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# Estimation of genetic parameters for female fertility traits in the Czech Holstein population

*Michaela Brzáková*, Ludmila Zavadilová, Josef Přibyl, Petr Pešek, Eva Kašná, Anita Kranjčevičová*

*Institute of Animal Science, Prague-Uhříněves, Czech Republic*

**Corresponding author: brzakova.michaela@vuzv.cz*

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**Abstract**: Genetic parameters for fertility traits in Czech Holstein population were estimated. The database obtained from the Czech-Moravian Breeders Corporation with 6 414 486 insemination records between years 2005–2015 was used. Date of calving of the selected animals was taken from the database of milk records from 2005–2015. Fertility traits were age at first service (AFS), age at first calving (AFC), days open (DO), calving interval (CI) and first service to conception interval in cows (FSC-C) and heifers (FSC-H). The heritability of each trait was estimated using single-trait animal models. The model included fixed effects of herd-year-season of birth, herd-year-month of calving, lactation order, parity, last calving ease, linear and quadratic regressions on age at first insemination in heifers or on age at first calving in cows. Random effects were animal, permanent environmental effect and random residual error. After edits, the final data set included up to 599 901 observations from up to 448 037 animals dependent on traits. The range of heritability estimates was from 0.010 to 0.058. The lowest heritability was for first service to conception interval in heifers, and the highest heritability was for age at first service. Variances of random permanent effects were higher than variance of additive genetic effect in all traits manifested in mature cows. Repeatability ranged from 0.060 to 0.090. Genetic correlations between traits were estimated using a bivariate animal model. High positive genetic correlations were found between AFS–AFC, DO–CI, FSC-C–DO and FSC-C–CI. A moderate genetic correlation was found between AFS–FSC-H and between AFC. A negative correlation was found between AFS–FSC-C. Correlations between other traits were close to zero. The results suggest that the level of these reproductive traits can be improved by selection of animals with high genetic merit.

**Keywords**: dairy cattle; fertility; heritability; genetic correlation; heifers; cows

Female fertility is one of the major factors affecting profitability of milk production in dairy cattle. Poor fertility parameters increase the cost of milk production through higher culling rate, costs of fertility treatments, higher number of inseminations and longer calving intervals. A long-term selection for yield traits has led to a decrease in reproductive performance in high-yielding breeds due to a negative genetic correlation between reproduction and milk production traits (Abe et al. 2009; Zink et al. 2012; Yamazaki et al. 2014). The problem was caused by little emphasis on reproductive traits in dairy cattle selection schemes. Currently, dairy breeding programs focus on improving functional and reproductive traits of dairy cows because ignoring fertility reduces the economic profit of a farm (Komlosi et al. 2010). Therefore it is necessary to incorporate fertility traits into selection programs to slow down deterioration or to improve fertility in dairy cattle.

Novel fertility traits have been incorporated into selection schemes over the world in the last

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years. The typical traits often used in breeding programs are calving interval, calving to first service interval, days open, non-return rates, days from first insemination to conception, the number of inseminations per conception, age at first calving and age at first service (Guo et al. 2014). There can be a problem with data recording because in many countries there is no suitable recording program for fertility traits. Days open and calving interval data can be calculated from milk recording data, and the other traits require the result of insemination (Gonzalez-Recio and Alenda 2005).

Currently, in the Czech Republic, the only evaluated fertility trait is conception rate. The result of insemination after 3 months after artificial insemination (AI) is evaluated. This trait has also been a part of Interbull evaluation since 2008. Conception rate records are collected by AI service technicians during insemination and rectal examination for pregnancy. Since 1995, the insemination records have been used in genetic evaluation with a linear model. Prediction of breeding values runs separately for cows and heifers. Breeding values for male (AI bull) and female fertility (inseminated cow/heifer) are predicted. The fertility component has the weight 0.12 in total merit index (SIH) in the Czech Republic (Plemdat 2018 – https://www.cmsch.cz/CMSCH.cz/media/lib_Plemdat/Popis_plodnost_H.pdf). The breeding goal of the Czech Holstein population encompasses age at first calving in the range of 23 to 27 months and calving interval until 400 days. Age at first calving and calving interval are incorporated into the breeding goal but they are not genetically evaluated. Other fertility traits have not been taken into account yet. In spite of the inclusion of fertility traits in total merit index, the level of reproductive traits has still been generally insufficient.

The objective of this study is to estimate genetic parameters for selected cow and heifer fertility traits using a linear animal model in the Czech Holstein population as a step toward the incorporation of novel fertility traits into routine genetic evaluation.

## MATERIAL AND METHODS

***Database description***. The databases of insemination, milk production, calving, and pedigree were obtained from the Czech-Moravian Breeders Corporation. All the databases were collected by technicians from the corporation. The database of inseminations containing 12.816.439 inseminations of all breeds from 1995 to 2015 was used. Data are routinely collected by AI service technicians by rectal examination for pregnancy and used for prediction of breeding values for conception rate in heifers and cows. Only heifers and cows of Holstein breed (75–100%) and data from 2005 to 2015 were used to estimate genetic parameters. After filtering, the data file contained only 6 414 486 inseminations. Date of calving was not presented in this database so the database of milk records performance was provided by the Czech-Moravian Breeders Corporation too and joined to previous data set to complete information. The pedigree information of Holstein cattle was available in one of the databases.

***Studied traits***. The fertility traits were categorized into two groups: "heifer-specific" and "cow-specific". The "heifer-specific" traits included age at first service (AFS) which was defined as the number of days from the birth of heifer to her first service and days from first service to conception for heifers (FSC-H). The "cow-specific" traits included age at first calving (AFC) defined as the number of days from the birth of cow to her first calving, days open (DO) defined as the number of days from calving to conceive, calving interval (CI) defined as the number of days between two successive calvings, and days from the first service to conception for cows (FSC-C).

***Data editing***. For variance components estimations some edits were done. The number of records before and after edit is presented in Table 1. Incomplete data and embryo-transfer donors and recipients were excluded. Only records between 2005 and 2015 were included into the genetic pa-

Table 1. Number of observations before and after edit

| Trait | Records *n* before edit | Animals *n* before edit | Records *n* after edit | Animals *n* after edit |
|---|---|---|---|---|
| AFS | 775 826 | 775 826 | 342 648 | 342 648 |
| AFC | 557 723 | 557 723 | 290 081 | 290 081 |
| FSC-H | 727 009 | 550 233 | 275 886 | 215 456 |
| FSC-C | 1 136 149 | 373 200 | 518 152 | 170 201 |
| DO | 1 102 648 | 565 408 | 599 901 | 307 612 |
| CI | 727 009 | 678 567 | 480 022 | 448 037 |

AFS = age at first service, AFC = age at first calving, FSC-H = days from first service to conception in heifers, FSC-C = days from first service to conception in cows, DO = days open, CI = calving interval rameter estimation. Each trait had another specific editing condition according to extreme values, the number of observations in each herd-year-month/season, the number of sires in each herd-year-month/season, the number of herds in which the bull was used and the number of inseminations per bull to ensure connectedness of records, predictability of effects and to reduce the computational demands (Table 2). Only data in the range of 20–300 days for days open and data in the range of 300–600 days for calving interval were applied. Records from the first 10 lactations were used in the analysis of FSC-C, DO and CI so the number of records is larger than the number of animals. Days from the first service to conception in cows and heifers were evaluated separately because these traits are influenced by different environmental and production conditions. For example, in cows, the fertility is strongly influenced by lactation stage and milk production. After these edits, the pedigree file included 621.454 to 882.287 animals (depending on a trait). A pedigree file containing animals with the observations and five generations of ancestors was created. Animals with unknown parents were assigned to phantom parent groups (created according to year and country of birth).

***Statistical and genetic analysis***. Heritability was calculated as the ratio of additive genetic variance to total phenotypic variance. Repeatability (r) was calculated as

$$r = (\sigma^2_a + \sigma^2_{pe})/\sigma^2_p$$

where:

$\sigma^2_a$ = additive genetic variance

$\sigma^2_{pe}$ = permanent environmental variance

$\sigma^2_p$ = phenotypic variance

Genetic correlations between traits were estimated using a bivariate model for each 2 combinations of traits. Multitrait animal model for all 6 traits was tried but it had a convergence problems. The methods and model equations were the same as the single-trait analyses.

A General Linear Model (GLM) procedure of SAS (Version 9.4, 2013) was used to identify the fixed effects that should be included in the models for genetic parameter estimation. Effects were included with regards to biological importance. All chosen effects were significant ($P < 0.05$).

The linear models for each trait are described below.

The model for AFS and AFC:

$$y = HYSb + Anim + E$$

The model for FSC-H:

$$y = HYSb + \beta_1 Age + \beta_2 Age^2 + Anim + E$$

The model for DO, CI and FSC-C:

$$y = HYSb + HYMc + Lac + CE + \beta_1 Age + \beta_2 Age^2 + Anim + PE + E$$

where:

$y$ = dependent variable

$HYSb$ = fixed effect of herd-year-season of birth

$HYMc$ = fixed effect of herd-year-month of calving

$Lac$ = fixed effect of lactation number

$CE$ = fixed effect of the last calving ease

$\beta_1, \beta_2$ = regression coefficients

$Age, Age^2$ = covariates of linear and quadratic regression of age at first insemination in heifers or on age at first calving in cows

$Anim$ = random direct animal effect

$PE$ = random permanent environmental effect

$E$ = random residual effect

Table 2. Structure and descriptive statistics of input data

| Trait | No. of sires | PED | HYSb | HYMc | Mean (days) | Min (days) | Max (days) | SD (days) |
|---|---|---|---|---|---|---|---|---|
| AFS | 2 468 | 882 287 | 5.837 | | 479.37 | 380 | 800 | 66.88 |
| AFC | 4 363 | 748 543 | 8.851 | | 766.77 | 650 | 1 200 | 74.23 |
| FSC-H | 2 312 | 737 362 | 5.034 | | 23.39 | 0 | 200 | 42.64 |
| FSC-C | 4 385 | 621 454 | 8.989 | 21.733 | 48.54 | 0 | 200 | 56.10 |
| DO | 4 385 | 709 287 | 11.515 | 26.025 | 124.26 | 20 | 300 | 60.20 |
| CI | 5 669 | 698 881 | 14.626 | 33.161 | 400.08 | 300 | 600 | 58.74 |

AFS = age at first service, AFC = age at first calving, FSC-H = days from first service to conception in heifers, FSC-C = days from first service to conception in cows, DO = days open, CI = calving interval, PED = number of animals in pedigree file, HYSb = number of herd-year-seasons of birth, HYMc = number of herd-year-months of calving, Mean = average value, Min = minimum value, Max = maximum value, SD = standard deviation of value

The description of the models in matrix notation are described below.

The model used for univariate and multivariate analyses for AFS, AFC and FSC-H:

$$Y = \mathbf{X}b + \mathbf{Z}a + e$$

where:

$Y$ = vector of observation

$\mathbf{X}$, $\mathbf{Z}$ = incidence matrices of the fixed effects and additive genetic random effects, respectively

$b$ = vector of fixed effects

$a$ = vector of additive genetic effects

$e$ = vector of residual effects

The models for DO, CI and FSC-C are subject to repeated records so the permanent environmental effect was included:

$$Y = \mathbf{X}b + \mathbf{Z}a + \mathbf{W}pe + e$$

where:

$Y$ = vector of observation

$\mathbf{X}$, $\mathbf{Z}$, $\mathbf{W}$ = incidence matrices of the fixed, additive genetic random effects, and permanent environmental effects, respectively

$b$ = vector of fixed effects

$a$ = vector of additive genetic effects

$pe$ = vector of permanent environmental effects

$e$ = vector of residual effects

We assumed that the direct animal effect, permanent environmental effect, and random residual effect follow the multivariate normal distribution with zero mean and the following covariance structure:

$$\mathrm{Var}\begin{Bmatrix} \boldsymbol{pe} \\ \boldsymbol{a} \\ \boldsymbol{e} \end{Bmatrix} = \begin{Bmatrix} \mathbf{I}\otimes\mathbf{P} & 0 & 0 \\ 0 & \mathbf{A}\otimes\mathbf{G} & 0 \\ 0 & 0 & \mathbf{I}\otimes\mathbf{E} \end{Bmatrix}$$

where:

$\boldsymbol{pe}$ = vector of random permanent environmental effects of animals with records

$\boldsymbol{a}$ = vector of additive genetic effects

$\mathbf{I}$ = identity matrix

$\mathbf{P}$ = (co)variance matrix for permanent environmental effects

$\mathbf{A}$ = numerator relationship matrix

$\mathbf{G}$ = (co)variance matrix for additive genetic effects

$\mathbf{E}$ = diagonal matrix of residual variances.

The estimation of variance components was carried out by using the multivariate mixed model program package (DMU) (Madsen and Jensen 2013) with the RJMC (Reversible Jump Markov Chain) module so the single and multiple trait Markov chain Monte Carlo was applied. The number of burn-in rounds was 100 000, the number of sampling rounds was 400 000, and the sampling interval was 100.

## RESULTS AND DISCUSSION

***Descriptive statistics***. Descriptive statistics of all fertility traits are shown in Table 2. The statistics are generally at the similar level compared to other countries although the strict comparison is not simple. The comparison between countries is not simple because the definition of traits and the breeding management may differ between the populations. The mean values for AFS and AFC are lower than those published by Haile-Mariam et al. (2003) but higher than those published by Jagusiak and Zarnecki (2006). The mean values for calving interval and days open reached higher values than reported Haile-Mariam et al. (2003) and Guo et al. (2014). Similar results as in our case were reported by Gonzalez-Recio and Alenda (2005) or Jagusiak and Zarnecki (2006). Longer calving interval is often connected with lower fertility due to undesirable conception rate. Days from first service to conception in heifer and cows have a great range of values and traits are often evaluated together for heifers and cows. In the period between calving and conception there are potential traits which can be evaluated (service period, non-return rate, interval between first and last insemination, number of insemination, etc.) but each trait has a different definition which makes a comparison difficult. Gonzalez-Recio and Alenda (2005) presented mean value of 36 days. Low mean value (16 days) for Canadian Holstein cattle was published by Jamrozik et al. (2005). Haile-Mariam et al. (2003), on the contrary reported higher value of 63 days in Australian Holstein.

***Genetic parameters***. Estimated genetic and non-genetic parameters are presented in Table 3. Genetic correlations are presented in Table 4.

***Age at first service and age at first calving***. AFS and AFC are important traits influencing replacement costs because a heifer is not commonly profitable until the second lactation. Also heifers with early sexual maturity and good fertility are economically advantageous thanks to lower feed consumption in the rearing period and lower labour costs. Synchronization of AFS in a herd

Table 3. Estimated variance (posterior mean ± posterior standard deviation), heritability and repeatability

| Trait | $\sigma^2_G$ | $\sigma^2_{PE}$ | $\sigma^2_E$ | $h^2$ | r |
|---|---|---|---|---|---|
| AFS | 92.32 ± 5.19 | | 1501.87 ± 5.37 | 0.058 | |
| AFC | 114.30 ± 8.93 | | 3556.09 ± 11.69 | 0.031 | |
| DO | 128.39 ± 5.94 | 170.09 ± 7.39 | 3117.43 ± 8.06 | 0.038 | 0.087 |
| CI | 108.91 ± 5.68 | 181.08 ± 8.34 | 2935.45 ± 9.14 | 0.034 | 0.090 |
| FSC-H | 18.14 ± 1.83 | | 1713.57 ± 4.87 | 0.010 | |
| FSC-C | 74.63 ± 4.78 | 104.99 ± 6.76 | 2816.67 ± 7.88 | 0.025 | 0.060 |

$\sigma^2_G$ = genetic variance with standard error, $\sigma^2_{PE}$ = variance of random permanent effect with standard error, $\sigma^2_E$ = residual variance with standard error, $h^2$ = heritability, r = repeatability, AFS = age at first service, AFC = age at first calving, DO = days open, CI = calving interval, FSC-H = days from first service to conception in heifers, FSC-C = days from first service to conception in cows

can also simplify management because the first calving is requested at the age of 24 months. Heritability of AFS in heifers was low. Guo et al. (2014) also reported a low heritability of 0.1 in Chinese Holstein. Jagusiak and Zarnecki (2006) published almost 10-times higher heritability (0.324) in Polish Holstein. De Haer et al (2013) estimated the heritability of 0.23.

AFC is a complex trait which contains information that the female has reached puberty and is able to conceive and deliver a calf (Bormann and Wilson 2010). It is defined as a period that the cow needs to reach maturity and to reproduce for the first time. AFC belongs to simply collected traits because the date of calving is always known. An earlier AFC can reduce rearing costs. Gavan et al. (2014) published that replacement costs decreased by 4.3% when AFC was between 24 and 25 months compared to 18% when AFC was of 21 months. Estimated heritability was of 0.031 in this study but many authors published higher heritabilities like 0.26 (Makgahlela et al. 2008) and 0.3 (Jagusiak and Zarnecki 2006). The low heritabilities of AFS and AFC should be related to a large residual variance; it means the age to get the first insemination varies greatly in this population.

***Days open and calving interval***. The length of CI and DO is strongly influenced by herd management. This is the reason why the heritability is low. Our estimated heritability for DO was of 0.038, which corresponds to heritability 0.03 estimated by Zink et al. (2012) in the first-parity Czech Holstein and VanRaden et al. (2004) who estimated heritability 0.037. Liu et al. (2008) estimated heritability 0.026 using multiple trait models. VanRaden et al. (2004) applied the upper limit of 305 days to DO and they found that the heritability increased as the upper limit decreased. Heritability of 0.053 and 0.056 was reported by Guo et al. (2014) for DO and CI, respectively. Gonzalez-Recio and Alenda (2005) published the heritability of 0.04 for both DO and CI.

The estimated heritability for CI was lower than heritability of 0.09 published by Haile-Mariam et al. (2003). Lower heritabilities (0.01, 0.022, and 0.024) were reported by Pryce et al. (2001), Kadarmideen et al. (2000), and Kadarmideen et al. (2003), respectively. Jagusiak and Zarnecki

Table 4. Estimated genetic correlations between analysed traits (posterior mean ± posterior standard deviation)

| | AFS | AFC | DO | CI | FSC-H | FSC-C |
|---|---|---|---|---|---|---|
| AFS | 1 | | | | | |
| AFC | 0.990 ± 0.0003 | 1 | | | | |
| DO | –0.060 ± 0.0019 | 0.156 ± 0.0019 | 1 | | | |
| CI | –0.129 ± 0.0017 | 0.291 ± 0.0018 | 0.987 ± 0.0003 | 1 | | |
| FSC-H | 0.197 ± 0.0017 | 0.360 ± 0.0017 | 0.008 ± 0.0019 | –0.047 ± 0.0014 | 1 | |
| FSC-C | –0.183 ± 0.0017 | 0.139 ± 0.0018 | 0.990 ± 0.0003 | 0.988 ± 0.0002 | –0.036 ± 0.0013 | 1 |

AFS = age at first service, AFC = age at first calving, DO = days open, CI = calving interval, FSC-H = days from first service to conception in heifers, FSC-C = days from first service to conception in cows

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(2006) presented the heritability of DO for the first, second and third parity of 0.051, 0.045, and 0.043, respectively.

Selection for a shorter calving interval can lead not only to better fertility but also to possible problems with premature calving. This is a reason why DO should be preferable to CI. Moreover, DO have higher heritability and genetic variance then CI and thus higher genetic progress can be expected in subsequent breeding. The same conclusion was drawn by Silva et al. (1992) and Toghiani Pozveh et al. (2009). These authors also claimed that there is a substantial additive genetic variance which can be used in a profitable breeding program. DO can be calculated as CI minus the gestation length. DO and CI are also dependent on pregnancy and successful delivery. Cows had a longer gestation length than heifers (Bahonar et al. 2009; Norman et al. 2009).

DO and CI are both strongly influenced by breeder's decisions based on the milk-production level and management protocol. It complicates selection because the length of DO and CI often depends on time when artificial insemination is performed. Thus the identification of animals with high genetic merit according to breeding values is necessary because the genetic potential for short CI and DO gives an opportunity for farmer to manage the herd in his own way. In high-yielding cows, early pregnancy can negatively influence milk yield, so a lot of farmers postpone first service after calving. To a certain extent these systematic effects of management could be taken into account by the herd-year-season but only in large balanced herds. Generally, the mentioned management practice is the cause of inaccuracies in genetic evaluation for CI or DO.

***Days from the first service to conception in heifers and cows***. FSC-H is defined as the number of days from the first service to conception in heifers and FSC-C as the number of days from the first service to conception in cows. Conception rate traits are commonly considered traits like the interval between the first and last insemination, the number of inseminations per service period or pregnancy within a specific number of days.

In our study we were interested only in the interval from the first service to conception because of data availability. The number of services for a successful conception seems to be hardly evaluatable due to frequent reinseminations occurring in our data. This trait is an indicator of the time that heifer or cow needs to become pregnant after first service. The interval from the first to last (successful) mating or insemination in cows and heifers seems to be a preferable trait for genetic evaluation and breeding. Usually, when a farmer decides to inseminate the cow or heifer, he will be doing it until the cow becomes pregnant (except for medical reasons). So the interval from first service to conception is less influenced by farmer's decision than DO or CI, but less heritable.

The heritabilities for FSC in heifers and cows were low. Liu et al. (2008) presented slightly higher heritability (0.014) for FSC-H, but lower heritability (0.01) for FSC-C. Similar results of 0.01 for cows and 0.012 for heifers were obtained by Zink et al. (2012) and by Kadarmideen et al. (2003), respectively. Lower FSC-H compared to FSC-C was reported previously by Jamrozik et al. (2005) and Kadarmideen et al. (2003). The same author claimed that a loss in pregnancy success at the first insemination could be attributed to the parturition and post-parturition events. Our finding for FSC-C was in agreement with Gonzalez-Recio and Alenda (2005), who published heritability of 0.03.

For all three traits evaluated in mature cows, permanent environmental effect of the cow had higher variance than additive genetic effect. Also Guo et al. (2014) published that repeatability (r) is often higher than heritability. In their study, repeatability was more than once higher than heritability in DO and CI (r was 0.060–0.090). Differences in all estimated variance components for each evaluated trait could be caused by differences in genetic variation between populations or applications of another statistical model.

***Genetic correlations***. Genetic correlations between all traits were estimated. High positive genetic correlations (0.98–0.99) were estimated between AFS–AFC, DO–CI, FSC-C–DO and FSC-C–CI. The genetic correlation between AFS and AFC was very high (0.99), probably because of the same physiological base. Jagusiak and Zarnecki (2006) presented a very high genetic correlation (0.98) between AFC and AFS, too. We found the strong, positive genetic correlation between days open and calving interval. This high genetic correlation is explained by the fact that they represent almost the same overlapping traits which result in the genetic correlation close to 1. The very high genetic correlation (0.99) was published by Jagusiak and Zarnecki (2006) and Gonzalez-Recio and

Alenda (2005). Zaabza et al. (2016) reported a slightly lower genetic correlation (0.81). A strong genetic correlation between FSC-C and DO was reported by Liu et al. (2017) and Ghiasi et al. (2011). A further strong positive correlation was found between the interval between first and last insemination and CI, DO (Gonzalez-Recio and Alenda 2005). In our study FSC-C also had a strong correlation with DO and CI. Strong genetic correlations were not found between FSC-H and DO, and FSC-H and CI. A moderate genetic correlation was found between AFS –FSC-H and between AFC and all fertility traits (expect AFS). Do et al. (2013) published genetic correlations of –0.060 and 0.080 between AFC and first and second CI, respectively. These values were lower than our estimation. Correlations of 0.12 and 0.15 were reported by Jagusiak and Zarnecki (2006) for AFC with CI and DO, respectively. Genetic correlations close to zero were estimated between AFS–DO, FSC-H–DO, FSC-H–CI, and FSC-C–FSC-H. Jagusiak and Zarnecki (2006) reported higher correlation of 0.44 between AFS–DO and correlation of 0.30 between AFS–CI. In our study, the correlation between AFS–CI was slightly negative (–0.13). A negative genetic correlation was also found between AFS–FSC-C. Jamrozik et al. (2005) published a correlation of –0.14 and thus confirmed this finding.

In the Czech Republic, the only evaluated fertility trait is conception rate. There are two separate evaluations for heifers and cows. Evaluation of conception rate (for heifers and cows) is divided into two subgroups (male and female fertility). So the breeding values for bull are estimated for heifers and cows. Herd-year-season of insemination, herd-year-season of birth, insemination order, age at the time of insemination, AI service technician + year of insemination, inseminated heifer (female fertility) and AI bull (male fertility) are included in single trait BLUP-animal model for heifers. For cows, herd-year-season of insemination, herd-year-season of birth, insemination order, age at the time of first calving, lactation order, days in milk (DIM), relative milk yield in first 100 days within herd, AI service technician + year of insemination, inseminated cow (female fertility), AI bull (male fertility) are included in the model. The genetic correlation between the conception rate and evaluated traits in this study is approximately 10%. This correlation is low but it is necessary to include more traits into the genetic evaluation because the current system in not sufficient. Novel traits could bring more possibilities of targeted selection. Fertility is a complex trait including many reproductive and health performances and conception rate defines only one part of it.

## CONCLUSION

Genetic parameters for six fertility traits in the Czech Holstein population were estimated using single and multi-trait animal models in heifers and cows. The heritability and repeatability estimates were generally low. Genetic correlations between traits were estimated using a bivariate model for each 2 combinations of traits. The genetic evaluation and following selection of animals with high genetic merit for fertility traits is the effective way how to improve the level of heifer and cow fertility. Genetic correlations between traits can be helpful in selection of high correlated traits. Additive genetic variance of all traits is sufficient for the effective selection of animals.

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