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Genetic correlations between test station and on-farm performance for backfat thickness and daily gain

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ABSTRACT

Performance test of boars (S-) and on-farm test of gilts (F-) for ultrasonic backfat thickness (BF) and daily live weight gain (LDG) were analyzed to estimate the magnitude of genotype-environment interaction (GxEI). GxEI was estimated as genetic correlation in multivariate animal model approach. The dataset consisted of 4583 records of boars and 12145 of gilts for three breeds: Swedish Landrace (SL), Large White (LW) and German Landrace (GL) in years 1990 - 1997 for the nucleus herd on farm Ptuj in Slovenia. Altogether, pedigree file contained 19076 animals. Separate analyses were performed for each breed using REML method in VCE 4. Estimated genetic correlations between corresponding traits in station and on-farm tests were high (above 0.9), except for LW (0.50 and 0.44 for BF and LDG, respectively). The heritability estimates were 0.11 - 0.35 for F-BF, 0.23 - 0.40 for S-BF, 0.14 - 0.23 for F-LDG and 0.13 - 0.31 for S-LDG. Common litter environment variance accounts for 6 - 23% of the phenotypic variance for BF and 7 - 25% for LDG.

(Keywords: pigs, genotype-environment interaction, backfat thickness, daily gain)

ZUSAMMENFASSUNG

Genetische Korrelationen zwischen Stations- und Feldtest für die Produktionsparameter Rückenspeckdicke und Tageszunahme

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Die Daten aus der Eigenleistungsprüfung der Eber und aus dem Feldtest der Jungsauen für Rückenspeckdicke (RS) und Tageszunahme (TZ) wurden analysiert, um die Größe der Genotyp-Umwelt-Interaktion (GxUI) zu schätzen. GxUI wurde als genetische Korrelation mit Hilfe eines multivariablen Tiermodells geschätzt. In die Analyse wurden 4583 Daten von Ebern und 12.145 von Jungsauen dreier Genoypen einbezogen (Schwedische Landrasse-SL, Large White-LW und Deutsche Landrasse-DL). Die Daten stammen aus einer Stammherde der Farm Ptuj in Slowenien von 1990 bis 1997. Die Herdbuchführung umfasst 19.076 Tiere. Für jeden Genotyp wurde eine gesonderte Analyse mit der REML-Methode in VCE 4 durchgeführt. Die geschätzten genetischen Korrelationen zwischen den untersuchten Merkmalen im Stations- und Feldtest waren hoch (über 0,9), außer für die LW Rasse (0.50 für RS und 0.44 für TZ). Die geschätzte Heritabilität für die RS lag im Stationstest zwischen 0.23 und 0.40, im Feldtest zwischen

0.11 und 0.35. Für die TZ lag die Heritabilität im Stationstest zwischen 0.13 und 0.31 und im Feldtest zwischen 0.14 und 0.23. Der Wurfeffekt trägt mit 6-23% bzw. 7-25% zur phänotypischen Variabilität der RS bzw. TZ bei.

(Schlüsselwörter: Schwein, Genotyp-Umwelt-Interaktion, Rückenspeckdicke, Tageszunahme)

INTRODUCTION

In pig breeding, performance testing on test stations is the base for selecting sire for next generation. Uniformity of environment, more accurate measurements, more traits measured are main reasons for station testing. Testing conditions often differ much from conditions for fatteners on the farm, so it may be expected some differences in genetic control of the same traits measured on the test station and in field. Because of that, breeding goal should be defined at commercial level (*Merks*, 1989), and selection at the nucleus level should include information from lower levels of breeding pyramid.

Differences in expression of the same genotype in different environments are defined as genotype-environment interactions (GxEI). The genotype involves breeds, lines, families, sires or simply individual animals, while environment includes effects such as location, housing, management, feeding. It is useful to know, if changes in a rank occur or if there is significant difference among expressions of the genotypes in different environments.

The method suggested by *Falconer* (1952) estimates the magnitude of GxEI as genetic correlation between observations of the same genotype in different environments. The same trait measured in two environments is considered as two correlated traits. A multivariate approach is the logical choice for estimation of genetic correlation between two traits. Where traits are measured on different individuals, information on relatives are used for estimation of genetic correlation. In early times, univariate approach was used, because no direct procedures were available for analysis of measurements taken on from different individuals (*Mathur* and *Schlote*, 1995). Studies from that time reported existence of GxEI interactions in pig breeding (reviewed by *Brascamp et al.*,1985; *Merks*, 1986; *Webb* and *Curran*, 1989). In 1989, *Van Diepen* and *Kennedy* applied mixed model approach and produced very high estimates of genetic correlations. From this, *De Vries* and *Sorensen* (1990) raised possibility that low genetic correlations from earlier studies were an artefact of the method of estimation. *Merks* and *van Oijen* (1994) and *Crump et al.* (1997) also estimated high genetic correlation for fattening traits using multivariate approach. On contrary, the study of *Tholen et al.* (1998) showed poor genetic correlations between adequate fattening and carcass traits measured on test station and in fattening herds.

The aim of this paper was to find out the existence of genotype-environment interactions (GxEI) in Slovenian pig population through estimating of genetic correlations between boars and gilts for fattening traits measured under different performance test. Due to structure of data, it was impossible to distinguish between GxEI and genotype-sex interaction like in study of *Crump et al.* (1997).

MATERIALS AND METHODS

In analysis, performance test records from boars and gilts of three breeds were taken from a purebred nucleus breeding herd on farm Ptuj in Slovenia. The data set consisted of 4583 test records for boars and 12145 for gilts which were collected from July 1990 to December 1997 (*Table 1*). Complete pedigree over several generations was available. Pedigree file contained 14703, 1805 and 2568 animals for Swedish Landrace (SL), Large White (LW), and German Landrace (GL), respectively. Near 13% of animals from pedigree were without records and around 5% were base animals.

Table 1

Data structure of performance records

Breed(1)	SL	LW	GL
Boars(2)	3147	575	861
Gilts(3)	9656	986	1503
Animals in pedigree(4)	14703	1805	2568
% of animals without records(5)	12.9	13.5	7.9
% of base animals(6)	5.5	9.1	4.6
N° of progenies per sire(7)	85.4	13.7	19.4
N° of progenies per dam(8)	3.1	4.7	4.4
N° of progenies per litter(9)	1.9	2.0	1.9

1. Tabelle: Datenstrurktur der Produktionsmerkmale

Genotyp(1), Eber(2), Jungsauen(3), Herdbuchtiere(4), Tiere ohne Abstammungsdaten(5), Tiere mit Abstammungsdaten(6), Geprüfte Nachkommen pro Vatertier(7), Geprüfte Nachkommen pro Muttertier(8), Geprüfte Ferkel pro Wurf(9)

Gilts were reared under commercial conditions, housed in groups and fed approximately to appetite. At around 100 kg, selection was based on daily live weight gain and ultrasonic backfat thickness. Before measuring, preselection based on subjective condition score was made. No individual food recording was carried out in gilts. Near 50% gilts were selected, the ratio depends a large extent on culling rate of sows and the number of gilts available. On the other hand, boars were penned individually and fed ad libitum. Same feed mixture with 14.6% of crude proteins was fed through entire test. Test was carried out in three stages: boars were first subjectively scored and selected before 30 kg. At 60 kg, between 40 and 60% of boars were culled on daily gain, feed conversion efficiency, and exterior abnormality. At the end of test at 100 kg, animals were selected according to index including duration of fattening, total feed consumption, and ultrasonic backfat thickness. Three to 15% of tested boars are selected annually as sires for the nucleus herd (*Kovač et al.,* 1999).

Boars have finished test between 95 and 107 kg live weight (*Table 2*), while weight at the test in gilts was one kilogram less and within wider range from 80 to 129 kg. Average backfat thickness in SL was 16.6 mm in boars and 16.7 mm in gilts. Gilts of other two breeds had 14.0 mm of backfat, while boars had 15.0 mm (LW) and 15.1 mm (GL), respectively. The standard deviations for backfat thickness ranged between 1.71 and 2.31 mm in boars, and between 1.87 and 2.36 in gilts. Averages for backfat thickness differed among breeds 1.5 mm in boars and 2.7 mm in gilts. All three breeds showed similar standard deviation in daily live weight gain (33 - 38 g). Daily live weight gain was close to 500 g in gilts and 600 g in boars with small differences among breeds. Average daily gain from 30 to 100 kg (TDG) on test station in boars was 870 g with standard deviation of 70 g.

Table 2

Basic statistics for analyzed traits in boars and gilts for three breeds

Breed(1)		SL			LW			GL		
Boars(2)	BF (mm)	16.6	±	2.31	15.0	±	2.15	15.1	±	1.71
	LDG (g)	609	±	33	594	±	38	585	±	34
	TDG (g)	874	±	69	884	±	76	856	±	69
	WT (kg)	99.8	±	3.00	100.2	±	3.21	99.5	±	2.87
Gilts(3)	BF (mm)	16.7	±	2.36	14.0	±	2.10	14.0	±	1.87
	LDG (g)	513	±	36	500	±	37	496	±	36
	WT (kg)	99.2	±	6.50	97.3	±	7.00	96.5	±	6.12

BF-Ultrasonic backfat thickness *(Ultraschall Rückenfettdicke),* LDG-Daily live weight gain *(Tägliche Zunahme),* TDG-Daily gain between 30 and 100 kg *(Tägliche Zunahme zwischen 30 und 100 kg),* WT–Weight on test. *(Körpergewicht)*

2. Tabelle: M*ittelwerte und Standardabweichungen für Eber und Jungsauen von drei Genotypen)*

Genotyp(1), Eber(2), Jungsauen(3)

Separate analyses were performed for each breed using REML method in VCE 4 (*Neumaier* and *Groeneveld,* 1998). For backfat thickness, the analysis was performed with two trait model, while model for daily gain contained daily live weight gain in gilts and boars as well as TDG. Daily gain from 30 to 100 kg in boars is one of traits on which boars are selected. Because of this, it was also included in analysis. The following linear model written in matrix notation was used in multiple trait analysis:

$$\mathrm{y} = \mathbf{X}\beta + \mathbf{Z}_{\mathrm{a}}\mathbf{a} + \mathbf{Z}_{\mathrm{c}}\mathbf{c} + \mathbf{e}$$

where $\mathbf{y}$ is the vector of observations, β is the vector of fixed effects, $\mathbf{a}$ is the vector of additive genetic effects, $\mathbf{c}$ is the vector of common litter environment effects, and $\mathbf{e}$ is the vector of residuals. Known incidence matrices $\mathbf{X}$, $\mathbf{Z_a}$, $\mathbf{Z_c}$ relate observations to fixed and random effects. The vector of fixed effects β contained month of test as year-month interaction for daily gain and additionally, weight on test as covariate for backfat thickness. The expectations of all random effects as well as covariances between random effects were zero. The following variance structure was assumed in analysis:

$$\mathrm{var}(\mathbf{a}) = \mathbf{G} = \mathbf{A} \otimes \mathbf{G}_{\mathrm{o}}$$

$$\mathrm{var}(\mathbf{c}) = \mathbf{C} = \mathbf{I}_{\mathrm{c}} \otimes \mathbf{C}_{\mathrm{o}}$$

$$\mathrm{var}(\mathbf{e}) = \mathbf{R} = \sum_{i=1}^{n}{}^{\oplus}\mathbf{R}_{\mathrm{ko}}$$

$$\mathrm{var}(\mathbf{y}) = \mathbf{V} = \mathbf{R} + \mathbf{Z}_{\mathrm{a}}\mathbf{G}\mathbf{Z}'_{\mathrm{a}} + \mathbf{Z}_{\mathrm{c}}\mathbf{C}\mathbf{Z}'_{\mathrm{c}}$$

where $\mathbf{G}$ is the matrix of additive genetic (co)variances, $\mathbf{A}$ is the numerator relationship matrix, $\mathbf{C}$ is the (co)variance matrix of the common litter environment, and complete residual covariance matrix $\mathbf{R}$ is direct sum of two types of $\mathbf{R}$ due to missing values. Covariance matrices $\mathbf{G_o}$, $\mathbf{C_o}$ and $\mathbf{R_{ko}}$ for traits measured on the same individual for backfat thickness and daily gain are presented below.

BACKFAT THICKNESS

$$\mathbf{G}_o = \begin{bmatrix} \sigma^2_{a_1} & \sigma_{a_1a_2} \\ \sigma_{a_2a_1} & \sigma^2_{a_2} \end{bmatrix}$$

$$\mathbf{C}_o = \begin{bmatrix} \sigma^2_{c_1} & \sigma_{c_1c_2} \\ \sigma_{c_2c_1} & \sigma^2_{c_2} \end{bmatrix}$$

$$\mathbf{R}_{1o} = \begin{bmatrix} \sigma^2_{e_1} & 0 \\ 0 & 0 \end{bmatrix} \mathbf{R}_{2o} = \begin{bmatrix} 0 & 0 \\ 0 & \sigma^2_{e_2} \end{bmatrix}$$

DAILY GAIN

$$\mathbf{G}_o = \begin{bmatrix} \sigma^2_{a_1} & \sigma_{a_1a_2} & \sigma_{a_1a_3} \\ \sigma_{a_2a_1} & \sigma^2_{a_2} & \sigma_{a_2a_3} \\ \sigma_{a_3a_1} & \sigma_{a_3a_2} & \sigma^2_{a_3} \end{bmatrix}$$

$$\mathbf{C}_o = \begin{bmatrix} \sigma^2_{c_1} & \sigma_{c_1c_2} & \sigma_{c_1c_3} \\ \sigma_{c_2c_1} & \sigma^2_{c_2} & \sigma_{c_2c_3} \\ \sigma_{c_3c_1} & \sigma_{c_3c_2} & \sigma^2_{c_3} \end{bmatrix}$$

$$\mathbf{R}_{1o} = \begin{bmatrix} \sigma^2_{e_1} & \sigma_{e_1e_2} & 0 \\ \sigma_{e_2e_1} & \sigma^2_{e_2} & 0 \\ 0 & 0 & 0 \end{bmatrix} \mathbf{R}_{2o} = \begin{bmatrix} 0 & 0 & 0 \\ 0 & 0 & 0 \\ 0 & 0 & \sigma^2_{e_3} \end{bmatrix}$$

RESULTS AND DISCUSSION

Variance component estimates for daily gain are summarized in *Table 3*. Estimated phenotypic variances for LDG were in range between 958.0 g^2 in GL boars and 1245.4 g^2 in LW gilts. Within breeds, there were small differences between sexes. TDG in boars is different trait with phenotypic variance estimated between 3818.1 g^2 in GL and 4457.7 g^2 in LW. Similar magnitude of variance components for residual and common litter environmental effect were estimated for LDG in both sexes in all three breeds. In his study on German and Australian data, *Brandt* (1994) estimated higher phenotypic variances for LDG (range 2400-3000 g^2). Joint analysis for daily gain on different intervals in boars and LDG in gilts on data from another Slovenian nucleus farm by *Kovač* (1992) showed more comparable estimates (1486.1 g^2). The LW population showed higher additive genetic variance (379.5 in boars and 279.2 in gilts) in comparison to the other two breeds (166.4 and 231.8 in SL and GL boars; around 130 in both Landrace gilts). Consequently, heritabilities (*Table 4*) in LW boars (0.31) and gilts(0.22) were higher. GL gilts also showed heritability of 0.23, while heritabilities for LDG were lower (013-0.14) in SL gilts and boars and GL boars. Heritability for LDG in gilts from *Kovač* (1992) was 0.24, while estimates from *Brandt* (1994) were in range 0.20 - 0.32. Common litter environment effect accounted for 7 to 25% of phenotypic variance in LW and GL boars, respectively.

The highest phenotypic variance for BF (*Table 5*) was estimated to 3.94 mm^2 for SL gilts. Similar result (3.74 mm^2) was obtained for SL boars. In smaller breeds, phenotypic variance was smaller. Additive genetic variance varied among breeds: 1.50 and 1.37 mm^2 for SL, almost three times smaller in GL (0.50 and 0.49 mm^2), while 1.20 and only 0.30 mm^2 in LW boars and gilts, respectively. LW gilts also showed highest residual variance component (2.31 mm^2). Reason for smaller genetic variance may be in possible closer genetic relationship in small size populations, which must be confirmed in the future. Variance for common litter environment of 0.41-0.50 mm^2 in boars was comparable with estimates in both Landrace gilts, while LW gilts (0.16 mm^2) differed a lot.

Table 3

Phenotypic variance and variance components from multivariate analysis for daily gain

Breed(3)	Boars(1)								Gilts(2)			
	LDG				TDG				LDG			
	σ^2_p	σ^2_a	σ^2_c	σ^2_e	σ^2_p	σ^2_a	σ^2_c	σ^2_e	σ^2_p	σ^2_a	σ^2_c	σ^2_e
SL	1044.7	131.9	180.3	732.5	4068.8	742.2	331.8	2994.7	1187.3	166.4	201.6	819.2
LW	1205.2	379.5	78.7	747.0	4457.7	1461.0	203.8	2792.8	1245.4	279.2	194.2	772.1
GL	958.0	134.2	240.4	583.4	3818.1	816.0	753.3	2248.8	1022.5	231.8	95.0	695.7

LDG - Daily live weight gain *(Tageszunahme Lebendgewicht)*, TDG - Daily gain between 30 and 100 kg *(Tageszunahme zwischen 30 und 100 kg),* σ^2_p-Phenotypic variance, σ^2_a-Additive genetic variance, σ^2_c-Common litter environmental variance *(Umwelt-Wurf-Varianz)*, σ^2_e-Residual variance *(Residualvarianz)*

3. Tabelle: Phänotypische Varianz und Varianzkomponenten aus der multivariablen Analyse für Tageszunahmen

Eber(1), Jungsauen(2), Genotyp(3)

Table 4

Proportions of variance components from multivariate analysis for daily gain

Breed(1)	Boars(2)				Gilts(3)	
	LDG		TDG		LDG	
	h^2	c^2	h^2	c^2	h^2	c^2
SL	0.13	0.17	0.18	0.08	0.14	0.17
LW	0.31	0.06	0.33	0.05	0.16	0.22
GL	0.14	0.25	0.21	0.20	0.23	0.09

LDG - Daily live weight gain *(Tageszunahme Lebendgewicht)*, TDG- Daily gain between 30 and 100 kg *(Tageszunahme zwischen 30 und 100 kg),* h^2–Heritability *(Heritabilität),* c^2-Common litter environmental variance as proportion of phenotypic variance *(Umwelt-Wurf-Varianz als Teil der phänotypischen Varianz)*

4. Tabelle: Varianzanteile aus der multivariabler Analyse für Tageszunahmen

Genotyp(1), Eber(2), Jungsauen(3)

Table 5

Phenotypic variance and variance components from bivariate analysis for backfat thickness

	Boars(2)				Gilts(3)			
Breed(1)	σ^2_p	σ^2_a	σ^2_c	σ^2_e	σ^2_p	σ^2_a	σ^2_c	σ^2_e
SL	3.74	1.50	0.46	1.79	3.94	1.37	0.59	1.98
LW	3.18	1.20	0.41	1.57	2.76	0.30	0.16	2.31
GL	2.21	0.50	0.50	1.21	2.19	0.49	0.32	1.39

σ^2_p-Phenotypic variance *(Phänotypische Varianz)*, σ^2_a-Additive genetic variance *(Additive genetische Varianz)*, σ^2_c-Common litter environmental variance *(Umwelt-Wurf-Varianz)*, σ^2_e-Residual variance *(Residualvarianz)*

5. Tabelle: Phänotypische Varianz und Varianzkomponenten aus der bivariablen Analyse für Rückenspeckdicke

Genotyp(1), Eber(2), Jungsauen(3)

Heritabilities for BF in boars (0.23-0.40) were higher in comparison to 0.11-0.35 in gilts (*Table 6*), which was expected because of more uniform environment on test stations than on farms. Very low heritability in LW gilts was a consequence of small additive genetic variance component (0.30 mm^2) comparing to rest of variance (*Table 5*). *Crump et al.* (1997) estimated comparable heritabilities for BF (0.28-0.36 and 0.25-0.46 in boars and gilts, respectively) with similar model. Additive genetic effect accounted for 23% of phenotypic variance in the study of *Kovač* (1992) and from 15 up to 52% of *Brandt* (1994).

Table 6

Proportions of variance components, phenotypic (r_p) and genetic correlation (r_a) for backfat thickness

	Boars(2)				Gilts(3)	
Breed(1)	h^2	c^2	h^2	c^2	r_a	R_p
SL	0.40	0.12	0.35	0.15	0.91	0.38
LW	0.38	0.13	0.11	0.06	0.50	0.12
GL	0.23	0.23	0.22	0.14	0.92	0.26

h^2–Heritability (*Heritabilität)*, c^2-Common litter environmental variance as proportion of phenotypic variance *(Umwelt-Wurf-Varianz als Teil der phänotypischen Varianz)*

6. Tabelle: Varianzantaile, phänotypische (r_p) und genetische Korrelationen (r_a) für Rückenspeckdicke

Genotyp(1), Eber(2), Jungsauen(3)

Between LDG in boars and gilts, low phenotypic correlations were estimated: 0.14, 0.19 and 0.22 in LW, GL, and SL, respectively (*Table 7*). Estimates were also low for phenotypic correlations between LDG in gilts and TDG in boars (from 0.10 to 0.17). Phenotypic correlations between LDG and TDG in boars were in range between 0.76 (LW) and 0.79 (SL). While genetic correlations for LDG between boars and gilts were high with 0.93 in SL and 1.00 in GL (*Table 7*). In LW population, genetic correlation was only 0.44. The explanation for low estimates, as reasoned Simianer (1991) in his simulation study, may be in small sample size and low heritabilities even if there is no GxEI interactions. The two daily gains measured in boars were also highly correlated (from 0.82 in GL to 0.93 in LW). Lower genetic correlations were expected between LDG in gilts and TDG in boars. However, they all lie between 0.82 and 0.93. *Merks* and *van Oijen* (1994), as well as *Crump et al*. (1997) also estimated very high genetic correlations for backfat thickness (0.81-1.00).

Table 7

Phenotypic (r_p) and genetic correlations (r_a) from multivariate analysis for daily gain

Breed (1)	r_a^*	r_p^*	r_a^{**}	r_p^{**}	r_a^{***}	r_p^{***}
SL	0.93	0.22	0.90	0.79	0.72	0.17
LW	0.44	0.14	0.93	0.76	0.68	0.10
GL	1.00	0.19	0.82	0.76	0.77	0.12

*Between LDG in boars and LDG in gilts *(Tageszunahmen bei Ebern und Jungsauen)*
**Between LDG and TDG in boars *(Tageszunahmen und Tageszunahmen zwischen 30 kg und 100 kg Lebendgewicht bei Ebern)*
***Between LDG in gilts and TDG in boars *(Tageszunahmen bei Jungsauen und Tageszunahmen zwischen 30kg und 100 kg Lebendgewicht bei Ebern)*

7. Tabelle: Phänotypische (r_p) und genetische Korrelationen (r_a) aus der multivariablen Analyse für Tageszunahmen

Genotyp(1)

If genetic correlation is good measure for the magnitude of G x E interactions, was argued in *Simianer* (1991), *Mathur* and *Horst* (1994) and *Mathur* and *Schdlote* (1995). Nevertheless, with high estimated genetic correlations (above 0.9) might be concluded on non-existence of G x E interactions and/or genotype-sex interactions from this data. On the other hand, high genetic correlations have their own significance. Including information from full- and halfsibs from on-farm test in the procedure for predicting of breeding values of boars from the test station means more accurate estimation and consequently, more efficient selection.

CONCLUSIONS

Slovenian data for backfat thickness and daily gain were analyzed using REML method and multitrait approach. The intention was to determine the magnitude of genotype-environment The heritability estimates for backfat thickness were 0.11- 0.35 in gilts and

0.23-0.40 in interactions boars. For daily live weight gain estimates for heritabilities were lower (0.14-0.31 and 0.14-0.23 in boars and gilts, respectively).

Common litter variance accounted for six to 25% of phenotypic variance for daily live weight gain. Similar proportion for common litter effect (6-23%) was estimated in backfat thickness, too.

Estimated genetic correlations were high (above 0.90 for backfat thickness and daily live weight gain), except for Large White breed with very small data set (0.44 and 0.50 for LDG and BF, respectively). Phenotypic correlations were much lower in comparison to genetic correlations (0.10-0.22 for LDG and 0.12-0.38 for BF).

In the future, the study will be extended to other nucleus herds in Slovenia, especially interesting will be analysis in small populations like LW and terminal sire breeds.

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