

COMPARISON BETWEEN SIRE AND ANIMAL MODEL TO ESTIMATE GENETIC (CO)VARIANCES FOR MILK YIELD TRAITS

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ABSTRACT

Records of 847 Friesian cows which completed one or more lactations of milk production kept at Sakha and El-Karda farms during the period from 1996 to 2002 were used to estimate the genetic and phenotypic (co)variances of and between three months and 305 day milk yield traits by using sire and animal model. Sire model, included the fixed effects of HYS and parity, Days open was used as a covariate, while the random effects were sire, cow and dam and residual effect. Animal model included the same effects in the sire model and increase the animal direct genetic effect and permanent environmental effect as the random effects. The average number of mixed model equations (MME), no. of iterations, CPU for solving and inverting and AG-Log Likelihood were higher for multi trait than single trait for both sire and animal model. Estimates of heritability (h^2) of milk traits, for sire model were moderate, ranged from 0.096 to 0.276 for single trait and from 0.116 to 0.264 for multiple traits. While the h^2 for milk traits from animal models ranged from 0.001 to 0.031 for single trait and from 0.046 to 0.062 for multiple traits. Heritability estimates for milk traits in single and multiple traits from both sire and animal model were nearly similar. Genetic correlations between yield traits were positive, high and near similar for both sire and animal model and ranged from 0.88 to 0.99. The high estimates of genetic correlation in the present study offer the possibility to select for yield traits as early ages, i.e., at 90 days of lactation. Also, this study indicate that, using of sire model is useful when, small number of observation and little pedigree information.

Keywords: Friesian cattle, genetic parameters, variance component estimation, milk traits

INTRODUCTION

Estimation of genetic parameters for dairy cattle are estimated by using sire model (Mixed model., Hardie *et al.*, 1978; Ashmawy and Khalil , 1990 and Atil and Khattab, 2000) and animal model (i.e., Ahlborn and Demfple, 1992; Suzuki and Van Vleck, 1994; Mantysaari *et al.*, 2002 and Kadramideen *et al.*, 2003). Misztal *et al.* (1994) found that the correlation between the sire and animal model breeding values for bulls with semen available were 0.92 for final score and 0.91 and 0.96 for the linear traits. The same authors also concluded that genetic merit of the mates was accounted for more completely by the animal model, resulting in important differences in breeding values

predictions between the two models. Gutierrez *et al.* (1994) with Spanish Holstein Friesian cows, comparison between sire and animal model, suggested that a sire model based estimating procedure for genetic parameters may be preferred when a small number of individuals, little pedigree information and highly unbalanced distribution of effects. Also, the same authors concluded that the cheapest in terms of computing costs was based on a sire model and the most expensive on an animal model. The present study was undertaken to estimate the genetic and phenotypic (co)variances of and between three months and 305 day milk yield traits of Friesian cows in Egypt by using sire and animal model.

MATERIALS AND METHODS

Data

Data of the present study were obtained from the history sheets of Sakha and El-Karda farms, belonging to the Animal Production Research Institute, Ministry of Agriculture, Dokki, Cairo, Egypt and comprising 847 cows which completed one or more lactations., calving during 1996 to 2002. Animal were mainly grazed on Egyptian clover (*Trifolium alexandrinum*) during December–May. They were fed on concentrate mixture along with rice straw and limited amount of clover hay when available during the rest of the year. Cows pregnant in the last two months were supplemented with extra concentrate. Artificial insemination (AI) was used at random for both farms. Heifers were first inseminated at 18 months of age. In subsequent lactations, cows were initially inseminated 60 -70 days postpartum. Cows were machine milked twice daily. Milk yield were recorded daily and both fat and protein percents are estimated weekly in laboratory by using system of Milko–Scan 130 series, type 10900. Maintained at (ILMTC) related to Animal Production Research Institute (APRI), this set have special program to estimate milk composition (fat, protein and lactose). Traits studied are milk yield, fat yield and protein yield in the first three months (MY3, FY3 and PY3, respectively) and milk yield, fat yield and protein yield in 10 months (MY10, FY10 and PY10, respectively). Complete records or less than 305 days in milk were included only if the cow remained in the herd for full 305 day period. Lactations that began with an abortion or in which milking was interrupted by injury or sickness were excluded. Days open was computed as the interval between parturition and the date of successful mating. Four seasons of calving were considered. Autumn (September–November), Winter (December–February), Spring (March–May) and Summer (June–August). Table1. Show the structure of data considered in the analysis, means, minimum, maximum of MY3, FY3, PY3, MY10, FY10 and PY10.

Statistical Analysis

The preliminarily analysis of data by using GLM procedure of the SAS Computational program (Statistical Analysis System, 2000) show the significant effect of HYS (herd–year–season of calving), parity and days open as a covariate on different traits studied. After that the data were analysis by Pest Program according to Groeneveld *et al.* (1998) using sire and animal model.

For sire model, the model of the analysis included the fixed effects of HYS and parity, the linear regression coefficient of the different traits on days open, the random effects of sire, cow and dam and random errors. Estimates of sire components (σ^2_s), cow components (σ^2_c), dam components (σ^2_d) and residual components of variance and covariance were computed according to method II of Henderson (1953). Heritability estimates (h^2) were calculated from four times the intraclass correlation among half sibs. Standard errors of h^2 and estimation of genetic correlation were obtained by computing technique described by Pest Program.

For animal model, the model of the analysis included the fixed effects of HYS, parity and the days open as a covariate, animal direct genetic effect, permanent environmental effect and residual effect. Heritability (h^2) was estimated by using the following equation ($h^2 = \sigma^2_a / \sigma^2_a + \sigma^2_{pe} + \sigma^2_e$), where, σ^2_a = additive genetic variance, σ^2_{pe} = permanent environmental variance and σ^2_e = random residual effects. More detail for the description of the mixed model equations were written by Mrode (1996).

RESULTS AND DISCUSSION

Means, minimum and maximum, SD and CV% for milk, fat and protein yields are presented in Table 1. The present means for 305-day milk (MY10), fat (FY10) and protein (PY10) were lower than those reported by Hardie *et al.* (1978), Ashmawy and Khalil (1990), Suzuki and Van Vleck (1994) and Mantysaari *et al.* (2002) worked on Friesian cows in different countries and ranged from 4295 to 11571 kg for MY10, from 162 to 419 kg for FY10 and from 138 to 361 kg for PY10 respectively.

Table 1: Structure of data used in analysis, unadjusted means, minimum, maximum, standard deviation (SD) and CV % for different traits studied in a herd of Friesian cows in Egypt.

Trait (kg)*	Mean	Minimum	Maximum	SD	CV %
MY3	1222	288	2888	393	32
FY3	42.48	10.20	115.10	15.43	36
PY3	32.50	7.80	76.20	10.98	34
MY10	3050	751	7077	979	32
FY10	105.54	25.10	237.90	43.74	41
PY10	81.61	20.40	184.80	26.29	32
Observations					
No. of records	1992				
No. of cows	847				
No. of sires	77				
No. of dams	483				
No. of Animals in relationship (A^{-1})	2144				
No. of parity	9				
No. of HYS	57				
Average of days open, day	142				

*MY3, FY3 and PY3 are milk yield, fat yield and protein yield in the first three months, respectively. MY10, FY10 and PY10 are milk yield, fat yield and protein yield in the ten months, respectively.

Also, the present means for MY3, FY3 and PY3 were lower than those obtained by Soliman *et al.* (1990) worked on Pinzgauer cows in Austria. The CV % were ranging between 32 to 41 % (Table 1). The estimates between 22 to 23 % for yield traits were reported by Ashmawy and Khalil (1990). The CV% of fat yields were slightly high compared with those of milk and protein. Similar results were obtained by Ashmawy and Khalil (1990). The higher CV % values of milk traits reflect a great variation between individuals in important productive traits.

Results given in Table 2 show that the average number of mixed model equations (MME), no. of iterations, CPU for solving and inverting and AG-Log Likelihood were higher for multi trait than single trait for both two models (Table 2). Probably because of increment the number of traits (Misztal *et al.* 1994). In addition, Garcia-Cortes (1995) estimated variance components by using animal model, found that the no. of iterations were 740 and 750 for analysis 12 and 4 traits, respectively. In addition, animal models were higher MME than sire models. This could be due to included permanent environmental effects in the model. While, animal models were slight lower for PCU for solving and inverting and AG- Log Likelihood than sire model. In this respect, Suzuki and Van Vleck (1994) using 10 data files of Japanese Holstein cows, concluded that the variance of the Log Likelihood in the simplex was less than 10^{-7} in all data files and for all milk traits. In general, number of iterations required to reach convergence could be affected by the number of animals, the number of random effects in the model and traits studies.

Estimates of heritability (h^2) of milk traits, from single and multiple traits for sire model are given in table 3 and 6. Estimates of h^2 were moderate from sire components, ranged from 0.096 to 0.276 for single trait and from 0.116 to 0.264 for multiple traits. The present estimates of h^2 for MY10, FY10 and PY10 were similar to those reported by Ashmawy and Khalil (1990) with British Friesian cows, found that h^2 estimates from sire components for milk, fat and protein yields were 0.25, 0.24 and 0.23, respectively. While, the present estimates were lower than those obtained by different workers on Friesian cows on different countries by using sire model (i.e., Gacula *et al.*, 1968 and El-Awady *et al.*, 2002) and ranged from 0.20 to 0.48 for MY10, from 0.24 to 0.30 for FY10 and from 0.23 to 0.29 for PY10, respectively. In addition, Hardie *et al.* (1978) with Holstein cows in Madison, using sire model, found that h^2 estimates for milk yield and fat yield were 0.27 and 0.38, respectively.

According to moderate values of h^2 for MY10, FY10 and PY 10, it can be concluded that the genetic improvement in milk yield and it is composition can be achieved through selection breeding programs as well as better managerial practices

Estimates of h^2 for milk traits from single and multiple trait animal models are presented in Tables 3 and 7, and ranged from 0.001 to 0.031 for single trait and from 0.046 to 0.062 for multiple trait animal model.

The present estimates were lower than estimates from sire model and also were lower than those estimated by many authors on different countries, using animal model (Ahlborn and Dempfle, 1992; Suzuki and Van Vleck, 1994; Mantysaari *et al.*, 2002 and Kadarmideen *et al.*, 2003) and ranged from 0.10 to 0.30.

Table 7: Heritability estimates on diagonal and genetic correlations (r_g) below diagonal, permanent correlation (r_{pe}) above diagonal and residual correlations between practices among different traits studied by using multi-traits animal model

Traits	MY10	FY10	PY10	MY3	FY3
MY10	0.057	0.999 (0.929)	1.000 (0.962)	0.998 (0.696)	0.998 (0.560)
FY10	0.980	0.046	1.00 (0.948)	0.994 (0.631)	1.000 (0.660)
PY10	0.986	0.999	0.048	0.996 (0.652)	0.999 (0.580)
MY3	0.958	0.882	0.898	0.062	0.992 (0.848)
FY3	0.999	0.985	0.990	0.949	0.052

Unexpected lower estimates of h^2 for milk traits (Tables 4 and 5) by using animal model, could be due to higher percentage of permanent and residual environmental factors. Also, the present result is the first attempt for calculated fat and protein percentages in government farms in Egypt, and the sample of cows which used in this study were taken from different parities in a short period (seven years) and also small number of observations.

In this respect, Gutierrez *et al.* (1994) with Spanish Holstein Friesian cows, comparison between sire and animal model, concluded that sire model based estimating procedure for genetic parameters may be preferred when a small number of individuals, little pedigree information and highly disequibrated distribution of effects characterize the data. Also, Soliman *et al.* (1990) with Pinzgauer cows, concluded that the lower h^2 estimates for fat and protein % could be explained on the basis of error components of variance (σ^2_e) and this inflation in σ^2_e could be attributed to the effects of some non genetic factors (e.g., gestation length, preceding dry period.....etc.) such effects were not considered in collecting in the data. In addition, Abdel Salam *et al.* (2001) analysis 2245 lactation records of Holstein Friesian herd of the International Company for Animal Wealth, using animal model, found that h^2 estimates for 305 day milk yield was 0.05 and concluded that the low h^2 estimates may be due to size of the data and natural editing of the data. Also, several factors must be considered for reliable estimation of genetic parameters (Suzuki and Van Vleck, 1994).

Estimates of h^2 for milk traits in single and multiple traits from both two models sire and animal model were near similar (Tables 6 and 7). Similar results were obtained by Kadarmideen *et al.* (2003) worked on Holstein Friesian cows in UK, found that h^2 estimates for milk yield was 0.280 (0.021) and 0.280 (0.020) when using single and multiple traits animal model, respectively. The same authors also, concluded that Multiple –trait analysis

improve accuracy of estimated breeding value (EBV) for each trait evolved by reducing variances of prediction error (PEV) of (EBV).

Genetic correlations between yield traits (Tables 6 and 7) were positive, high and near similar for both two models (sire and animal model) and ranged from 0.882 to 0.999. Estimates of genetic correlation between MY10, FY10 and PY10 were higher than those reported by Hardie *et al.* (1978), Ashmawy and Khalil (1990), Soliman *et al.* (1990), Ahlborn and Dempfle (1992) and Kadarmideen *et al.* (2003) and ranged from 0.68 to 0.89. The present results indicated that selection for high yielding cows would cause a correlated increase in fat and protein yields. In addition, the first three months of milk traits can be good indicators of production in 305 day milk, fat and protein yield. Most of the estimates in the literature (e.g. Soliman *et al.* 1990) showed that the genetic correlations between initial yield traits and 305 day in milk traits were positive and high (< 0.85). Estimates of permanent correlations among milk traits were positive and high and ranged from 0.992 to 1.00 (Table 7). These results suggested that it is important to improve the environmental.

Finally, from the moderate estimate of h^2 for milk traits in a closed herd of Friesian cows, in Egypt by using sire model, reported herein, it can be concluded that genetic improvement of milk yield traits can be achieved through selective breeding. This gives encouragement for Friesian breeders to improve milk traits of their breed through selection (Soliman *et al.*, 1990). Higher estimates of genetic correlation in the present study offer the possibility to select for yield traits as early ages, .i.e., at 90 days of lactation. The using of sire model is useful when, small number of observation and little pedigree information.

REFERENCES

- Abdel-Salam, S. A. M ;El-Said U. M.; Abou-bakr, S and Ibrahim, M. A. M. (2001). Phenotypic and genetic parameters of milk production traits of Holstein commercial herd in Egypt. *Egypt. J. of Anim. Prod.* 38:87-96.
- Ahlborn, G.; Dempfle, L.(1992) Genetic parameters for milk production and body size in New Zealand Holstein-Friesian and Jersey. *Livest. Prod. Sci.*, 31: 205-219.
- Ashmawy, A. A.; Khalil, M.H.(1990) Single and multiple trait selection for lactation in Holstein Friesian cows. *Egypt. J. Anim. Prod.* 27:171-184.
- Atil, H.; Khattab, A. S. (2000) A comparison of different methods of estimating sire transmitting ability of some milk traits in a herd of Holstein Friesian cattle. *Arch. Tierz. Dummerstorf.* 43: 115-122.
- El-Awady, H. G.; El-Arian, M. N.; Khattab, A. S.(2002) Genetic improvement for milk traits of Friesian cows through selection indexes. 53rd Annual Meeting of European of Animal Production. (1-4 Setember, Cairo, Egypt).
- Gacula, M. C.; Gaunt, S. N.; Damon, R. A. (1968) Genetic and environmental parameters of milk constituents for five breeds. II- Some genetic parameters. *J. Dairy Sci.*, 51: 435.

- Gargia- Cortes, L. A.; Moreno, C.; Varona, I.; Rico, M.; Altarriba, L.(1995) (co) variance components estimation of yield traits between different lactations using an animal model. *Livest. Prod. Sci.*, 43: 111-117.
- Groeneveld, E.; Kovac, M.; Wang, T. (1998) PEST User, Manual A software package for multivariate and estimation. Department of Animal Science University of Illinois Germany, pp80.
- Gutierrez, J. P.; Canon, J.; Rico, M.(1995) Comparison of two models for estimation of variance components in a sample of Spanish Holstein Friesian. *J. Anim. Breed. Genet.* 111: 169-174.
- Hardie, A. R.; Jensen, E. L.; Tyler, W. J.(1978) Genetic and economic implications of single trait selection for protein and solids- not fat. *J. Dairy Sci.*, 61: 96.
- Henderson, C. R. (1953) Estimation of variance and covariance components. *Biometrics.* 9: 226-252.
- Kadarmideen, H.N.; Thompson, R.; Coffeny, M. P.; Kossaibati, M. A.(2003) Genetic parameters and evaluation from single and multiple trait analysis of dairy cow fertility and milk production. *Livest. Prod. Sci.*, 75: 213-322.
- Mantysaari , P.; Ojala, M.; Esa, A. Mantysaari (2002) Measures of before and after breeding daily gains of dairy replacements heifers and their relationship with first lactation milk production traits. *Livest. Prod. Sci.*, 75:313-322.
- Misztal, I.; Lawlor, T. J.; Short, T. H. (1994) Implementation of single and multiple trait animal models for genetic evaluation of Holstein type traits. *J. Dairy Sci.*, 76: 1421-1432.
- Mrode, R. A. (1996) Linear models for the prediction of animal breeding values. Animal Data Center Fox Talbot House Green ways Business Park Bellinger Close Chippenham Wits, UK., 184PP.
- SAS. Statistical Analysis System- user's Guide. 2000 Stat, Version 8.2. Cary (NC: SAS Institute Inc.).
- Soliman, I.M.; Khalil, M. H.; Ashmawy, A. A.; Essl, A. (1990) Analysis of milk production traits of Pinzgauer cattle in Austria. *J. Anim. Breed. Genet.*, 107: 43-51.
- Suzuki, M.; Van Vleck,. L. D. (1994) Heritability and repeatability for milk production traits of Japanese Holstein from an animal model. *J. dairy Sci.*, 77: 583:588.

مقارنة بين استخدام نموذج الأب ونموذج الحيوان لتقدير التباينات الوراثية
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استخدم فى هذه الدراسة سجلات 847 بقرة فريزيان لها موسم حليب أو أكثر والتابعة لمحطات البحوث الزراعية بكل من سخا والقرضا التابعين لمعهد بحوث الإنتاج الحيوانى - وزارة الزراعة المصرية خلال الفترة من 1996 - 2002 وذلك لتقدير التباينات والتباينات المشتركة المظهرية والوراثية لصفات إنتاج اللبن عند 3 شهور من بداية موسم الحليب وكذلك عند 305 يوم من نفس الموسم باستخدام نموذج الأب ونموذج الحيوان. فى حالة نموذج الأب استخدمت التأثيرات الثابتة لكل من القطيع- السنة- الموسم ، موسم الحليب - كما استخدمت فى التحليل مدة الأيام المفتوحة كعامل انحدار، بينما استخدم كل من الأب والبقرة كمتغيرات عشوائية. بينما فى حالة نموذج الحيوان استخدمت نفس التأثيرات المستخدمة فى حالة نموذج الأب وأضيف إليها التأثير الوراثى المباشر للحيوان وكذلك التأثير البيئى الدائم كمتغيرات عشوائية. كانت المكافئات الوراثية لصفات إنتاج اللبن المتحصل عليها من نموذج الأب معتدلة القيم وتراوحت ما بين 0.096 إلى 0.276 للصفات الفردية بنما تراوحت نفس القيم ما بين 0.116 إلى 0.264 للصفات المتعددة. فى حين تراوحت المكافئات الوراثية لنفس الصفات باستخدام النموذج الحيوانى ما بين 0.001 إلى 0.031 للصفات الفردية وما بين 0.046 إلى 0.062 للصفات لمتعددة. كانت المكافئات الوراثية لصفات إنتاج اللبن فى حالة الصفات الفردية والصفات المتعددة والمتحصل عليها من كل من نموذج الأب ونموذج الحيوان متقاربة تقريبا. كانت معاملات الارتباط الوراثى بين الصفات المختلفة لإنتاج اللبن موجبة وعالية ومتساوية تقريبا فى حالة استخدام كل من كل من نموذج الأب ونموذج الحيوان وتراوحت ما بين 0.88 إلى 0.99. ومن هذه الدراسة يمكن الاستنتاج أن معاملات الارتباط الوراثى العالية بين الصفات المدروسة تمكن من الانتخاب لتلك الصفات فى عمر مبكر (90 يوم من بداية موسم الحليب) إضافة إلى أن استخدام نموذج الأب لتقدير التباينات الوراثية يمكن الاستفادة منه فى حالة وجد عدد محدود من المشاهدات ومعلومات قليلة عن النسب.

قام بتحكيم البحث

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Table 2: Average of mixed model equation (MME), No. of iterations, CPU-time for solving and for inverting for different Single and Multi-traits studied by using sire and animal model.

Items	Sire Model							Animal Model						
	Traits (STSM)						MTSM	Traits (STAM)						MTAM
	MY3	FY3	PY3	MY10	FY10	PY10		MY3	FY3	PY3	MY10	FY10	PY10	
MME	1474	1474	1474	1474	1474	1474	7370	3058	3058	3058	3058	3058	3058	15290
No. of records	32	33	33	30	37	30	118	30	37	27	34	30	40	103
CPU for solving	0.48	0.58	0.55	0.47	0.53	0.53	2.77	0.53	0.58	0.56	0.52	0.52	0.45	2.64
CPU for inverting	0.00	0.00	0.02	0.02	0.02	0.02	1.69	0.02	0.02	0.02	0.00	0.02	0.02	1.17
AG Log Likelihood	1205	1173	1189	1442	1395	1449	9251	1809	1767	1791	2057	2005	2070	6271

Table 3. Variance components estimates for single traits for sire and animal model

Traits	Sire Model						Animal Model			
	σ^2_s	σ^2_d	σ^2_c	σ^2_e	$h^2s \pm S.E$	$h^2d \pm S.E$	σ^2_a	σ^2_{Pe}	σ^2_e	$h^2a \pm S.E$
MY3	14203	3659	0.00	79747	0.148±0.019	0.584±0.019	2113	14786	79941	0.022±0.055
FY3	17.67	3.50	0.00	124.25	0.096±0.010	0.488±0.018	0.00	19.83	125	0.00±0.00
PY3	9.84	2.72	0.00	62.63	0.144±0.011	0.524±0.018	2.34	9.42	62.83	0.031±0.055
MY10	149775	44496	0.00	519816	0.248±0.015	0.840±0.020	5958	176105	521172	0.008±0.069
FY10	178.76	48.53	0.00	643.90	0.224±0.015	0.820±0.019	0.00	211.43	646.91	0.000±0.000
PY10	106.89	35.92	0.00	376.89	0.276±0.017	0.824±0.020	0.00	132.33	378.49	0.000±0.000

Table 4. Estimation of covariance components for milk traits by using multi-traits sire model

Traits	Sire component					Cow component					Dam component					Residual component				
	MY10	FY10	PY10	MY3	FY3	MY10	FY10	PY10	MY3	FY3	MY10	FY10	PY10	MY3	FY3	MY10	FY10	PY10	MY3	FY3
1	42592	1405	1204	13084	425	138926	4911	3779	41804	1540	12240	304	231	4118	130	518865	19655	13459	140812	4463
2		47	40	428	14		175	134	1455	54		8	6	95	3		641	466	4483	184
3			34	369	12			103	1127	42			5	72	3			377	3549	124
4				4055	13				13138	472				72	4				79059	2581
5					4					472					1					123

Table 5. Estimation of covariance components for milk traits by using multi-traits animal model

Traits	Genetic component					Permanent component					Residual component				
	MY10	FY10	PY10	MY3	FY3	MY10	FY10	PY10	MY3	FY3	MY10	FY10	PY10	MY3	FY3
1	40413	1239	981	14930	552	143546	5053	3947	41061	1441	519447	16975	13483	140969	4472
2		40	31	430	17		178	139	1441	51		643	467	4497	185
3			24	344	13			109	1128	40			378	3564	125
4				6007	202				11800	410				79052	2583
5					8					15					123

Table 6: Heritability estimates from sire , cow and dam component on diagonal and genetic correlations below diagonal among different traits studied byusing multi-traits sire model

Traits	Sire component					Cow component					Dam component				
	MY10	FY10	PY10	MY3	FY3	MY10	FY10	PY10	MY3	FY3	MY10	FY10	PY10	MY3	FY3
1	0.245					0.780					0.068				
2	0.996	0.216				0.997	0.804				0.975	0.036			
3	0.999	0.999	0.264			0.999	0.999	0.796			0.972	1.000	0.036		
4	0.996	0.985	0.991	0.164		0.979	0.961	0.969	0.536		0.961	0.876	0.868	0.060	
5	0.996	0.991	0.998	0.990	0.116	0.988	0.984	0.983	0.983	0.48	0.986	0.999	0.998	0.900	0.040

