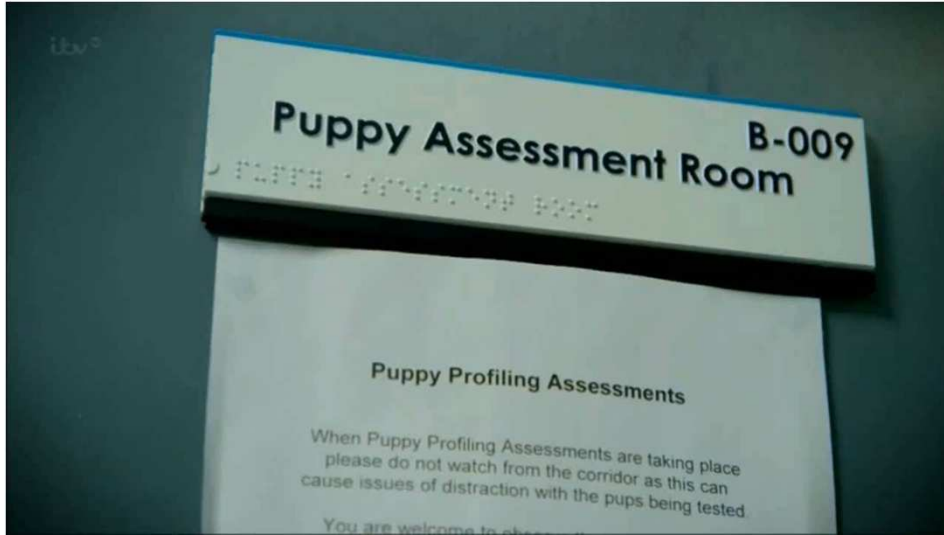
Component	Description
1	Following
2a	Retrieve – response to stimulus
2b	Retrieve – response to assessor
3	Restraint
4	Noise
5a	Stroking – response to stimulus
5b	Stroking – response to assessor
6a	Squirrel – response to stimulus
6b	Squirrel – response to assessor
7	Tunnel
8	Ramp





PPA video


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Tunnel

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## Ramp


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## Description of dataset 1

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- Two years of data from April 2012 to April 2014 used in analyses.
- For this analysis only Labrador Retriever (Lab), Golden Retriever (G Ret) and their crosses bred by Guide Dogs were included.





## Description of dataset 2



- Resultant dataset consisted of PPA results for 2127 puppies from 298 litters.
- Average litter size was 7.1 pups.
- 62 unique sires and 229 unique dams.
- 47% of the puppies were female and 53% were male.



## Description of dataset 3



Breed	Number of pups
Golden Retriever X Labrador	950
Labrador Retriever	704
Lab x (G Ret x Lab)	315
Golden Retriever	119
G Ret x (G Ret x Lab)	39
Total	2127



## Crossbreed genetic analysis



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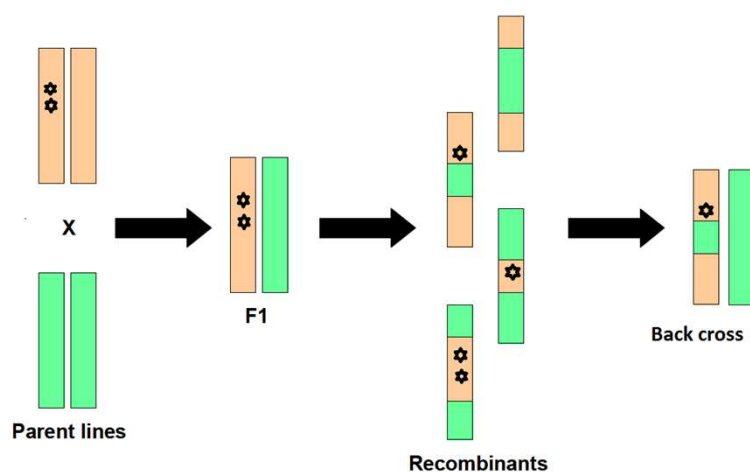
- Simple crossbreed models used.
- Method described by Van der Werf and de Boer (1989).
- Expected heterosis and recombination loss for each individual was calculated from the proportion of Labrador Retriever and Golden Retriever of their sire and dam.



## Heterosis and recombination loss



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## Crossbreed genetic analysis 2



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- Expected heterosis value is the probability that the two alleles at any one locus originate from different breeds.
- Expected recombination loss value is the probability that any two loci inherited from the same parent originate from different breeds.



## Crossbreed genetic analysis 2



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Breed	Heterosis	Recombination loss	Labrador fraction
Golden Retriever	0	0	0
Labrador Retriever	0	0	1
GR x LR	0.5	0	0.5
GR x (GR x LR)	0.25	0.125	0.25
LR x (GR x LR)	0.25	0.125	0.75
(GR x LR) x (GR x LR)	0.25	0.25	0.5



## Description of models



- Heritabilities and other genetic parameters estimated using univariate linear mixed models in ASReml.
- Model used included sex and year of birth as fixed effects and age at test as a covariate.
- Breed fraction and calculated heterosis and recombination loss were included as covariates.
- Litter and test batch were included as random effects.



## Description of models 2



- Genetic correlations between PPA components estimated by running multiple bivariate models between pairs of components.
- 55 models.





## Heritability estimates



Component	$h^2$	p value
1 - Following	0.24 (0.09)	$p < 0.01$
2a - Retrieve (stimulus)	0.21 (0.07)	$p < 0.01$
<b>2b - Retrieve (assessor)</b>	<b>0.21 (0.07)</b>	<b><math>p &lt; 0.01</math></b>
3 - Restraint	0.14 (0.08)	NS
4 - Noise	0.01 (0.03)	NS
<b>5a - Stroking (stimulus)</b>	<b>0.24 (0.09)</b>	<b><math>p &lt; 0.01</math></b>
<b>5b - Stroking (assessor)</b>	<b>0.19 (0.07)</b>	<b><math>p &lt; 0.01</math></b>
6a - Squirrel (stimulus)	0.13 (0.07)	$p < 0.05$
<b>6b - Squirrel (assessor)</b>	<b>0.09 (0.05)</b>	<b><math>p &lt; 0.01</math></b>
7 - Tunnel	0.16 (0.07)	$p < 0.01$
<b>8 - Ramp</b>	<b>0.13 (0.07)</b>	<b><math>p &lt; 0.05</math></b>



## Litter effects



- Litter effect estimates were all small but detectably larger than zero except that for component 4 (noise).
- Estimates ranged from 0.07 (s.e. 0.03) for component 2a (retrieve – response to assessor) to 0.14 (s.e. 0.04) for components 3 (restraint) and 5a (stroking – response to stimulus).







## Batch effects



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- Batch effect estimates were all small and not detectably larger than zero except that for component 4 (noise).
- The estimate for component 4 was 0.11 (s.e. 0.03).



## Crossbreeding effect estimates



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Trait	Heterosis	Recombination loss	Labrador fraction
1 - Following	0.01 (0.17)	0.13 (0.79)	-0.25 (0.34)
2a - Retrieve (stimulus)	0.08 (0.17)	<b>-1.62 (0.78)</b>	-0.15 (0.34)
2b - Retrieve (assessor)	0.01 (0.18)	-1.27 (0.81)	-0.46 (0.36)
3 - Restraint	0.01 (0.17)	-0.26 (0.73)	<b>0.69 (0.27)</b>
4 - Noise	-0.07 (0.10)	0.47 (0.41)	0.11 (0.10)
5a - Stroking (stimulus)	-0.12 (0.18)	-0.04 (0.83)	0.54 (0.35)
5b - Stroking (assessor)	0.05 (0.19)	-0.65 (0.84)	-0.58 (0.36)
6a - Squirrel (stimulus)	<b>-0.35 (0.16)</b>	-0.62 (0.72)	-0.29 (0.29)
6b - Squirrel (assessor)	-0.14 (0.16)	-1.26 (0.67)	-0.36 (0.24)
7 - Tunnel	-0.11 (0.16)	<b>-1.56 (0.72)</b>	-0.06 (0.28)
8 - Ramp	<b>-0.31 (0.14)</b>	0.34 (0.63)	0.08 (0.24)



## Other effects



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- None of the non-crossbreeding fixed effect estimates and regression coefficients were detectably larger than zero except for PPA component 2a (retrieve – response to assessor).
- For component 2a, age at test and sex were both significant.
- Estimates of 0.04 (s.e. 0.02) for age at test and 0.14 (s.e. 0.05) for being female.



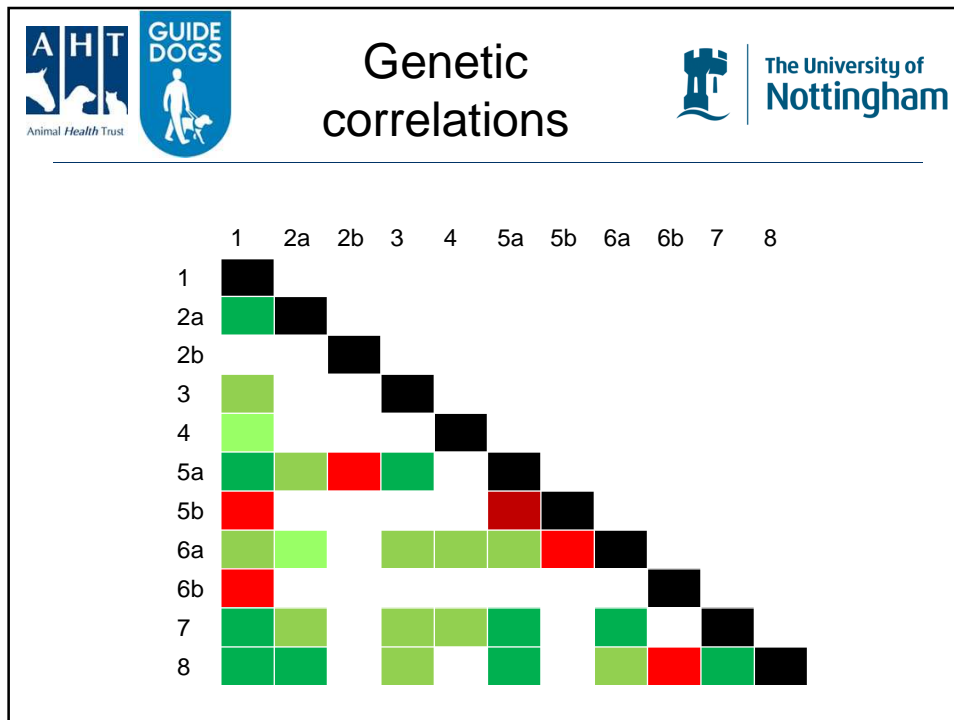
## Genetic correlations





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- Half of the models failed to converge or produced estimates which were not detectably larger than zero.
- The majority of genetic correlation estimates which were detectably larger than zero were moderate to large and positive.
- Antagonistic genetic correlations were identified between six pairs of PPA components.






## Conclusions





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- Nine of the 11 PPA components showed low to moderate heritabilities.
- EBVs for these components might be valuable for future selection decisions.
- Little evidence of beneficial or detrimental effects of crossbreeding on scores for PPA components.




## Next steps



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- Re-run bivariate models with additional data.
- Principal components analysis, then heritability estimation and EBVs for these components?
- Selection index for PPA?





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## Acknowledgements

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