

Method Article

Selective Breeding Under a Hierarchical Mating using OSBORNE Index Web APP

ABSTRACT

ICT led transmutation of processes and practices is apparent in almost all aspects of human activities. Better egg production techniques are recommended, to satisfy in-house and export demand. Knowledge about a particular breeding technique is required for its perfect implementation. These techniques require a kind of data mining and statistical analysis for mating sires and dams. In the era of 5G, Web Apps can provide better options for providing timely, precise analyzed information to poultry owners or breeders. As per Osborne, the maximum efficiency of egg production can be obtained by selection on the basis of a combination of family average and individual record. This paper proposes a device responsive web app for Osborne Index for hierarchical mating using selective breeding.

Keywords: Selective Breeding, Hierarchical Mating, Osborne Index, Web App, Poultry

1. INTRODUCTION

India is one of the leading producers of poultry meat in the world. The increase in the average income and the urban population has led to a tremendous increase in poultry demand and a steady increase in consumption over the years. In 2022, the consumption of poultry meat in India was found to be over four million metric tons. To meet the growing demand, the poultry population in the country has grown at a rapid pace. In 2003, the poultry and livestock population in India were almost the same but the poultry sector has grown a lot more comparatively ever since. In 2019, the population of poultry in India was over 800 million. This was a 16 percent increase over the last five years [1].

Poultry is one of the fastest-growing segments of the agricultural sector in India today. While the production of crops has been rising at a rate of 1.5 to 2.0 percent per annum, that of eggs and broilers has been rising at a rate of 8.0 to 10.0 percent per annum. As a result, India is now the world's third egg producer in the world (Egg, hen in shell, Source: FAO). The potential in the sector is due to a combination of factors - growth in per capita income, a growing urban population and falling real poultry prices [2].

Lush and Lerner discussed the relative merits of individual selection and family selection in breeding for traits with low heritability. It is well known fact that for traits of low heritability, selection of complete families of full or half-sibs with regard to individual performance is more efficient as compared to selection on the basis of individual phenotypes. For traits with higher heritability, the situation may be reversed, but in all cases, maximum efficiency can be obtained by selection based on combination of family average and individual record. In poultry and other animal populations the family classification is a hierarchical one, consisting of several sires each mated to several dams and each mating producing several offspring [3].

As the size of sire family is quite large as compared to dam family, the selection of progenies on the basis of sire family is easier than the dam family. The pullets should be housed in individual California cages for obtaining individual production records. Combined selection is based on the information of both i.e., the individual phenotype and family averages. The gain expected from combined selection is always higher than those obtained from either mass selection or family selection alone, particularly for low heritable traits like egg production in poultry. The Osborne index selection is type of the combined selection which includes the individual production, dam family average and sire family average for single trait. Hence, it is also called single trait multi source index [3], [4].

In the last few years ICT has flourished and assisted Agricultural domain in each and every stage of crop life cycle [5]– [7]. Even poultry farming is also benefited by ICT and has been a boon for poultry breeders and owners [8]– [11].

The poultry farmers are not acquainted with data mining or statistical analysis and to provide information on few clicks for poultry breeders, a tool is required to generate Osborne index for progenies selection. This paper proposes a web application for generating Osborne index for selection of progenies based on sire family to house pullets in individual California cages.

2. METHODOLOGY

A responsive web-based tool is preferred for the generation of Osborne index, so that poultry breeders can easily generate index. This web application is divided into three layers viz. presentation layer, business layer and data access layer. User interface or presentation layer was developed using Angular, for business layer or server-side code was developed using C Sharp and deployed on IIS server. For data access layer excel file were preferred. The users interact via presentation layer and provide sire's egg collection details in an excel file. For convenience, poultry breeders can maintain data regarding egg collection in an excel file. Calculation of Osborne Index is divided into three stages.

In the first stage of Osborne index generation mean is calculated for sire wise egg details in sheet 1 and in sheet 2 parental relation between sire and dam family. The poultry breeders are supposed provide excel file containing sire wise egg details. Users can select trait from excel file and provide missing values. The system will generate frequency table as per class interval and start range provided for the selected trait. Users can omit unwanted classes and calculate standard Mean for it. Along with standard mean, user also get overall all idea about how data is distributed by Number of observations, Standard Error, Coefficient of variation, Standard Deviation, Min value, and Max value.

The Standard Mean is used as input for generating ANOVA and estimating heritability in the second stage. Heritability is an important genetic parameter used in the fields of breeding that estimates the degree of variation in a trait that is due to genetic variation. Heritability can be calculated by paternal half sib correlation method using the following procedure and is used as one of the important inputs in calculation of Osborne index.

$$\text{Correction term: } (Y_{..})^2 / n.$$

$$\text{Total sum of squares} = \sum_{i,j} Y_{ij}^2 - \frac{(Y_{..})^2}{n}$$

$$\text{Sum of squares (correlated)} = \frac{\sum (Y_{i.})^2}{n_i}$$

$$\sigma_s^2 = MS_S - MS_W / K$$

$$h^2 = \frac{4 \sigma_s^2}{\sigma^2}$$

$$\sigma_s^2 + \sigma_w^2$$

$$\text{Standard error of } h^2: \frac{4 \times \sqrt{\frac{2(n-1)(1-t)^2 [1+(k-1)t]^2}{k^2(n-s)(s-1)}}}{k^2(n-s)(s-1)}$$

Where:

\bar{Y} =Sum of all observations,

N=Number of observations,

$\sum \sum Y^2_{ij}$ =Sum of squares of all observations,
i j

MS_S =Mean square between sire,

MS_W =Mean square within sire,

h^2 =Heritability of sire trait.

Last or third step is for generation of Osborne index. It takes mean and heritability as input and provides Osborne index for all sires and dams. The Osborne index is used to select the individuals to be the parents for next generation based on egg production using below formulas:

$$I(\text{Female})=(P-\bar{P})+W2(Fd-\bar{P})+W3(Fs-\bar{P})$$

$$I(\text{Male})= W2(Fd-\bar{P})+W3(Fs-\bar{P})$$

$$W2=2n(1-h^2)/4+(n-2)h^2$$

$$W3=4n-d(1-h^2)(2-h^2)/[4+(\bar{n}-2)h^2][4+\{\bar{n}(1+d)-2\}h^2]$$

Where:

P = Individual's own performance,

\bar{P} = Flock average,

Fd= Dam family average.

Fs= Sire family average,

n = Number of pullets per dam,

\bar{n} = Average number of pullets per dam,

d = Number of dams per sire,

h^2 = Heritability of the trait under selection.

W2 = Weightage to be given to the dam family averages.

W3 = Weightage to be given to the sire family averages.

3. RESULTS

The three stages or steps required for Osborne index generation are available as menu options in the home page of web application. The user can proceed to each stage after completing the previous one. In case if mean and heritability is available then they can directly select Osborne option from menu.

In first step as stated in methodology for mean calculation upload excel file containing two sheets. Sheet 1 contains details of sire's egg collection whereas second sheet contains parental relation of sire and dam family. Here, one must provide class interval, starting point and omit unwanted data by removing classes of garbage data. This process is shown in Fig. 1 and Fig. 2. After adding selected data from appropriate class intervals, the user clicks on calculate button and gets excel file as output. This Excel file contains selected data, frequency distribution, and in the last sheet Selected Trait, Number of observations, Calculated Mean, Standard Error, Coefficient of variation, Standard Deviation, Min value, and Max value as shown in Fig. 3.

SELECT FIELD TO ANALYZE

WBN
 SIRE
 DAM
 TEN60

Enter class interval

Enter Start Range

Fig. 1 – Select class interval for calculation of mean.

Home Mean Heritability Osborne

TEN60

Remove UnSelect	Class Interval	No	%
<input type="checkbox"/>	<1	0	0
<input type="checkbox"/>	1-10	0	0
<input checked="" type="checkbox"/>	11-20	0	0
<input checked="" type="checkbox"/>	21-30	3	0.274
<input checked="" type="checkbox"/>	31-40	9	0.823
<input checked="" type="checkbox"/>	41-50	33	3.016
<input checked="" type="checkbox"/>	51-60	81	7.404
<input checked="" type="checkbox"/>	61-70	148	13.528
<input checked="" type="checkbox"/>	71-80	228	20.841
<input checked="" type="checkbox"/>	81-90	287	26.234
<input checked="" type="checkbox"/>	91-100	186	17.002
<input checked="" type="checkbox"/>		91	8.318
<input checked="" type="checkbox"/>		25	2.285
<input checked="" type="checkbox"/>	121-130	3	0.274

Fig. 2 - Deselect class interval to exclude data from calculation of mean.

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Individual Mean									
Sr No	Trait	Obs	Mean	SE	CV%	SD	Min	Max	
1	TEN40	1094	80.872	0.494	0.202	16.329	27	124	

Fig. 3 – Selected Trait, Number of observations, Calculated Mean, Standard Error, Coefficient of variation, Standard Deviation, Min value, and Max value.

In the second step estimated heritability can be derived. To derive heritability, ANOVA is the generated. Fig. 4 shows output of second step. In the third step the Osborne index is calculated and Fig. 5 shows that it requires folk average and estimated heritability as input. In Fig. 6 and 7 show Osborne index for sire and dam.

Poultry Research Station,AAU,Anand				
ANOVA				
Source	d.f	SS	MS	CAL F
Bet Sire	119	45101.73	379.006	1.49803
Within Sire	976	246931.3	253.003	
Total	1095	292033		

Estimate of heritability	
Comp	Value
MSs	379.006
MSw	253.003
h ² s	0.207
SE	0.081

Fig. 4 – ANOVA and estimated Heritability

Upload Excel File For OSB

Choose File: filed.m.xlsx

WBN
 SIRE
 DAM
 TEN40

Upload

Fig. 5 – Select trait and provide mean and heritability for generation of Osborne index.

Poultry Research Station,AAU,Anand												
WBN	SIRE	DAM	TEN40	FD	FS	N	AVEN	D	W2	W3	OSBTEN40	
3005	69	273	96	83.5	79.286	2	3.5	4	0.793	2.563	13.147	
3010	69	275	69	87	79.286	3	3.5	4	1.131	2.563	-9.006	
3011	69	275	89	87	79.286	3	3.5	4	1.131	2.563	10.994	
3014	69	275	103	87	79.286	3	3.5	4	1.131	2.563	24.994	
3019	69	276	80	72.75	79.286	8	3.5	4	2.42	2.563	-24.592	
3020	69	276	66	72.75	79.286	8	3.5	4	2.42	2.563	-38.592	
3023	70	278	73	84.5	84.375	4	2	4	1.437	2.011	4.386	
3040	71	283	118	86.4	81.286	5	3.5	2	1.716	1.604	47.278	
3041	71	283	71	86.4	81.286	5	3.5	2	1.716	1.604	0.278	
3042	71	284	70	68.5	81.286	2	3.5	2	0.793	1.604	-20.019	
3048	72	286	72	72	75.5	1	1.5	4	0.418	1.704	-21.734	
3358	99	393	98	89.5	78.5	2	2	2	0.793	1.178	21.176	
3377	101	401	99	88.5	84.125	6	2.667	3	1.971	1.898	39.337	
3379	101	401	81	88.5	84.125	6	2.667	3	1.971	1.898	21.337	
3382	101	401	92	88.5	84.125	6	2.667	3	1.971	1.898	32.337	
3396	103	410	83	87.857	78.267	7	7.5	2	2.205	2.014	12.283	
3421	105	418	100	83.714	80.316	7	4.75	4	2.205	2.782	23.848	
3423	105	418	54	83.714	80.316	7	4.75	4	2.205	2.782	-22.152	
3424	105	419	86	78.5	80.316	2	4.75	4	0.793	2.782	1.7	
3429	105	420	82	73.833	80.316	6	4.75	4	1.971	2.782	-14.293	
3430	105	420	97	73.833	80.316	6	4.75	4	1.971	2.782	0.707	
3454	108	429	66	66	74.222	1	2.25	4	0.418	2.136	-35.293	
3459	108	430	56	75.6	74.222	5	2.25	4	1.716	2.136	-48.123	
3466	109	433	58	80.571	80.625	7	4	2	2.205	1.698	-23.955	
3469	109	433	80	80.571	80.625	7	4	2	2.205	1.698	-1.955	

Fig. 6 – Osborne index for Sire in last column for trait TEN40 OSBTEN40 and for Dam OSBM in second sheet.

SIRE	DAM	MWBN	OSBM
1	1	4004	-4.133
1	3	4010	
2	5	4015	
2	5	4016	
2	8	4022	-5.931
3	9	4029	10.379
4	14	4040	-23.312
6	23	4062	-68.549
9	35	4084	-24.052
11	44	4106	-57.466
13	52	4129	-9.992
14	55	4148	10.865
16	63	4176	10.824
16	63	4177	10.824
16	63	4181	10.824
18	69	4188	-20.442
19	76	4206	-0.673
21	81	4221	-25.106
21	81	4232	-25.106
23	90	4246	9.745
23	90	4249	9.745
23	90	4251	9.745
23	92	4257	21.241
24	94	4260	-2.516
24	94	4261	-2.516
24	94	4264	-2.516
24	96	4273	23.807
25	98	4278	12.262

Fig. 7 – Osborne index for Dam OSBM in second sheet.

4. CONCLUSION

Developing a web application for Osborne index generation offers significant vantage for poultry and poultry breeders. Firstly, it provides unparalleled accessibility and convenience, allowing generation of Osborne index from anywhere with an internet, intranet or extranet on any device i.e. from desktop pc to smart mobile. This eliminates the need for or investing money for computer, its management and installation of software everywhere.

For poultry breeders this tool is a boon as it performs several operations instantly for deriving Osborne index for selection of progenies on the basis of sire family to house pullets in individual California cages for better egg production.

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