

The genetics of resilience and its relationships with egg production traits and antibody traits in chickens

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Additional file 1 Tables S1 to S16

Table S1. Estimates of genetic (below the diagonal) and phenotypic (above the diagonal, italic) correlations with standard errors (in parentheses) between the resilience indicators ln(variance), skewness, and autocorrelation based on average batch production for the same life periods, but with different intervals for White.

trait	period	interval	<i>phenotypic correlation</i>		
			1 week	2 weeks	3 weeks
genetic correlations	ln(variance)	1 week	-	^a	<i>0.93 (0.001)</i>
		25-83 2 weeks	^a	-	^a
		3 weeks	0.97 (0.01)	^a	-
		1 week	-	<i>0.93 (0.001)</i>	<i>0.83 (0.002)</i>
		83-end 2 weeks	0.99 (0.003)	-	<i>0.86 (0.002)</i>
		3 weeks	0.98 (0.01)	0.999 (0.004)	-
	skewness	1 week	-	<i>0.82 (0.002)</i>	<i>0.70 (0.003)</i>
		25-83 2 weeks	0.89 (0.02)	-	<i>0.82 (0.002)</i>
		3 weeks	0.87 (0.03)	0.97 (0.01)	-
		1 week	-	^b	^b
		83-end 2 weeks	^b	-	^b
		3 weeks	^b	^b	-
	autocorrelation	1 week	-	<i>0.72 (0.003)</i>	<i>0.56 (0.004)</i>
		25-83 2 weeks	0.90 (0.03)	-	^a
		3 weeks	0.86 (0.05)	^a	-
		1 week	-	^b	^b
		83-end 2 weeks	^b	-	^b
		3 weeks	^b	^b	-

^a Analysis did not converge.

^b Not tested, because one or both traits were not heritable (i.e. not significantly different from zero).

Table S2. Estimates of genetic (below the diagonal) and phenotypic (above the diagonal, italic) correlations with standard errors (in parentheses) between the resilience indicators ln(variance), skewness, and autocorrelation based on average batch production for the same life periods, but with different intervals for Brown.

trait	period	interval	<i>phenotypic correlation</i>		
			1 week	2 weeks	3 weeks
genetic correlations	ln(variance)	1 week	-	^a	<i>0.95 (0.001)</i>
		25-83 2 weeks	^a	-	^a
		3 weeks	0.98 (0.01)	^a	-
		1 week	-	<i>0.93 (0.001)</i>	<i>0.86 (0.004)</i>
		83-end 2 weeks	0.99 (0.01)	-	^a
		3 weeks	0.95 (0.07)	^a	-
	skewness	1 week	-	<i>0.87 (0.001)</i>	<i>0.76 (0.002)</i>
		25-83 2 weeks	0.94 (0.03)	-	^a
		3 weeks	0.90 (0.05)	^a	-
		1 week	-	^b	^b
		83-end 2 weeks	^b	-	^b
		3 weeks	^b	^b	-
autocorrelation	25-83	1 week	-	<i>0.76 (0.002)</i>	<i>0.57 (0.004)</i>
		2 weeks	0.84 (0.04)	-	<i>0.79 (0.002)</i>
		3 weeks	0.84 (0.04)	0.68 (0.06)	-
	83-end	1 week	-	^b	^b
		2 weeks	^b	-	^b
		3 weeks	^b	^b	-

^a Analysis did not converge.

^b Not tested, because one or both traits were not heritable (i.e. not significantly different from zero).

Table S3. Estimates of genetic (below the diagonal) and phenotypic (above the diagonal, italic) correlations with standard errors (in parentheses) between the resilience indicators ln(variance), skewness, and autocorrelation based on average batch production for 1-week-intervals, but for different life periods for White.

	trait	period	<i>phenotypic correlations</i>	
			25-83	83-end
genetic correlations	ln(variance)	25-83	-	<i>0.10 (0.01)</i>
		83-end	0.80 (0.04)	-
	skewness	25-83	-	^a
		83-end	^a	-
	autocorrelation	25-83	-	<i>0.17 (0.01)</i>
		83-end	0.73 (0.07)	-

^a Not tested, because one or both traits were not heritable (i.e. not significantly different from zero).

Table S4. Estimates of genetic (below the diagonal) and phenotypic (above the diagonal, italic) correlations with standard errors (in parentheses) between the resilience indicators ln(variance), skewness, and autocorrelation based on average batch production for 1-week-intervals, but for different life periods for Brown.

	trait	period	<i>phenotypic correlations</i>	
			25-83	83-end
genetic correlations	ln(variance)	25-83	-	<i>-0.04 (0.01)</i>
		83-end	0.76 (0.07)	-
	skewness	25-83	-	<i>-0.03 (0.01)</i>
		83-end	-0.46 (0.13)	-
	autocorrelation	25-83	-	<i>0.19 (0.01)</i>
		83-end	0.80 (0.08)	-

Table S5. Estimates of genetic (below the diagonal) and phenotypic (above the diagonal, italic) correlations with standard errors (in parentheses) between the resilience indicators ln(variance), skewness, and autocorrelation based on average batch production for the same life periods with 1-week-intervals for White.

			<i>phenotypic correlation</i>		
	trait	period	ln(variance)	skewness	autocorrelation
genetic correlation	ln(variance)	25-end	-	-0.32 (0.01)	0.56 (0.01)
		25-83	-	-0.33 (0.01)	0.42 (0.01)
		83-end	-	a	0.17 (0.01)
	skewness	25-end	-0.71 (0.05)	-	0.06 (0.01)
		25-83	-0.46 (0.07)	-	0.03 (0.01)
		83-end	a	-	a
	autocorrelation	25-end	0.32 (0.06)	0.07 (0.08)	-
		25-83	-0.01 (0.08)	-0.21 (0.09)	-
		83-end	0.18 (0.08)	a	-

^a Not tested, because one or both traits were not heritable (i.e. not significantly different from zero).

Table S6. Estimates of genetic (below the diagonal) and phenotypic (above the diagonal, italic) correlations with standard errors (in parentheses) between the resilience indicators ln(variance), skewness, and autocorrelation based on average batch production for the same life periods with 1-week-intervals for Brown.

			<i>phenotypic correlation</i>		
	trait	period	ln(variance)	skewness	autocorrelation
genetic correlation	ln(variance)	25-end	-	-0.29 (0.01)	0.58 (0.004)
		25-83	-	-0.32 (0.01)	0.51 (0.005)
		83-end	-	-0.07 (0.01)	0.15 (0.01)
	skewness	25-end	-0.63 (0.09)	-	0.06 (0.01)
		25-83	-0.67 (0.11)	-	0.04 (0.01)
		83-end	0.65 (0.09)	-	0.10 (0.01)
	autocorrelation	25-end	0.34 (0.08)	-0.32 (0.13)	-
		25-83	0.14 (0.10)	-0.55 (0.15)	-
		83-end	0.42 (0.11)	0.36 (0.13)	-

Table S7. Estimates of genetic and phenotypic (italic) correlations with standard errors (in parentheses) between the resilience indicators ln(variance), skewness, and autocorrelation based on average batch production and expected individual production for the same life periods with 1-week-intervals for White and Brown.

trait	period	genetic correlation		<i>phenotypic correlation</i>	
		White	Brown	White	Brown
ln(variance)	25-83	0.95 (0.01)	0.98 (0.01)	<i>0.88 (0.001)</i>	<i>0.90 (0.001)</i>
	83-end	0.996 (0.002)	0.99 (0.01)	<i>0.92 (0.001)</i>	<i>0.81 (0.002)</i>
skewness	25-83	0.27 (0.08)	0.001 (0.14)	<i>0.52 (0.004)</i>	<i>0.55 (0.004)</i>
	83-end	^a	0.99 (0.01)	^a	<i>0.78 (0.002)</i>
autocorrelation	25-83	0.62 (0.06)	0.73 (0.06)	<i>0.67 (0.003)</i>	<i>0.70 (0.003)</i>
	83-end	0.92 (0.02)	0.97 (0.02)	<i>0.85 (0.001)</i>	<i>0.84 (0.002)</i>

^a Not tested, because one or both traits were not heritable (i.e. not significantly different from zero).

Table S8. Estimates of variance components (σ^2), heritability (h^2), and maternal environmental effect (m^2) for the full production cycle (i.e. all eggs between start and end), the early production cycle (i.e. between start and 25 weeks of age), the 'traditional' production cycle (i.e. between 25 and 83 weeks of age), and the time period after the 'traditional' production cycle (i.e. between 83 weeks of age and end) with standard errors (SE) for White and Brown.

trait	line	σ_a^2 (SE)	σ_m^2 (SE)	σ_e^2 (SE)	σ_p^2 (SE)	h^2 (SE)	m^2 (SE)
full	White	405.97 (31.87)	NS	2030.85 (24.33)	2436.80 (23.54)	0.17 (0.01)	NS
	Brown	501.34 (57.23)	78.59 (17.66)	3965.68 (45.14)	3965.68 (45.14)	0.11 (0.01)	0.02 (0.004)
early	White	20.12 (0.91)	NS	23.64 (0.48)	43.75 (0.57)	0.46 (0.02)	NS
	Brown	18.62 (1.17)	0.90 (0.21)	32.69 (0.66)	52.21 (0.63)	0.36 (0.02)	0.02 (0.004)
25-83	White	106.12 (10.99)	5.25 (2.66)	856.90 (9.28)	968.26 (8.76)	0.11 (0.01)	0.01 (0.003)
	Brown	211.10 (28.57)	46.91 (10.13)	2437.13 (25.54)	2695.10 (23.08)	0.08 (0.01)	0.02 (0.004)
83-end	White	99.67 (7.33)	NS ^a	467.27 (5.57)	566.94 (5.47)	0.18 (0.01)	NS ^a
	Brown	59.20 (5.63)	5.65 (1.62)	370.85 (4.32)	435.70 (3.95)	0.14 (0.01)	0.01 (0.004)

NS: maternal environmental effect not significantly different from zero.

^a Tended to be significantly different from zero (i.e. $0.05 < p \leq 0.10$).

Table S9. Estimates of genetic (below the diagonal) and phenotypic (above the diagonal, italic) correlations with standard errors (in parentheses) between egg production traits for the full production cycle (i.e. all eggs between start and end), the early production cycle (i.e. between start and 25 weeks of age), the 'traditional' production cycle (i.e. between 25 and 83 weeks of age), and the time period after the 'traditional' production cycle (i.e. between 83 weeks of age and end) for White.

	trait	<i>phenotypic correlation</i>			
		full	early	25-83	83-end
genetic correlation	full	-	0.25 (0.01)	0.91 (0.001)	0.82 (0.002)
	early	0.21 (0.04)	-	0.17 (0.01)	0.02 (0.01)
	25-83	0.93 (0.01)	0.03 (0.05)	-	0.52 (0.005)
	83-end	0.89 (0.01)	-0.06 (0.04)	0.75 (0.03)	-

Table S10. Estimates of genetic (below the diagonal) and phenotypic (above the diagonal, italic) correlations with standard errors (in parentheses) between egg production traits for the full production cycle (i.e. all eggs between start and end), the early production cycle (i.e. between start and 25 weeks of age), the 'traditional' production cycle (i.e. between 25 and 83 weeks of age), and the time period after the 'traditional' production cycle (i.e. between 83 weeks of age and end) for Brown.

	trait	<i>phenotypic correlation</i>			
		full	early	25-83	83-end
genetic correlation	full	-	0.33 (0.01)	0.96 (0.0004)	0.72 (0.003)
	early	0.28 (0.06)	-	0.27 (0.01)	0.05 (0.01)
	25-83	0.97 (0.005)	0.03 (0.05)	-	0.53 (0.004)
	83-end	0.89 (0.02)	-0.03 (0.06)	0.82 (0.04)	-

Table S11. Estimates of genetic and phenotypic (italic) correlations with standard errors (in parentheses) between the resilience indicators ln(variance), skewness, and autocorrelation based on average batch production for the same life periods with 1-week-intervals and egg production traits for the full production cycle (i.e. all eggs between start and end), the early production cycle (i.e. between start and 25 weeks of age), the 'traditional' production cycle (i.e. between 25 and 83 weeks of age), and the time period after the 'traditional' production cycle (i.e. between 83 weeks of age and end) for White.

		period	full	early	25-83	83-end
genetic correlation	ln(variance)	25-83	-0.82 (0.02)	0.05 (0.05)	-0.72 (0.04)	-0.88 (0.02)
		83-end	-0.62 (0.05)	0.10 (0.05)	-0.43 (0.06)	-0.81 (0.03)
	skewness	25-83	0.11 (0.08)	-0.15 (0.06)	-0.05 (0.09)	0.33 (0.08)
		83-end	<i>a</i>	<i>a</i>	<i>a</i>	<i>a</i>
	autocorrelation	25-83	-0.04 (0.07)	-0.06 (0.06)	0.25 (0.09)	-0.23 (0.07)
		83-end	-0.16 (0.08)	-0.07 (0.07)	-0.03 (0.09)	-0.22 (0.08)
phenotypic correlation	ln(variance)	25-83	<i>-0.60 (0.004)</i>	<i>-0.01 (0.01)</i>	<i>-0.58 (0.004)</i>	<i>-0.48 (0.005)</i>
		83-end	<i>-0.13 (0.01)</i>	<i>0.04 (0.01)</i>	<i>0.06 (0.01)</i>	<i>-0.34 (0.01)</i>
	skewness	25-83	<i>-0.11 (0.01)</i>	<i>-0.05 (0.01)</i>	<i>-0.15 (0.01)</i>	<i>-0.02 (0.01)</i>
		83-end	<i>a</i>	<i>a</i>	<i>a</i>	<i>a</i>
	autocorrelation	25-83	<i>-0.37 (0.01)</i>	<i>-0.04 (0.01)</i>	<i>-0.37 (0.01)</i>	<i>-0.27 (0.01)</i>
		83-end	<i>-0.24 (0.01)</i>	<i>-0.03 (0.01)</i>	<i>-0.15 (0.01)</i>	<i>-0.30 (0.01)</i>

Table S12. Estimates of genetic and phenotypic (italic) correlations with standard errors (in parentheses) between the resilience indicators ln(variance), skewness, and autocorrelation based on average batch production for the same life periods with 1-week-intervals and egg production traits for the full production cycle (i.e. all eggs between start and end), the early production cycle (i.e. between start and 25 weeks of age), the 'traditional' production cycle (i.e. between 25 and 83 weeks of age), and the time period after the 'traditional' production cycle (i.e. between 83 weeks of age and end) for Brown.

		period	full	early	25-83	83-end
genetic correlation	ln(variance)	25-83	-0.84 (0.03)	-0.14 (0.07)	-0.83 (0.04)	-0.77 (0.04)
		83-end	-0.46 (0.08)	0.18 (0.07)	-0.42 (0.09)	-0.59 (0.07)
	skewness	25-83	0.53 (0.14)	-0.21 (0.11)	0.49 (0.15)	0.70 (0.11)
		83-end	-0.95 (0.04)	0.06 (0.07)	-0.91 (0.05)	-0.98 (0.02)
	autocorrelation	25-83	0.22 (0.10)	-0.12 (0.08)	0.38 (0.11)	-0.02 (0.09)
		83-end	-0.25 (0.10)	-0.04 (0.09)	-0.11 (0.11)	-0.42 (0.09)
phenotypic correlation	ln(variance)	25-83	<i>-0.59 (0.004)</i>	<i>-0.06 (0.01)</i>	<i>-0.59 (0.004)</i>	<i>-0.42 (0.01)</i>
		83-end	<i>0.10 (0.01)</i>	<i>0.06 (0.01)</i>	<i>0.18 (0.01)</i>	<i>-0.10 (0.01)</i>
	skewness	25-83	<i>-0.16 (0.01)</i>	<i>-0.11 (0.01)</i>	<i>-0.21 (0.01)</i>	<i>0.04 (0.01)</i>
		83-end	<i>-0.35 (0.01)</i>	<i>-0.02 (0.01)</i>	<i>-0.25 (0.01)</i>	<i>-0.50 (0.005)</i>
	autocorrelation	25-83	<i>-0.33 (0.01)</i>	<i>-0.06 (0.01)</i>	<i>-0.35 (0.01)</i>	<i>-0.18 (0.01)</i>
		83-end	<i>-0.28 (0.01)</i>	<i>-0.05 (0.01)</i>	<i>-0.21 (0.01)</i>	<i>-0.35 (0.01)</i>

Table S13. Estimates of variance components (σ^2), heritability (h^2), and maternal environmental effect (m^2) of the antibody traits keyhole limpet hemocyanin (KLH)-binding IgM natural antibody titer and KLH-binding IgG natural antibody titer with standard errors (SE) for White and Brown.

trait	line	σ_a^2 (SE)	σ_m^2 (SE)	σ_e^2 (SE)	σ_p^2 (SE)	h^2 (SE)	m^2 (SE)
IgM	White	0.41 (0.06)	NS	0.83 (0.04)	1.24 (0.04)	0.33 (0.04)	NS
	Brown	0.38 (0.06)	NS	0.66 (0.04)	1.04 (0.04)	0.37 (0.05)	NS
IgG	White	0.11 (0.03)	NS	1.56 (0.04)	1.67 (0.04)	0.07 (0.02)	NS
	Brown	0.34 (0.07)	NS	1.27 (0.06)	1.61 (0.06)	0.21 (0.04)	NS

NS: maternal environmental effect not significantly different from zero.

Table S14. Estimates of genetic (below the diagonal) and phenotypic (above the diagonal, italic) correlations with standard errors (in parentheses) between the antibody traits keyhole limpet hemocyanin (KLH)-binding IgM natural antibody titer and KLH-binding IgG natural antibody titer for White and Brown.

		<i>phenotypic correlation</i>			
		White		Brown	
	trait	IgM	IgG	IgM	IgG
genetic correlation	IgM	-	<i>0.26 (0.02)</i>	-	<i>0.24 (0.02)</i>
	IgG	0.84 (0.07)	-	0.24 (0.12)	-

Table S15. Estimates of genetic and phenotypic (*italic*) correlations with standard errors (in parentheses) of the resilience indicators ln(variance), skewness, and autocorrelation based on average batch production for the same life periods with 1-week-intervals and the antibody traits keyhole limpet hemocyanin (KLH)-binding IgM natural antibody titer and KLH-binding IgG natural antibody titer for White.

	period	genetic correlation		<i>phenotypic correlation</i>	
		IgM	IgG	IgM	IgG
ln(variance)	25-83	-0.09 (0.11)	0.06 (0.17)	<i>0.01 (0.02)</i>	<i>-0.01 (0.02)</i>
	83-end	-0.12 (0.12)	-0.02 (0.18)	<i>0.03 (0.02)</i>	<i>0.01 (0.02)</i>
skewness	25-83	0.08 (0.13)	-0.18 (0.19)	<i>0.004 (0.02)</i>	<i>0.0002 (0.02)</i>
	83-end	a	a	a	a
autocorrelation	25-83	0.16 (0.12)	0.21 (0.18)	<i>-0.02 (0.02)</i>	<i>-0.03 (0.02)</i>
	83-end	0.15 (0.15)	0.13 (0.21)	<i>-0.001 (0.02)</i>	<i>-0.01 (0.02)</i>

^a Not tested, because the resilience indicator trait was not heritable (i.e. not significantly different from zero).

Table S16. Estimates of genetic and phenotypic (*italic*) correlations with standard errors (in parentheses) of the resilience indicators ln(variance), skewness, and autocorrelation based on average batch production for the same life periods with 1-week-intervals and the antibody traits keyhole limpet hemocyanin (KLH)-binding IgM natural antibody titer and KLH-binding IgG natural antibody titer for Brown.

	period	genetic correlation		<i>phenotypic correlation</i>	
		IgM	IgG	IgM	IgG
ln(variance)	25-83	-0.03 (0.30)	-0.27 (0.32)	<i>a</i>	<i>a</i>
	83-end	-0.21 (0.34)	-0.24 (0.39)	<i>a</i>	<i>a</i>
skewness	25-83	-0.16 (0.42)	0.16 (0.48)	<i>a</i>	<i>a</i>
	83-end	0.28 (0.34)	-0.09 (0.39)	<i>a</i>	<i>a</i>
autocorrelation	25-83	-0.09 (0.31)	-0.15 (0.33)	<i>a</i>	<i>a</i>
	83-end	0.03 (0.42)	0.56 (0.42)	<i>a</i>	<i>a</i>

^a Phenotypic correlation could not be estimated, because traits were collected on different individuals.