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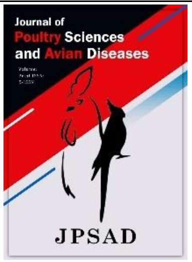

Genetic correlation estimates between direct and maternal genetic effects and estimates of the proportion of maternal permanent environmental variance to phenotypic variance for some important traits in Iranian fowls: A meta-analysis

Sedigheh Gholipour[1], Navid Ghavi Hossein-Zadeh[1*], Abdol Ahad Shadparvar[1], Hassan Darmani Kuhi[1]

[1] Department of Animal Science, Faculty of Agricultural Sciences, University of Guilan, Guilan, Iran

*** Corresponding author email address**: nhosseinzadeh@guilan.ac.ir

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ABSTRACT

Accurate estimation of genetic parameters is essential for setting selection plans in breeding programs. Over the past years, various studies reported the genetic parameters for different growth, reproduction, and egg quality traits in Iranian native fowls. These assessments were obtained using a variety of methods and from studies of different populations of native fowls, leading to significant variation in genetic parameter estimates. This study aimed to perform a meta-analysis based on a random-effects model to overcome the diversity of reported genetic parameters for economically important traits of Iranian native fowls. To summarize these results, a data set of information related to different growth, reproduction, and egg quality traits including 68 estimates of the proportion of maternal environmental variance to phenotypic variance (c^2) and 38 genetic correlation estimates between direct and maternal genetic effects from articles published between 2007 and 2019 were used. Mean estimate of the proportion of maternal environmental variance to phenotypic variance for the studied traits showed that the highest estimate was related to body weight at hatch (0.273) and the lowest was for egg weight at the first day of laying (0.021). Estimation of proportion of maternal environmental variance to phenotypic variance was not significant for EN ($P>0.05$), but for other traits were significant ($P<0.05$). The genetic parameter estimates reported in this meta-analysis study are exploitable in breeding schemes when reliable estimates are not accessible for economically important traits in Iranian native fowls.

Keywords: *Genetic parameters; Growth traits; Iranian native fowls; Systematic review*

1 Introduction

Increasing population along with increasing food demand has increased the demand for protein of animal origin. One of the sources of this protein is poultry products. Low fat, a higher percentage of protein, minerals, vitamins, and better digestibility have increased the desire for chicken more than red meat. Nutritional resources for humans are limited and this has led to many studies and programs to increase the yield of agricultural products, especially livestock products. Native breeds are generally considered

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as valuable genetic resources in any country and are a useful source of protein for rural families due to their adaptation to the method of breeding in unfavorable and open rural conditions. Therefore, preserving these breeds along with planning for their increase and profitability is essential (1). Iran has many potential natural resources, among these resources we can mention the country's native chickens, which after years of natural selection and tolerance of various environmental, today are considered as a national capital and genetic reserve compatible with non-industrial breeding conditions. Native chickens are of great economic importance for breeders in small towns and villages, because things like the lower cost of keeping chickens compared to cattle and sheep farming, the adaptability and resistance of native chickens to adverse biological conditions and disease, creating employment and increasing income. Rural households and the optimal use of unusable waste in rural conditions have made native chickens one of the most important genetic reserves as well as one of the important and easy sources of animal protein, especially in rural conditions.

Before designing any breeding program, extensive studies on the genetic characteristics of economic traits should be done and to improve the average production and growth, the parameters related to these traits should be carefully calculated. Therefore, one of the most effective ways to improve the genetics of these populations in breeding programs and increase the production capacity of the poultry population is to estimate accurately the genetic parameters of economically important traits. Over the past few decades, several studies have been performed to estimate genetic parameters using different statistical methods for different traits of the native fowls in Iran. These studies have variable quality in terms of sample size and sometimes have conflicting results. In individual studies, there is uncertainty about estimates, and the results may have been measured with a specific error which can hurt breeding decisions and programs. Accurate estimation of genetic parameters is necessary to increase the accuracy of breeding value estimates, and one of the effective ways to increase the accuracy of estimates is the use of new and scientific methods such as meta-analysis. Using meta-analysis to integrate results leads to more reliable estimates and declines unnecessary duplication of animal studies (2). In addition, because of the more exploratory nature of animal studies compared to clinical trials, a meta-analysis of animal studies has greater potential for uncovering likely heterogeneity sources (3). It also provides new information that was not possible by analyzing each study individually. Meta-analysis is a methodology that merges different individual and independent results from studies that have a common field and leads to a report with a single result and higher statistical power (4). Because of the variability of the scope of genetic parameter estimates and also the possibility of errors in the literature and published articles, it is necessary to achieve a single range of estimates using meta-analysis, and this single domain will be useful in breeding programs (5).

In a previous study by the same authors, the results of a meta-analysis of heritabilities for economically important traits and their genetic correlations were reported (5). But, this study aimed to conduct a meta-analysis based on a random-effects model to combine different published genetic correlation estimates between direct and maternal genetic effects and the proportion of maternal permanent environmental variance to phenotypic variance for some economic traits in Iranian native fowls. The present results will help the breeders when accurate genetic parameter estimates for different traits are not accessible in Iranian native fowls.

2 Methods and Materials

2.1 *Collecting required information and inclusion criteria*

At first, to find studies related to the research topic, a systematic search of published studies from databases was performed to identify all sources reporting genetic parameter estimates and genetic correlations for growth, reproduction, and egg quality traits in Iranian native fowls; and then, the desired information was extracted from them. Databases used include Research Gate (https://www.researchgate.net), Google Scholar (https://www.scholar.google.com) and SID (https: //www.sid.ir). According to Higgins et al. (2003), the required and appropriate amount of data is one research (6), but some other sources consider at least two studies are sufficient. In addition, publication bias decreases with increasing the number of studies. Also, due to the increase in sample size and consequent reduction in standard error, the accuracy of estimates would be increased (7).

The most comprehensive search was conducted using synonyms and derivatives of the following keywords: meta-analysis, genetic parameters, growth traits, production traits, economically important traits, egg quality traits, components of variance, Iranian native fowls, and reproductive traits.

To summarize the results, a data set of information that related to genetic parameters of different growth, reproduction, and egg quality traits of Iranian native fowls, including 68 estimates of the proportion of maternal environmental variance to phenotypic variance (c^2) and 38 genetic correlation estimates between direct and maternal genetic effects from articles published between 2007 and 2019 were used in the present study.

2.2 Studied traits

The studied traits were grouped as growth traits [body weight at hatch (BW1), body weight at eight weeks of age (BW8), body weight at 12 weeks of age (BW12)], reproductive traits [age at sexual maturity (ASM), weight at sexual maturity (WSM), egg number during the first three months of laying period (EN), mean egg weight at 28th, 30th, and 32nd weeks (MEW), egg weight at the first day of laying (FEW)], and egg quality traits shell weight (SHW)].

2.3 Data editing and preparation

After collecting the required information on genetic parameter estimates for the studied traits, the data were edited and prepared using the Microsoft Excel program. Information required for the analysis included the proportion of maternal environmental variance to phenotypic variance, the correlation between direct and maternal additive genetic effects, and their standard errors. However, the information related to data structure included researcher's characteristics, type of breed, number of years for data collection, number of records, estimation method, model and method of analysis, phenotypic mean, standard deviation, and coefficient of variation. Weighted descriptive statistics were estimated using the data set provided. The methods used to estimate the variance components were restricted maximum likelihood (REML) and Bayesian inference using mixed animal models. Only articles published in valid journals were considered. When the same estimates were published from different articles, only the latest publication information was used in the analysis. In addition, meta-analysis was performed only for traits that had at least two relevant estimates from different articles. Whereas if the standard error for the genetic parameter estimates was not reported, the approximate amount of standard error was estimated by the following formula using the combined-variance method (8):

$$SE_{ij} = \sqrt{\frac{\left(\frac{\sum_{k=1}^{k} s_{ik}^2 n_{ik}^2}{\sum_{k=1}^{k} n_{ik}}\right)}{\acute{n}_{ij}}}$$

where SE_{ij} is the predicted standard error for the published parameter estimate for the i^{th} trait in the j^{th} article that has not reported the standard error, s_{ik} is the published standard error for the parameter estimate for the i^{th} trait in the k^{th} article that has reported the standard error, n_{ik} is the number of used records to predict the published parameter estimate for the i^{th} trait in the k^{th} article that has reported the standard error, and n'_{ij} is the number of used records to predict the published parameter estimate for the i^{th} trait in the j^{th} article that has not reported the standard error.

Most meta-analyses do not use their published correlation estimates because they usually do not have a normal distribution. On the contrary, the published correlation is converted to the Fisher's Z scale, and all analyses are performed using the converted values. Then, the estimated parameter and its confidence interval are converted to correlation for re-presentation(9). The approximate normal scale based on the Fisher's Z scale conversion is as follows (9, 10):

$$Z_{ij} = 0.5\left[1n\left(1 + r_{gij}\right) - 1n\left(1 - r_{gij}\right)\right]$$

The r_{gij} is the correlation published for the i^{th} trait in the j^{th} article. The following equation is also used to return to the original scale (9):

$$r_{gij}^{*} = \frac{e^{2zij} - 1}{e^{2zij} + 1}$$

In this equation, r^*_{gij} is the retransformed genetic correlation for the i^{th} trait in the j^{th} article and Z_{ij} is Fisher Z transformation.

2.4 Estimation of the weighted mean of parameter estimates

In this study, meta-analysis was performed based on a random-effects model using CMA software version 2.2 to calculate the effect size for estimating genetic parameters (9). This software can analyze data using random and fixed-effects models. However, publication bias, effect size summaries, heterogeneity between different studies, forest plots, and funnel plots were drawn using this software.

The following model was used for data analysis:

$$\hat{\theta}_j = \bar{\theta} + u_j + e_j$$

where $\hat{\theta}_j$ is the published parameter estimate in the j^{th} article, $\bar{\theta}$ is the population-weighted mean parameter, u_j is the among study component of the deviation from the mean, assumed as $u_i \sim N(0, \tau^2)$, where τ^2 is the variance representing the amount of heterogeneity among studies, e_j is the within-study component due to sampling error in the parameter estimate in the j^{th} article, assumed as $e_j \sim N(0, \sigma^2_e)$, where σ^2_e is the within-study variance.

The meta-analysis results for each study are summarized and plotted. Overall estimates, the average effect size, and 95% confidence interval are designed in a plot known as a forest plot. In this plot, the horizontal line represents the confidence interval for each study, and the square represents the effect sizes, the size of which is proportional to the inverse variance of the effect size (studied weight) or sample size.

2.5 *Estimation of heterogeneity*

In the present study, I^2 statistic and Q test were used to measure the degree of heterogeneity among studies (9). Changes between study levels and heterogeneity were assessed using the Q test. The smaller the numerical value of Q, there is less heterogeneity between studies. Increasing the numerical value of this statistic indicated an increase in the degree of heterogeneity in the studied populations. Since the Q test is weak in detecting heterogeneity in studies with a small number of studies, so the numerical value of Q was measured with P-value and the significance level was set at 0.10 (11, 12). Higgins et al. (2003) sought to quantify heterogeneity between studies and defined I^2 statistic as a percentage of the heterogeneity that is part of the total variance of the study because it does not depend on the number of studies, unlike the Q statistic. Although, the Q statistic helped to identify heterogeneity, the I^2 statistic was also used to measure heterogeneity as follows (6):

$$I^2(\%) = \frac{Q-(K-1)}{\mathrm{Q}} \times 100$$

where Q is x^2 heterogeneity statistic (Chi-square) and K is the number of studies. Q was actually Cochran's test (Cochran, 1954). The present test was performed to determine the rationale for the assumption that all collected studies estimate an underlying population parameter and that the variability of the study estimates was random. Cochran statistics were as follows:

$$Q = \sum_{j=1}^{k} W_j \left(\widehat{\theta}_j - \bar{\theta}\right)^2$$

where w_j is the parameter estimate weight (assumed as the inverse of published sampling variance for the parameter, $\frac{1}{s_j^2}$) in the j^{th} article; $\widehat{\theta}_j$ and $\bar{\theta}$ were defined above in the random-effects model, and k is the number of used articles.

Negative values of I^2 were considered equal to zero. Therefore, the range of this index was between zero percent (0%) to one hundred percent (100%). When the I^2 statistic is equal to zero, it means that all variability in estimating the effect sizes is due to sampling errors and is a sign that no heterogeneity is observed. The degree of heterogeneity was considered negligible if the I^2statistic was in the range of zero percent (0%) to forty percent (40%). A value of 40% to 60% often indicated moderate heterogeneity, and a value of 60% to 100% was considered significant heterogeneity (6, 12). The 95% lower and upper limits for the estimated parameters were calculated as follows:

$$LL_{\bar{\theta}} = \bar{\theta} - 1.96 \times SE_{\bar{\theta}}$$

$$UL_{\bar{\theta}} = \bar{\theta} + 1.96 \times SE_{\bar{\theta}}$$

and $SE_{\bar{\theta}}$ the predicted standard error for the estimated parameter $\bar{\theta}$ was as follows:

$$SE_{\bar{\theta}} = \sqrt{\frac{1}{\sum_{j=1}^{k} W_j}}$$

2.6 *Determination of publication bias*

Parameter estimates for different traits were examined by Egger’s linear regression test if they were found to be homogeneous, provided there were at least three studies to determine the presence or absence of publication bias. According to this test, for each of the parameters of the studied traits, if the publication bias was detected ($P<0.10$), the trim-and-fill method was used to estimate the number of missing studies, and to correct the final estimate. In this method, initially, the asymmetric part of the funnel plot was removed, which is called trimming. Finally, the filling was performed by replacing the deleted or missing studies with the missing symmetric part. Also, the overall mean estimation and its corresponding variance were calculated. In contrast, funnel plots were used to draw the range of estimates. The use of a funnel plot is a common method for investigating publication bias in studies. In this plot, the effect size is plotted for studies against the standard error of effect size (or other specified indicators). The symmetrical funnel plot indicates the absence of any missing studies.

3 Results

3.1 *Mean proportion of maternal environmental variance to phenotypic variance*

Table 1 presents the mean proportion of maternal environmental variance to phenotypic variance, standard error, 95% confidence interval, Q test, and I^2 statistic to test the heterogeneity of studies. Mean estimate of the proportion of maternal environmental variance to phenotypic variance for the studied traits showed that the highest estimate was related to BW1 (0.273) and the lowest was for FEW (0.021). Estimation of proportion of maternal environmental variance to phenotypic variance was not significant for EN ($P>0.05$), but for other traits were significant ($P<0.05$; Table 1). The value of Q statistic was high for BW1, BW8, BW12, ASM, EN, and MEW. Also, the numerical value of the Q test was significant for these traits ($P<0.10$). In addition, the value of the I^2 statistic for these traits was above 60%, which indicates the significant heterogeneity of these traits. The value of the Q test and I^2 statistic for WSM were 13.287 and 62.369%, respectively, and showed moderate heterogeneity. The value of the Q test for FEW was negligible ($P>0.10$; Table 1). The I^2 statistic for this trait was 0%, which indicates that this trait is homogeneous. Since the FEW was homogeneous, Egger's linear regression test was performed to detect the presence or absence of possible publication bias. The results of this test are presented in Table 2 shows that the P-value for Egger's linear regression test was equal to 0.46, which is greater than 0.10; therefore, the publication bias was not detected for FEW. The trim-and-fill method determined one missing study for this trait (Table 2). According to Figure 1, one study to the right side of the plot was needed to correct the asymmetry of this plot. In this plot, the hollow points were the mean proportion of maternal environmental variance to phenotypic variance for the FEW. Black spots were missing studies that were detected by the trim-and-fill method. The white and hollow diamond represented the mean and confidence interval for existing studies for the FEW. Black diamond indicated the mean and confidence interval of missing studies. A forest plot for the ASM is shown in Figure 2. The estimated effect size along with its 95% confidence interval is presented in this plot.

Table 1. The number of contributing articles (N), Effect size and heterogeneity (I^2 index and Q statistics) of the proportion of maternal environmental variance to phenotypic variance (c^2) (± SE) estimates, and 95% confidence interval for different economically important traits in Iranian native fowls obtained from the random-effects model of meta-analysis.

Trait*	N	c^2	SE	95% CI	P-value	Q	P-value	I^2
BW1	11	0.273	0.026	0.223-0.324	0.000**	1331.907	0.000***	99.249
BW8	13	0.076	0.023	0.031-0.121	0.001**	4309.136	0.000***	99.722
BW12	8	0.032	0.007	0.018-0.046	0.000**	50.87	0.000***	86.24
ASM	10	0.037	0.005	0.027-0.048	0.000**	58.193	0.000***	84.534
WSM	6	0.030	0.005	0.021-0.039	0.000**	13.287	0.021***	62.369
EN	8	0.084	0.067	-0.048-0.215	0.212 (ns)	7017.192	0.000***	99.9
FEW	4	0.021	0.003	0.015-0.027	0.000**	0.897	0.826 (ns)	0
MEW	8	0.029	0.007	0.016-0.043	0.000**	53.129	0.000***	86.825

* BW1, body weight at hatch; BW8, body weight at eight weeks of age; BW12, body weight at 12 weeks of age; ASM, age at sexual maturity; WSM, weight at sexual maturity; EN, egg number during the first three months of laying period; FEW, egg weight at the first day of laying; MEW, mean egg weight at 28th, 30th, and 32nd weeks.

**$P<0.05$.

***$P<0.10$.

^{ns} non-significant ($P>0.05$, $P>0.10$).

Table 2. Results from statistical tests to evaluate publication bias and the trim-and-fill method to correct funnel plot asymmetry in mean proportion of maternal environmental variance to phenotypic variance estimates of that trait did not present heterogeneity.

Trait*	Egger's test p-value	Trim-and-fill method Number of missing	Mean	95% CI
FEW	0.46	1	0.021	0.015-0.027

*For traits, see Table 1.
Missing: Number of missing studies.

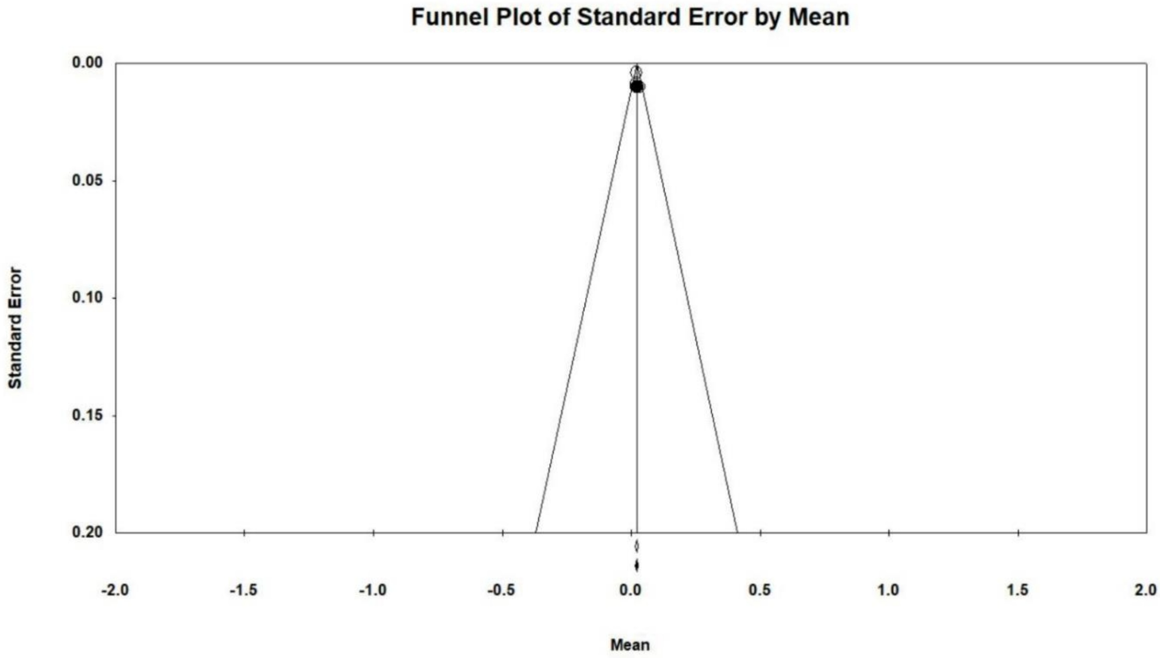
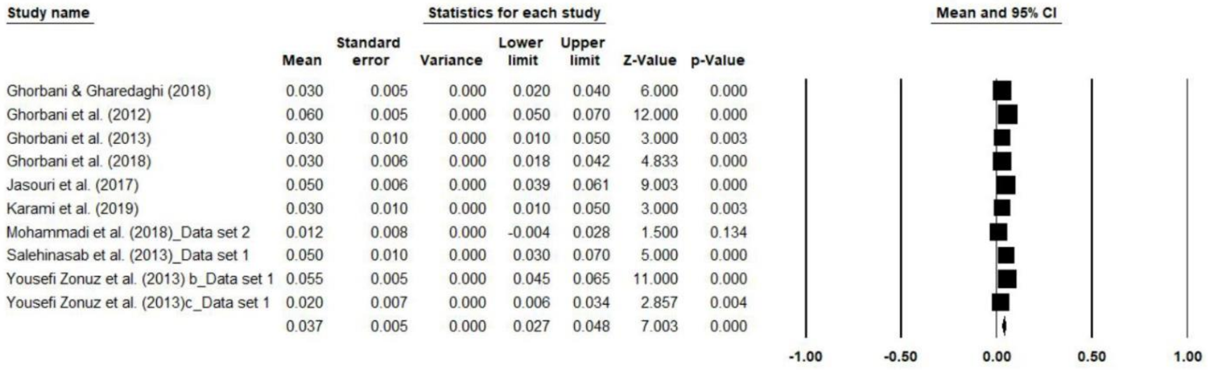


Figure 1. Funnel plot of mean proportion of maternal environmental variance to phenotypic variance estimates for FEW. The solid dots are the potentially missing studies imputed from the trim-and-fill method. The open diamond represents the mean and confidence interval of the existing studies and the solid diamond represents the mean and confidence interval if the theoretically imputed studies were included in the meta-analysis.



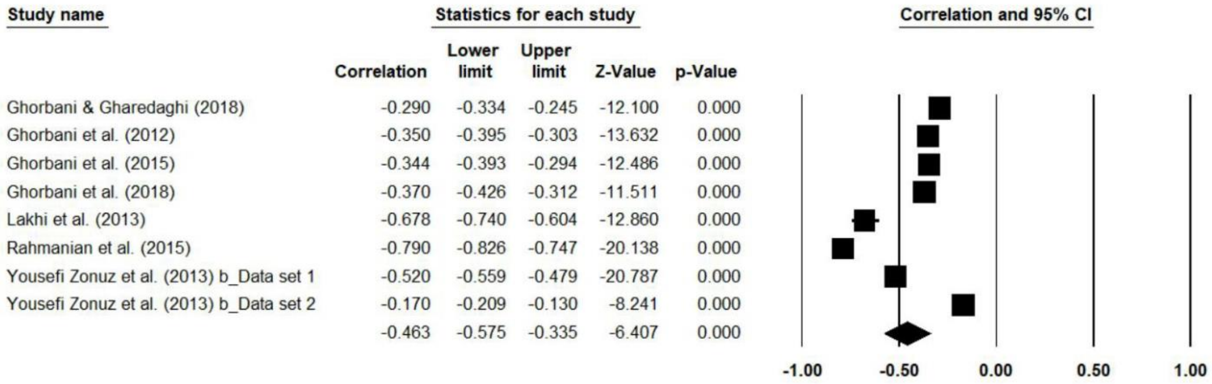
Study name	Mean	Standard error	Variance	Lower limit	Upper limit	Z-Value	p-Value
Ghorbani & Gharedaghi (2018)	0.030	0.005	0.000	0.020	0.040	6.000	0.000
Ghorbani et al. (2012)	0.060	0.005	0.000	0.050	0.070	12.000	0.000
Ghorbani et al. (2013)	0.030	0.010	0.000	0.010	0.050	3.000	0.003
Ghorbani et al. (2018)	0.030	0.006	0.000	0.018	0.042	4.833	0.000
Jasouri et al. (2017)	0.050	0.006	0.000	0.039	0.061	9.003	0.000
Karami et al. (2019)	0.030	0.010	0.000	0.010	0.050	3.000	0.003
Mohammadi et al. (2018)_Data set 2	0.012	0.008	0.000	-0.004	0.028	1.500	0.134
Salehinasab et al. (2013)_Data set 1	0.050	0.010	0.000	0.030	0.070	5.000	0.000
Yousefi Zonuz et al. (2013) b_Data set 1	0.055	0.005	0.000	0.045	0.065	11.000	0.000
Yousefi Zonuz et al. (2013)c_Data set 1	0.020	0.007	0.000	0.006	0.034	2.857	0.004
	0.037	0.005	0.000	0.027	0.048	7.003	0.000

Figure 2. The forest plots of individual studies and the overall outcome for the proportion of maternal environmental variance to phenotypic variance estimates of ASM in Iranian native fowls. The mean effect size, calculated according to a random-effects model, is indicated by the diamond at the bottom of each plot. The size of the squares illustrates the weight of each study relative to the mean effect size. Smaller squares represent less weight. The horizontal bars represent the 95% confidence intervals for the study.

3.2 *Mean estimates of the correlation between direct and maternal additive genetic effects*

Table 3 presents the effect size and mean estimate of the correlation between direct and maternal additive genetic effects, Q test, and I^2 statistic for the studied traits obtained from the random-effects model of meta-analysis. The mean estimate of the correlation between direct and maternal additive genetic effects was negative, moderate, and upward for all studied traits. Also, all correlation estimates were significant ($P<0.05$). Table 3 shows that the numerical values of the Q test for BW8, EN, and FEW were very high and significant, which indicate the existence of heterogeneity in these traits ($P<0.10$). Also, the value of the I^2 statistic for these traits was more than 60%, which indicates significant heterogeneity. In contrast, the values of I^2 statistics for ASM, WSM, and MEW were 40.42%, 0%, and 30.228%, respectively, which showed that the degree of heterogeneity in the WSM was equal to zero. For ASM and MEW, the degrees of heterogeneity were nearly low and negligible. Due to the homogeneity of estimates for these traits, Egger's linear regression test was performed to investigate the presence or absence of possible publication bias. The results of this test and the trim-and-fill test are presented in Table 4. The P-value of Egger's linear regression test for ASM, WSM, and MEW traits was estimated to be 0.049, 0.035, and 0.675, respectively, indicating that there is a publication bias for ASM and WSM. However, no publication bias was observed for MEW ($P>0.10$; Table 3). Figure 3 shows a forest plot for summarizing individual studies of the weighted correlation between direct and maternal additive genetic effects for the BW8.

The mean correlation between direct and maternal additive genetic effects for BW8 is marked with a diamond shape at the bottom of the plot. In this plot, the squares represent the sample size, and the size of the squares indicates the weight of each study relative to the average effect size. Smaller squares show less weight. Horizontal lines represent a 95% confidence interval for each study. Figure 4 shows the funnel plot of the weighted correlation between the direct and maternal additive and genetic effects of MEW. The trim-and-fill method did not detect a missing number of studies for this trait (Table 4). Thus, the funnel plot of the mean correlation between direct and maternal additive genetic effects for MEW is quite symmetric. Based on the trim-and-fill method, the ASM needed four studies and for the WSM, two studies were needed on the right side of the funnel plot to correct the asymmetry of the plot for these traits (results not shown).



Study name	Statistics for each study				
	Correlation	Lower limit	Upper limit	Z-Value	p-Value
Ghorbani & Gharedaghi (2018)	-0.290	-0.334	-0.245	-12.100	0.000
Ghorbani et al. (2012)	-0.350	-0.395	-0.303	-13.632	0.000
Ghorbani et al. (2015)	-0.344	-0.393	-0.294	-12.486	0.000
Ghorbani et al. (2018)	-0.370	-0.426	-0.312	-11.511	0.000
Lakhi et al. (2013)	-0.678	-0.740	-0.604	-12.860	0.000
Rahmanian et al. (2015)	-0.790	-0.826	-0.747	-20.138	0.000
Yousefi Zonuz et al. (2013) b_Data set 1	-0.520	-0.559	-0.479	-20.787	0.000
Yousefi Zonuz et al. (2013) b_Data set 2	-0.170	-0.209	-0.130	-8.241	0.000
	-0.463	-0.575	-0.335	-6.407	0.000

Figure 3. The forest plots of individual studies and the overall outcome for the correlation between direct and maternal additive genetic effects estimates of BW8 in Iranian native fowls. Detailed information is provided in Figure 2.

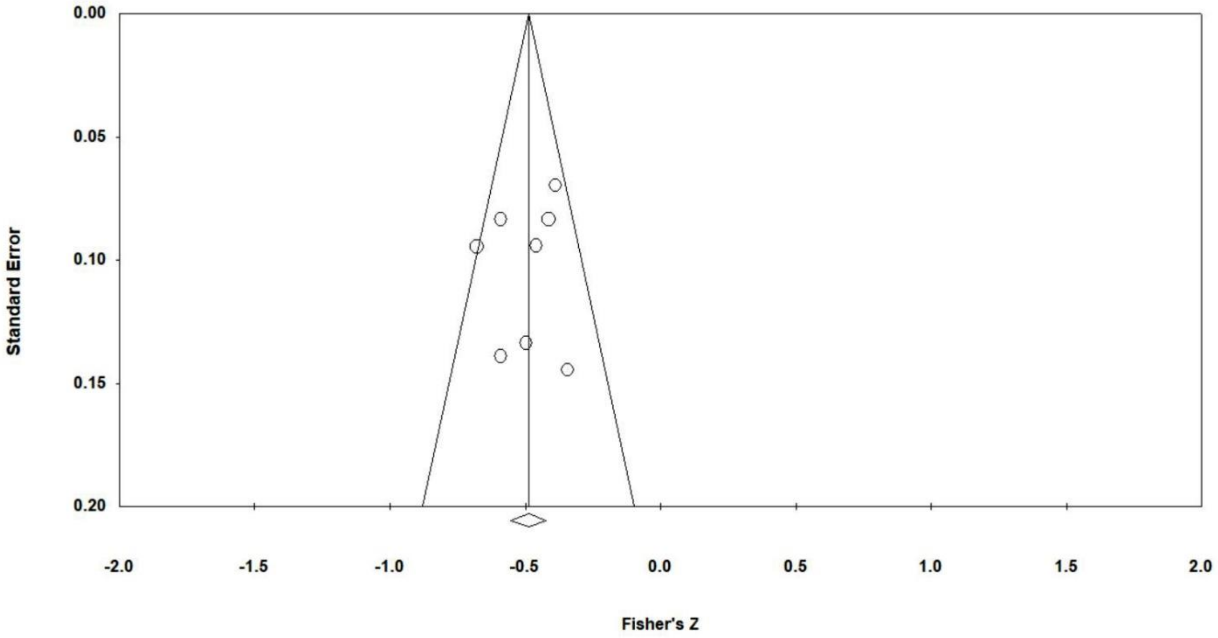


Figure 4. Funnel plot of mean correlation between direct and maternal additive genetic effects estimates for MEW. Detailed information is provided in Figure 1.

Table 3. The number of contributing articles (N), Effect size and heterogeneity (I^2 index and Q statistics) of the correlation between direct and maternal additive genetic effects (r_{am}) estimates, and 95% confidence interval for different economically important traits in Iranian native fowls obtained from the random-effects model of meta-analysis.

Trait*	N	r_{am}	95% CI	P-value	Q	P-value	I^2
BW8	8	-0.463	-0.575- -0.335	0.000**	378.806	0.000***	98.152
ASM	8	-0.543	-0.635- -0.435	0.000**	11.749	0.109 (ns)	40.42
WSM	4	-0.304	-0.461- -0.129	0.001**	2.65	0.449 (ns)	0
EN	7	-0.662	-0.770- -0.517	0.000**	294.531	0.000***	97.963
FEW	3	-0.627	-0.762- -0.440	0.000**	101.442	0.000***	98.028
MEW	8	-0.456	-0.518- -0.389	0.000**	10.041	0.186 (ns)	30.286

*For traits, see Table 1.
**P<0.05.
***P<0.10.
^{ns} non-significant (P>0.05, P>0.10).

Table 4. Results from statistical tests to evaluate publication bias and the trim-and-fill method to correct funnel plot asymmetry in mean the correlation between direct and maternal additive genetic effects estimates of that trait did not present heterogeneity.

Trait*	Egger's test p-value	Trim-and-fill method Number of missing	Mean	95% CI
ASM	0.029	4	-0.445	-0.514- -0.370
WSM	0.035	2	-0.245	-0.405- -0.071
MEW	0.675	0	-0.456	-0.518- -0.389

*For traits, see Table 1.
Missing: Number of missing studies.

4 Discussion

During recent years, discussions on the management of genetic resources of domestic livestock have started globally and these have generally focused on strategies for the preservation of breeds under the risk of extinction (13). The importance of preserving native genetic resources and the use of optimal production methods and new breeding methods play an effective role in increasing the livestock production quality in any country. Therefore, there is an urgent need to provide accurate estimates of genetic parameters. Definition of genetic goals helps us a lot in setting long-term goals, designing breeding programs, a better understanding of the genetic mechanisms of traits, and predicting the expected response from selection programs (14). A review of the literature provides different genetic parameter estimates of the important economic traits in different breeds of Iranian native fowls. The difference between estimates reported in various studies may be due to variations in environmental and managerial conditions, genetic structure differences in the study population, type and size of the study population, and different approaches applied for estimating heritability. Meta-analysis using a random-effect model allows the integration and combination of heritability estimates and correlation for economically important traits. The implementation of meta-analysis based on a random-effects model in the field of animal genetics and breeding mainly originates from the interest of making inferences at the population level (15, 16). Meta-analyses are considered as interesting techniques because they make it possible for us to determine a biological response through empirical modeling from a body of studies. Its outcomes are also useful to build or evaluate mechanistic models (12, 17). Due to their accuracy and precision, the use of meta-analysis models helps us to unravel particular trends and relationships which cannot be found by other methods. Besides, they assist us in testing hypotheses that can never be investigated in individual studies (9).

The results of this meta-analysis showed that correlations between direct and maternal additive genetic effects for all traits were negative. The main reason behind the high negative correlation between direct and maternal additive genetic effects can be found in different factors including lack of concern for maternal effects during the recent years, the intensity of selection based on direct additive genetic value during consecutive generations, better adaptation of species in nature, lower quality of eggshell and possibly incompatibility of statistical models (18, 19). The maternal genetic effect can be defined as the effect of maternal genotype on the studied traits that can affect the offspring's function. A review of the literature suggests that removal of any maternal effects from the model of analysis would lead to overestimation of the direct additive genetic variance and would finally lead to overestimation of the genetic parameters. Thus, considering the maternal effects would contribute to a more accurate estimation of the (co) variance components as well as genetic parameters of fowl's performance traits. Accordingly, making selections based on direct breeding values, without any notice to additive maternal effects, would lead to the reduction of effective maternal potentials for some reproductive traits in the course of each generation. The medium negative correlation estimates between direct and maternal genetic effects for under study traits implied that it would be difficult to improve direct and maternal ability jointly for these traits in native fowls of Iran. The wide confidence interval estimated for genetic correlations between some traits indicates a relatively smaller data set and diversity between studies (5). The repeatability estimate for a given trait would depend on permanent environmental variance, and the permanent environmental effect due to the dam (c^2) can be assigned to maternal environment effects, multiple hatch influences on production performance, feeding level during the late phase of incubation and maternal behavior of the hen. Except for BW1 which had a medium c^2, the low magnitude of permanent environmental effects for other traits indicated that neglecting them in a selection model will bias upwards the other estimates of genetic parameters.

In conclusion, this meta-analysis provided pooled genetic correlation estimates between direct and maternal genetic effects and estimates of the proportion of maternal permanent environmental variance to phenotypic variance for some important traits in Iranian native fowls. Because of the importance of accurate genetic parameter estimates for improving economic traits in the breeding programs, the average genetic parameter estimates reported in this meta-analysis are exploitable in breeding designs when reliable estimates are not available for these in Iranian native fowls.

Conflict of Interest

No potential conflict of interest was reported by the authors.

Authors Contributions

SG participated in the provision of data set, meta-analysis of data and drafted the manuscript. NGHZ designed and conceived this study and contributed to the meta-analysis of data, interpretation of the results and writing of the manuscript. AAS and HDK contributed to the conception of study and writing of the manuscript. All authors read and approved the final manuscript.

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