



Association between Single Nucleotide Polymorphisms of Fatty Acid Synthase and Fat Deposition in the Liver of the Overfed Goose

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- Supplementary Data -

Supplementary Table S1. Relationship between different genotype combinations and the performance of geese

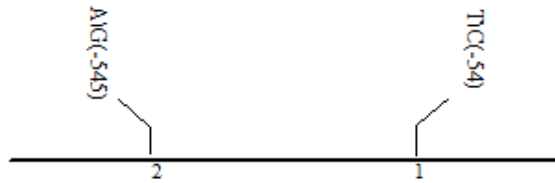
Genotype	Sample number	Fatty liver (g)	Abdominal fat (g)	Intestinal fat (g)	Genotype	Sample number	Fatty liver (g)	Abdominal fat (g)	Intestinal fat (g)
AACCEE	8	503.81±28.33 ^a	415.10±32.35 ^a	321.25±17.37 ^a	AADDEE	1	680.00±0.00 ^a	370.45±0.00 ^a	260.11±0.00 ^a
AACCFE	3	531.72±57.75 ^a	450.20±45.09 ^a	450.20±30.55 ^a	AADDEF	1	890.00±0.00 ^a	500.50±0.00 ^a	330.13±0.00 ^a
AACCEF	3	813.30±46.26 ^a	416.67±47.03 ^a	323.33±38.44 ^a	AADDFE	1	870.00±0.00 ^a	420.50±0.00 ^a	410.50±0.00 ^a
AACDFE	2	600.00±70.82 ^a	445.25±55.00 ^a	340.11±20.00 ^a	ABDDEE	5	880.00±71.61 ^a	450.50±24.49 ^a	340.10±37.20 ^a
AACDEF	5	694.00±55.96 ^a	352.23±46.41 ^a	356.23±27.13 ^a	ABDDEF	1	1,140.00±0.00 ^a	340.35±0.00 ^a	312.10±0.00 ^a
AACDEE	11	617.71±43.76 ^a	449.09±18.80 ^a	350.31±13.35 ^a	ABDDFE	3	930.02±57.81 ^a	470.24±11.55 ^a	420.12±45.09 ^a
ABCCEF	6	733.31±81.70 ^a	418.33±22.12 ^a	366.67±20.60 ^a	ABCDFE	20	854.51±40.28 ^a	400.30±22.04 ^a	370.33±16.92 ^a
ABCCFE	4	748.85±100.07 ^a	435.25±41.33 ^a	380.20±39.37 ^a	ABCDFE	9	794.42±200.14 ^a	370.22±73.31 ^a	320.20±116.73 ^a

Different letters indicate counterparts in the same row having significant difference between the average value (Mean± standard error) ($p < 0.05$).

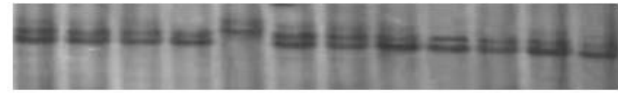
Supplementary Table S2. Hardy-Weinberg test of the genotypes

	P ₁			P ₂			P ₈		
	EE	FF	EF	CC	DD	CD	AA	AB	BB
Observed number	47	47	30	44	68	14	39	85	0
Observed frequency	0.380	0.380	0.242	0.355	0.549	0.113	0.315	0.385	0
Theoretic frequency	0.324	0.490	0.186	0.400	0.466	0.137	0.432	0.451	0.118
Theoretic number	40.20	60.67	23.06	49.60	57.78	16.99	53.57	55.89	14.59
χ^2	6.36			1.96			19.12		

$df \geq 1$, $P_{0.01} = 6.63$, $P_{0.05} = 3.84$. P₁ site was imbalanced, and P₂ site was balanced.

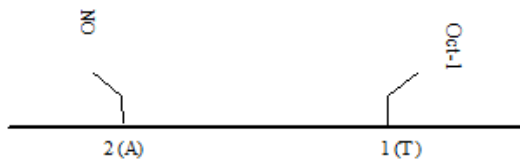


Supplementary Figure S1. Position of the SNPs in the *FAS* gene 5' region. The number in brackets represents the loci of base mutation, and the number in figure shows the relative position of polymorphic loci in 5' region. SNPs, single nucleotide polymorphisms; *FAS*, fatty acid synthase.

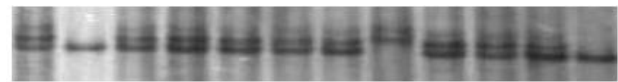


EF EF EF FF EE EF EF EF FF FF EF EF

Supplementary Figure S4. SSCP band patterns of PCR product amplified by P1. SSCP, single-strand conformation polymorphism; PCR, polymerase chain reaction.



Supplementary Figure S2. Predicted transcription factor binding in the 5' region SNPs before mutation. The number in brackets represents the loci of base mutation, and the number in figure shows the relative position of polymorphic loci in 5' region. SNPs, single nucleotide polymorphisms.



CD CC CD CD CD CD CD DD CD CD CD CC

Supplementary Figure S5. SSCP band patterns of PCR product amplified by P2. SSCP, single-strand conformation polymorphism; PCR, polymerase chain reaction.



Supplementary Figure S3. Predicted transcription factor binding in the 5' region SNPs after mutation. The number in brackets represents the loci of base mutation, and the number in figure shows the relative position of polymorphic loci in 5' region. SNPs, single nucleotide polymorphisms.



AB AB AB AB AA AB AB AA AB AB AB AB

Supplementary Figure S6. SSCP band patterns of PCR product amplified by P8. SSCP, single-strand conformation polymorphism; PCR, polymerase chain reaction.