

The Genetic Basis of White Tigers

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History of coat color genetics

- Coat color is the most obvious phenotypic trait in mammal, and has served as an ideal model to understand how genotype determines phenotype.
- Coat color genetics has been studied for over 100 years, mainly in lab mouse, and identified more than 150 coat color genes



New opportunity for coat color genetics



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New opportunity for coat color genetics





Objective of this study



Sample collection

- Blood or tissue samples from 20 unrelated white tigers and 110 orange tigers were collected from different resources.
- Blood samples from a full tiger pedigree (7 white, 9 orange) were provided by Chimelong Safari Park, Guangzhou.



Candidate sequencing approach



Candidate sequencing results

Candidate gene	Sequencing region	NO of SNPs identified	Phenotype associated SNPs
MC1R	CDS	1	none
ASIP	CDS	1	none
TYR	CDS, UTRs	2	none
TYRP1	CDS	1	none
SLC7A11	CDS	2	none
SLC18A2	CDS	0	none

• 5 white tigers and 5 orange tigers

Alternative Strategy



Result of family-based GWAS



172,554 SNPs were used for GWAS analysis

Homology of Scaffold75 and 1458



Critical region for white trait



Causal mutation screening

Gene	CDS SNP NO	AA change	Gene description
DNAJC21	2	N/A	DnaJ (Hsp40) homolog, subfamily C, member 21
SLC45A2	1	A477V	solute carrier family 45, member 2
ADAMTS12	4	D1125A	ADAM metallopeptidase with thrombospondin type 1 motif, 12
TARS	2	N/A	threonyl-tRNA synthetase
YWHAE	1	N/A	14-3-3 protein epsilon
PTIG0011772	1	N/A	PDZD2 PDZ domain containing 2
RNASEN	3	N/A	ribonuclease 3

SLC45A2 is a known pigmentation gene, whose mutations cause hypopigmentation in human, lab mouse, horse, chicken and fish.

ADAMTS12 is a gene responsible for the inflammatory response.

Mutation Validation

Table 1. Correlation between Tiger Coat Color Phenotypes and *SLC45A2* Genotypes

		Phenotype	
Gene	Genotype	White	Wild-Type
SLC45A2	A477V/A477V	20 (7)	0
	A477V/+	0	1 (9)
	+/+	0	109
ADAMTS12	D1125A/D1125A	20 (7)	19
	D1125A/+	0	30 (9)
	+/+	0	60
	missing data	0	1
Total		20 (7)	110 (9)

Prediction of A477V impact



Newton et al (2001) and Fukamachi et al (2001) predicted SLC45A2 is a 12 transmembrane transporter protein.

The MAPP score of A477V is 35.49, suggesting significant impact to SLC45A2

SLC45A2 structure prediction



How does SLC45A2 determine pigmentation ?

- SLC45A2 locates on the membrane of melanosome in melanocyte.
- SLC45A2 shares similar structure and the signature domain of sucrose/proton co-transporter in plants.
- SCRT, the *Drosophila melanogaster* homology of SLC45A2, is proved to be a sucrose/proton co-transporter.
- The activity of tyrosinase (TYR) is regulated by the melanosomal pH.

How does SLC45A2 determine pigmentation ?

- The activity of SLC45A2 in *underwhite* mouse was only about 20% of that found in wild type mouse.
- Premature melanosome was secreted in *underwhite* mouse.
- Crenated melanosome was found in the melanocyte of underwhite mouse.

How does SLC45A2 determine pigmentation ?

We proposed: SLC45A2 is a sucrose/proton cotransporter and mediate melanin synthesis by regulating melanosomal pH and/or osmotic balancing.









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Xu X., Dong G. X., Hu X. S., Miao L., Zhang X. L., Zhang D. L., Yang H. D., Zhang T. Y., Zou Z. T., Zhang T. T., Zhuang Y., Bhak J., Cho Y. S., Dai W. T., Jiang T. J., Xie C., Li R., Luo S. J. (2013) The genetic basis of white tigers. Curr. Biol. 23: 1031-1035.

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