Mathematics Model of Inheritance Three Different Traits in Genetics with Matrix Approach

Jufra*, Asrul Sani, Sardin
Department of Mathematics, Halu Oleo University
* Corresponding Author. E-mail: jufra.uho@gmail.com

ARTICLE INFO	ABSTRACT
	Mathematical models can solve problems to find out which individuals are superior from crosses in the field of genetics. The matrix form of the mathematical model using the concept of matrix diagonalization can solve these problems. The general definition of matrix diagonalization is $D = P^{-1}AP$ with the diagonalized matrix elements obtained from the probability of crossing the average parent and the recessive parent. The mathematical model of a cross between the average parent and recessive parent can be formulated as $x^n = Ax^{n-1}$. The behavior of the solution from the cross is in the form of an explicit equation which can be formulated as $x^n = A^n x^0 = P^{-1}D^n P x^0$. From the calculation results, it is found that in the nth generation, where the limit for n goes to infinity, all offspring from crossing normal parents with offspring with genotypes are normal genotypes. In contrast, all offspring from crossing recessive parents with offspring with genotypes are heterozygous.

INTRODUCTION

The decline of hereditary traits has a molecular basis, that is, the exact replication of Deoxyribonucleic Acid (DNA) and produces copies of genes that can be passed on from the parent to the offspring (Campbell, 2002). A single gene governs many traits in plants, animals, and microbes. Genes in diploid individuals are allele pairs and each of their offspring. The inheritance of a trait that can be known from parents to offspring genetically is called heredity. This inheritance law follows an orderly pattern and repeats itself from generation to generation (Crowder, 2007). The development of genetic science is characterized by discovering genes and chromosomes, which subsequently develop towards molecular genetics. The discovery of recombinant DNA opened up the development of genetic engineering. In gene therapy efforts, genetic engineering technology provides hope in various fields such as the pharmaceutical industry, health, society and humanity, agriculture, and law (Nusantari, 2018).

Crossbreeding is the mating between genetically different individuals or populations to produce a combination of traits from the parent or the recombination of genes in the offspring. Crosses can occur between individuals of different species and individuals within a single species, commonly known as crosses between strains or accessions (Alianto & Huda, 2008). With the crossing, we can get new seeds of good quality because of the combination of traits and can also give rise to new types due to the crossing of the two different traits or

individuals of their nature. For example, to increase the production of string beans, it is necessary to use high-yielding varieties. The results of crosses between genotypes of long beans can be seen through the diversity observed in the offspring generation. The results of crosses between different groups show that there is diversity between the results of crossing (Sa'diyah, et al., 2013). The problem of knowing which individuals are superior to the results of crossing arises in biology. Mathematical models can solve these problems by bringing existing mathematical models into matrix form with the concept of matrix diagonalization.

Mathematical modeling is a field of mathematics used to represent and explain physical systems or problems into mathematical statements. The mathematical representation resulting from this process is known as a mathematical model. Forming, analyzing, and using mathematical models is one of the mathematics applications that can represent life problems into mathematical statements (Haryanto, et al., 2015). Mathematical models can be equations, inequalities, or even matrix models. Applying linear algebra solves many problems in and outside the field of mathematics. Matrices are one example of the use of mathematics that can facilitate analyzing biological problems, especially in genetics (Yuliani & Mashuri, 2012).

Studying genetics will not be separated from the nature of heredity. These hereditary traits are found in the genotype, which is the form or genetic arrangement of a character that an individual contains. In the concept of classical genetics, Mendel found traits in plants following some simple mathematical calculations known as "Mendel's Law of Inheritance."Therefore, mathematics is one of the sciences very much related to the science of genetics that can determine the type of genotype of the offspring linked in chromosomes (Syafwan & Nurwati, 2015). A matrix diagonalization analysis can be carried out to find an individual superior from several generations by continuously crossing individuals. The matrix used is derived from the parent genotype opportunity table. From such analysis can be known the traits that appear in individuals within a generation (Nurmia, et al., 2017).

Research on applying matrix diagonalization to investigate trait inheritance has already been carried out. For example, a study conducted by (Jusriani, 2018) under the title "Application of Matrix Diagonalization to the Determination of the Chances of the Nth Generation Genotype."In the study, the results of the chances of heredity from all crosses would be average Homozygous. The case study in the study is to take two different properties. Furthermore, a similar study has been carried out (Salmiati, 2016) titled "Application of Matrix Diagonalization in Genotype Inheritance in Nth Generation with Two Different Traits."In the study, the distribution of genotypes produced in nth-generation offspring on dihybrid-controlled crossing was that all of them would have genotypes (average). In the previous two studies, the application of matrix diagonalization to determine the probability of Nth generation genotypes only took 2 different properties. The result showed that genotypic distribution in nth generation offspring over dihybrid controlled crosses that would all have is AABB genotypes. Unlike previous studies that only took two different traits (dihybrid), this study took three different traits (trihybrid) in genetics with a matrix approach.

Based on the thoughts above, the problem in this study is how the mathematical and behavioral models solve the inheritance of three different traits in genetics with matrix equality. The aim is to obtain a mathematical model and complete the inheritance of trihybrid in genetics with a matrix approach.

METHOD

The research method used in this n research is a literature method, a study or activity to collect information relevant to the topic or problem that is the object of the study. Information in this whitish study is obtained from books and journals.

Research Procedure

The procedure for this study is as follows:

1) Make a cross between large seeds with a smooth texture and round shape (AABBCC) and small seeds with a wrinkled texture and elongated shape (aabbcc) so that the first offspring will be obtained first Filial (F_1) is large seeds with a smooth texture and round shape (AaBbCc). Further, make an intermediate cross AaBbCc and AaBbCc so will be obtained a second Filial (F_2)

2) Conducting a reverse cross between possible offspring the entire set of possible combinations of these alleles AA,Aa,BB,Bb,CC,Cc (AoBoCo) and parental parents (AABBCC and aabbcc).

3) Formed a table of genotype opportunities from the results of reverse crossing between offspring AoBoCo and parental parents (AABBCC and aabbcc)

4) Forms a linear equation from the table of chances based on the genotype of the selected parent.

5) We are forming equations in matrix notation in such a way that a matrix is obtained with the elements present on the matrix according to the table of opportunities of each genotype.

6) Determines the matrix's eigenvalues and the eigenvectors corresponding to the eigen values.

7) Forming a matrix P of eigenic vectors thenn determines the inverse of the matrix P .
8) Furthermore, the matrix t can be diagnosed i so that it cannot form an explicit equation and look for the limit value of the explicit equation.
9) Perform numerical simulations for the parental crossover of broods (AABBCC and aabbcc) with typed offspring AoBoCo .
10) Conclude from the results of such studies.

RESULTS AND DISCUSSION

The Probability of Crossover Genotypes 3 Different Traits

Table 1. *Punnet-Square Crosses of 3 Different Traits*

Gamet	ABC	ABc	AbC	aBC	Abc	aBc	abC	abc
ABC	AABBCC	AABBCc	AABbCC	AaBBCC	AABbCc	AaBBCc	AaBbCC	AaBbCc
ABc	AABBCc	AABBcc	AABbCc	AaBBCc	AABbcc	AaBBcc	AaBbCc	AaBbcc
AbC	AABbCC	AABbCc	AAbbCC	AaBbCC	AAbbCc	AaBbCc	AabbCC	AabbCc
aBC	AaBBCC	AaBBCc	AaBbCC	aaBBCC	AaBbCc	aaBBCc	aaBbCC	aaBbCc
Abc	AABbCc	AABbcc	AAbbCc	AaBbCc	AAbbcc	AaBbcc	AabbCc	Aabbcc
aBc	AaBBCc	AaBBcc	AaBbCc	aaBBCc	AaBbcc	aaBBcc	aaBbCc	aaBbcc
abC	AaBbCC	AaBbCc	AabbCC	aaBbCC	AabbCc	aaBbCc	aabbCC	aabbCc
abc	AaBbCc	AaBbcc	AabbCc	aaBbCc	Aabbcc	aaBbcc	aabbCc	aabbcc

Based on the eight crosses above shows the crossing and the possibilities of the resulting offspring. Furthermore, it will present the chances of a possible genotype in offspring for the entire possible combination of the parent's genotype based on the crossover results.

From the matrix above, the inverse of the matrix can be determined with the help of Software Maple 13, and then the matrix is obtained as follows.

Mathematical Models with Matrix Approach

$$P = \begin{bmatrix} 1 & -1 & -1 & -1 & 1 & 1 & 1 & -1 \\ 0 & 1 & 0 & 0 & -1 & -1 & 0 & 1 \\ 0 & 0 & 1 & 0 & -1 & 0 & -1 & 1 \\ 0 & 0 & 0 & 1 & 0 & -1 & -1 & 1 \\ 0 & 0 & 0 & 0 & 1 & 0 & 0 & -1 \\ 0 & 0 & 0 & 0 & 0 & 1 & 0 & -1 \\ 0 & 0 & 0 & 0 & 0 & 0 & 1 & -1 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 \end{bmatrix}$$

From the matrix P above, the inverse of the matrix P can be determined with the help of Maple 13 Software, and then the matrix is obtained as follows :

$$P^{-1} = \begin{bmatrix} 1 & 1 & 1 & 1 & 1 & 1 & 1 & 1 \\ 0 & 1 & 0 & 0 & 1 & 1 & 0 & 1 \\ 0 & 0 & 1 & 0 & 1 & 0 & 1 & 1 \\ 0 & 0 & 0 & 1 & 0 & 1 & 1 & 1 \\ 0 & 0 & 0 & 0 & 1 & 0 & 0 & 1 \\ 0 & 0 & 0 & 0 & 0 & 1 & 0 & 1 \\ 0 & 0 & 0 & 0 & 0 & 0 & 1 & 1 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 \end{bmatrix}$$

Because the matrix P has such an inverse that it $P^{-1}AP$ is a diagonal matrix so that, $D = P^{-1}AP$

$$D = \begin{bmatrix} 1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 1/2 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 1/2 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 1/2 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 1/4 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 1/4 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 1/4 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1/8 \end{bmatrix}$$

Based on the equation $x^n = A^n x^0$, then it can be obtained

$$x^n = A^n x^0$$
$$= PD^n P^{-1} x^0 \tag{1}$$

$$
\begin{bmatrix} a_n \\ b_n \\ c_n \\ d_n \\ e_n \\ f_n \\ g_n \\ h_n \end{bmatrix} =
\begin{bmatrix}
1 & -1 & -1 & -1 & 1 & 1 & 1 & -1 \\
0 & 1 & 0 & 0 & -1 & -1 & 0 & 1 \\
0 & 0 & 1 & 0 & -1 & 0 & -1 & 1 \\
0 & 0 & 0 & 1 & 0 & -1 & -1 & 1 \\
0 & 0 & 0 & 0 & 1 & 0 & 0 & -1 \\
0 & 0 & 0 & 0 & 0 & 1 & 0 & -1 \\
0 & 0 & 0 & 0 & 0 & 0 & 1 & -1 \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 1
\end{bmatrix}
\begin{bmatrix}
(1)^n & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & (1/2)^n & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & (1/2)^n & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & (1/2)^n & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & (1/4)^n & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & (1/4)^n & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & (1/4)^n & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & (1/8)^n
\end{bmatrix}
$$

$$
\begin{bmatrix}
1 & 1 & 1 & 1 & 1 & 1 & 1 & 1 \\
0 & 1 & 0 & 0 & 1 & 1 & 0 & 1 \\
0 & 0 & 1 & 0 & 1 & 0 & 1 & 1 \\
0 & 0 & 0 & 1 & 0 & 1 & 1 & 1 \\
0 & 0 & 0 & 0 & 1 & 0 & 0 & 1 \\
0 & 0 & 0 & 0 & 0 & 1 & 0 & 1 \\
0 & 0 & 0 & 0 & 0 & 0 & 1 & 1 \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 1
\end{bmatrix}
\begin{bmatrix} a_0 \\ b_0 \\ c_0 \\ d_0 \\ e_0 \\ f_0 \\ g_0 \\ h_0 \end{bmatrix}
$$

By using Maple 13 Software, the Equation System formed :

$$a_n = a_0 + \left(1 - \left(\frac{1}{2}\right)^n\right) b_0 + \left(1 - \left(\frac{1}{2}\right)^n\right) c_0 + \left(1 - \left(\frac{1}{2}\right)^n\right) d_0 + \left(1 - 2\left(\frac{1}{2}\right)^n + \left(\frac{1}{4}\right)^n\right) e_0$$
$$+ \left(1 - 2\left(\frac{1}{2}\right)^n + \left(\frac{1}{4}\right)^n\right) f_0 + \left(1 - 2\left(\frac{1}{2}\right)^n + \left(\frac{1}{4}\right)^n\right) g_0 + \left(1 - 3\left(\frac{1}{2}\right)^n + 3\left(\frac{1}{4}\right)^n - \left(\frac{1}{8}\right)^n\right) h_0$$

$$b_n = \left(\frac{1}{2}\right)^n b_0 + \left(\left(\frac{1}{2}\right)^n - \left(\frac{1}{4}\right)^n\right) e_0 + \left(\left(\frac{1}{2}\right)^n - \left(\frac{1}{4}\right)^n\right) f_0 + \left(\left(\frac{1}{2}\right)^n - 2\left(\frac{1}{4}\right)^n + \left(\frac{1}{8}\right)^n\right) h_0$$

$$c_n = \left(\frac{1}{2}\right)^n c_0 + \left(\left(\frac{1}{2}\right)^n - \left(\frac{1}{4}\right)^n\right) e_0 + \left(\left(\frac{1}{2}\right)^n - \left(\frac{1}{4}\right)^n\right) g_0 + \left(\left(\frac{1}{2}\right)^n - 2\left(\frac{1}{4}\right)^n + \left(\frac{1}{8}\right)^n\right) h_0$$

$$d_n = \left(\frac{1}{2}\right)^n d_0 + \left(\left(\frac{1}{2}\right)^n - \left(\frac{1}{4}\right)^n\right) f_0 + \left(\left(\frac{1}{2}\right)^n - \left(\frac{1}{4}\right)^n\right) g_0 + \left(\left(\frac{1}{2}\right)^n - 2\left(\frac{1}{4}\right)^n + \left(\frac{1}{8}\right)^n\right) h_0$$

$$e_n = \left(\frac{1}{4}\right)^n e_0 + \left(\left(\frac{1}{4}\right)^n - \left(\frac{1}{8}\right)^n\right) h_0$$

$$f_n = \left(\frac{1}{4}\right)^n f_0 + \left(\left(\frac{1}{4}\right)^n - \left(\frac{1}{8}\right)^n\right) h_0$$

$$g_n = \left(\frac{1}{4}\right)^n g_0 + \left(\left(\frac{1}{4}\right)^n - \left(\frac{1}{8}\right)^n\right) h_0$$

$$h_n = \left(\frac{1}{8}\right)^n h_0 \qquad \text{where n = 1,2, ...} \tag{2}$$

Equations (1) is an explicit equation for the probability of all eight genotypes in the n-th generation in terms of the probability of the initial genotype. Because $\left(\frac{1}{2}\right)^n$ it tends to approach 0 towards n the infinite, the limit of the equation above is as follows.

$$\lim_{n\to\infty} a_n = \lim_{n\to\infty} \left(a_0 + \left(1 - \left(\frac{1}{2}\right)^n\right) b_0 + \left(1 - \left(\frac{1}{2}\right)^n\right) c_0 + \left(1 - \left(\frac{1}{2}\right)^n\right) d_0 + \left(1 - 2\left(\frac{1}{2}\right)^n + \left(\frac{1}{4}\right)^n\right) e_0 \right.$$
$$\left. + \left(1 - 2\left(\frac{1}{2}\right)^n + \left(\frac{1}{4}\right)^n\right) f_0 + \left(1 - 2\left(\frac{1}{2}\right)^n + \left(\frac{1}{4}\right)^n\right) g_0 + \left(1 - 3\left(\frac{1}{2}\right)^n + 3\left(\frac{1}{4}\right)^n - \left(\frac{1}{8}\right)^n\right) h_0 \right)$$
$$= a_0 + b_0 + c_0 + d_0 + e_0 + f_0 + g_0 + h_0 = 1$$

$$\lim_{n\to\infty} b_n = \lim_{n\to\infty} \left(\left(\frac{1}{2}\right)^n b_0 + \left(\left(\frac{1}{2}\right)^n - \left(\frac{1}{4}\right)^n\right) e_0 + \left(\left(\frac{1}{2}\right)^n - \left(\frac{1}{4}\right)^n\right) f_0 + \left(\left(\frac{1}{2}\right)^n - 2\left(\frac{1}{4}\right)^n + \left(\frac{1}{8}\right)^n\right) h_0 \right) = 0$$

$$\lim_{n\to\infty} c_n = \lim_{n\to\infty} \left(\left(\frac{1}{2}\right)^n c_0 + \left(\left(\frac{1}{2}\right)^n - \left(\frac{1}{4}\right)^n\right) e_0 + \left(\left(\frac{1}{2}\right)^n - \left(\frac{1}{4}\right)^n\right) g_0 + \left(\left(\frac{1}{2}\right)^n - 2\left(\frac{1}{4}\right)^n + \left(\frac{1}{8}\right)^n\right) h_0 \right) = 0$$

$$\lim_{n\to\infty} d_n = \lim_{n\to\infty} \left(\left(\frac{1}{2}\right)^n d_0 + \left(\left(\frac{1}{2}\right)^n - \left(\frac{1}{4}\right)^n\right) f_0 + \left(\left(\frac{1}{2}\right)^n - \left(\frac{1}{4}\right)^n\right) g_0 + \left(\left(\frac{1}{2}\right)^n - 2\left(\frac{1}{4}\right)^n + \left(\frac{1}{8}\right)^n\right) h_0 \right) = 0$$

$$\lim_{n\to\infty} e_n = \lim_{n\to\infty} \left(\left(\frac{1}{4}\right)^n e_0 + \left(\left(\frac{1}{4}\right)^n - \left(\frac{1}{8}\right)^n\right) h_0 \right) = 0$$

$$\lim_{n\to\infty} f_n = \lim_{n\to\infty}\left(\left(\frac{1}{4}\right)^n f_0 + \left(\left(\frac{1}{4}\right)^n - \left(\frac{1}{8}\right)^n\right)h_0\right) = 0$$

$$\lim_{n\to\infty} g_n = \lim_{n\to\infty}\left(\left(\frac{1}{4}\right)^n g_0 + \left(\left(\frac{1}{4}\right)^n - \left(\frac{1}{8}\right)^n\right)h_0\right) = 0$$

$$\lim_{n\to\infty} h_n = \lim_{n\to\infty}\left(\left(\frac{1}{8}\right)^n h_0\right) = 0 \qquad \text{where n = 1,2, ...} \tag{3}$$

So the chances of hereditary genotypes n going to infinity are obtained, namely:
$a_n = a_0 + b_0 + c_0 + d_0 + e_0 + f_0 + g_0 + h_0 = 1$
$b_n = c_n = d_n = e_n = f_n = g_n = h_n = 0$
From the approach of the limit above to n go towards infinity obtained the value $a_n = 1$ and $b_n = 0$ $c_n = 0$, , $d_n = 0$, $e_0 = 0$, $f_0 = 0$, $g_0 = 0$, $h_0 = 0$, so that at that limit all descendants in the population will have a genotype AABBCC

Numerical Analysis
Numerical Analysis For Crossing and AABBCCAoBoCo
In AABBCC and AoBoCo crosses, numerical analysis can be performed by taking $n = 1, 2, ... ,30$.

Tabel 2. AABBCC and AoBoCo Genotype Illustration Results

n	a_n	b_n	c_n	d_n	e_n	f_n	g_n	h_n
1	0,5787037	0,1157407	0,1157407	0,1157407	0,0231481	0,0231481	0,0231481	0,0046296
2	0,7702546	0,0700231	0,0700231	0,0700231	0,0063657	0,0063657	0,0063657	0,000578
3	0,880136	0,0382668	0,0382668	0,0382668	0.0016638	0.0016638	0.0016638	0,0000723
4	0,938793	0,0199743	0,0199743	0,0199743	0,000425	0,000425	0,000425	0,000009
5	0,9690744	0,0102008	0,0102008	0,0102008	0,0001074	0,0001074	0,0001074	0,0000011
6	0,9844562	0,0051542	0,0051542	0,0051542	0,000027	0,000027	0,000027	0,0000001
7	0,9922078	0.0025906	0.0025906	0.0025906	0.0000068	0.0000068	0.0000068	0
8	0,9960988	0.0012987	0.0012987	0.0012987	0.0000017	0.0000017	0.0000017	0
9	0,9980481	0.0006502	0.0006502	0.0006502	0.0000004	0.0000004	0.0000004	0
10	0,9990238	0.0003253	0.0003253	0.0003253	0.0000001	0.0000001	0.0000001	0
11	0,9995118	0.0001627	0.0001627	0.0001627	0	0	0	0
12	0,9997559	0.0000814	0.0000814	0.0000814	0	0	0	0
13	0,9998779	0.0000407	0.0000407	0.0000407	0	0	0	0
14	0,999939	0.000203	0.000203	0.000203	0	0	0	0
15	0,9999695	0.0000102	0.0000102	0.0000102	0	0	0	0
16	0,9999847	0.0000051	0.0000051	0.0000051	0	0	0	0
17	0,9999924	0.0000025	0.0000025	0.0000025	0	0	0	0
18	0,9999964	0.0000013	0.0000013	0.0000013	0	0	0	0
19	0,9999962	0.0000006	0.0000006	0.0000006	0	0	0	0
20	0,999999	0.0000003	0.0000003	0.0000003	0	0	0	0
21	0,9999995	0.0000002	0.0000002	0.0000002	0	0	0	0
22	0,9999998	0	0	0	0	0	0	0
22	0,9999998	0	0	0	0	0	0	0
23	0,9999999	0	0	0	0	0	0	0
24	0,9999999	0	0	0	0	0	0	0
25	1	0	0	0	0	0	0	0
26	1	0	0	0	0	0	0	0
27	1	0	0	0	0	0	0	0

n	a_n	b_n	c_n	d_n	e_n	f_n	g_n	h_n
28	1	0	0	0	0	0	0	0
29	1	0	0	0	0	0	0	0
30	1	0	0	0	0	0	0	0

Table 2 shows that if it is approached with $n = 1, 2, …, 30$, then for a_n, it will close the value of 1 in the 25th to nth generation, it will be AABBCC genotype. For b_n, c_n and d_n in the 22nd generation to the nth generation, there were no more descendants with the genotype AABBCc, AABbCC, and AaBBCC. For e_n, f_n and g_n in the 11th generation to the nth generation, there were no more offspring with genotypes AABbCc, AaBBCc and AaBbCC. For h_n, in the 7th generation to the nth generation, there ara no more descendants of the AaBbCc genotypes.

Implementations for Table 2 show that in the first generation to a_n is as large 0,5787037 or 57% , the second generation is obtained a_n is as large 0,7702546 or 77%, and the third generation a_n is as large 0,880136 or 88%. The fourth generation is obtained a_n as large 0,938793 or 93%. So, the crossing AABBCC and AoBoCo in the fourth generation have already reached the level of trust 93%. This shows that superior offspring can be obtained by making four crosses, namely typed offspring with a AABBCC level of trust 93%. More details of the crossing and AABBCCAoBoCo can beseen in Figure 1. Following
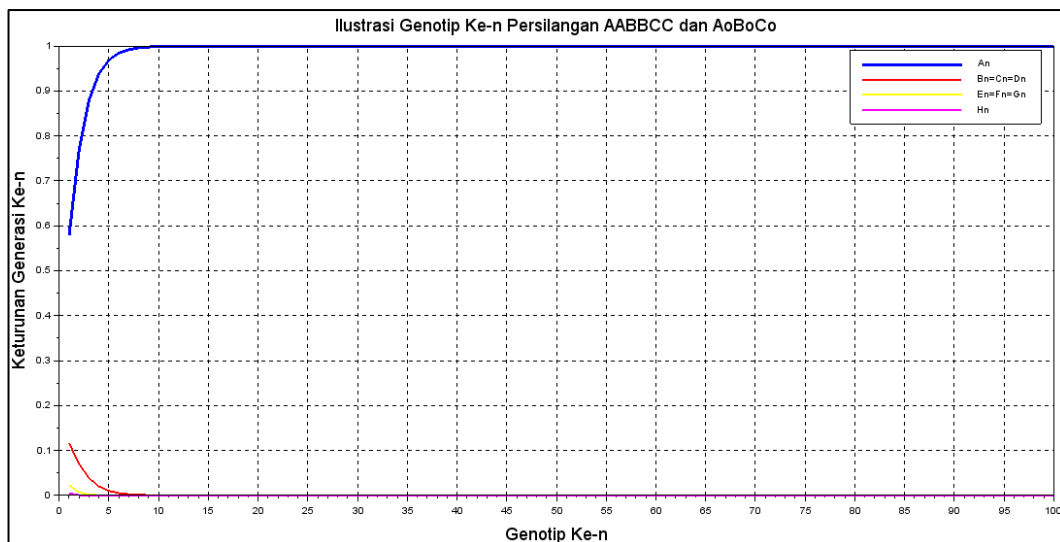

Figure 1. Illustration of the nth genotype Cross of aabbcc and AoBoCo

Figure 1 above shows that a_n will be stable or convergent at numbers 1 to infinity. This figure shows that the offspring of the AABBCC genotype will always exist in each iteration. Thus the genotype of the cross between AABBCC and AoBoCo in the nth generation will produce offspring with the AABBCC genotype (a_n). Meanwhile, $b_n, c_n, d_n, e_n, f_n, g_n, h_n$ will be stable from 0 to infinity. This figure shows offspring with genotypes AABBCc, AABbCC, AaBBCC, AABbCc, AaBBCc, AaBbCC, and AaBbCc will not appear in every iteration. This indicates that the AABBCC crosses with AoBoCo in the nth generation there are no more descendants of AABBCc, AABbCC, AaBBCC, AABbCc, AaBBCc, AaBbCC, AaBbCc. So it can be concluded that the inheritance of traits from crosses between AABBCC and AoBoCo in the nth generation will produce offspring with the AABBCC genotype (normal homozygous).

Numerical Analysis For Crossing aabbbcc and AoBoCo

In aabbcc and AoBoCo crosses, numerical analysis can be performed by taking $n = 1, 2, …, 30$. So the illustration can be seen in the table below.

Tabl*e* 3. Genotype Illustration Results of Crossing aabbcc and AoBoCo

n	a_n	b_n	c_n	d_n	e_n	f_n	g_n	h_n
1	0,5787037	0,1157407	0,1157407	0,0231481	0,1157407	0,0231481	0,0231481	0,015625
2	0,7702546	0,0700231	0,0700231	0,0063657	0,0700231	0,0063657	0,0063657	0,0019531
3	0,880136	0,0382668	0,0382668	0.0016638	0,0382668	0.0016638	0.0016638	0,0002441
4	0,938793	0,0199743	0,0199743	0,000425	0,0199743	0,000425	0,000425	0,0000305
5	0,9690744	0,0102008	0,0102008	0,0001074	0,0102008	0,0001074	0,0001074	0,0000038
6	0,9844562	0,0051542	0,0051542	0,000027	0,0051542	0,000027	0,000027	0,0000005
7	0,9922078	0.0025906	0.0025906	0.0000068	0.0025906	0.0000068	0.0000068	0
8	0,9960988	0.0012987	0.0012987	0.0000017	0.0012987	0.0000017	0.0000017	0
9	0,9980481	0.0006502	0.0006502	0.0000004	0.0006502	0.0000004	0.0000004	0
10	0,9990238	0.0003253	0.0003253	0.0000001	0.0003253	0.0000001	0.0000001	0
11	0,9995118	0.0001627	0.0001627	0	0.0001627	0	0	0
12	0,9997559	0.0000814	0.0000814	0	0.0000814	0	0	0
13	0,9998779	0.0000407	0.0000407	0	0.0000407	0	0	0
14	0,999939	0.000203	0.000203	0	0.000203	0	0	0
15	0,9999695	0.0000102	0.0000102	0	0.0000102	0	0	0
16	0,9999847	0.0000051	0.0000051	0	0.0000051	0	0	0
17	0,9999924	0.0000025	0.0000025	0	0.0000025	0	0	0
18	0,9999964	0.0000013	0.0000013	0	0.0000013	0	0	0
19	0,9999962	0.0000006	0.0000006	0	0.0000006	0	0	0
20	0,999999	0.0000003	0.0000003	0	0.0000003	0	0	0
21	0,9999995	0.0000002	0.0000002	0	0.0000002	0	0	0
22	0,9999998	0	0	0	0	0	0	0
22	0,9999998	0	0	0	0	0	0	0
23	0,9999999	0	0	0	0	0	0	0
24	0,9999999	0	0	0	0	0	0	0
25	1	0	0	0	0	0	0	0
26	1	0	0	0	0	0	0	0
27	1	0	0	0	0	0	0	0
28	1	0	0	0	0	0	0	0
29	1	0	0	0	0	0	0	0
30	1	0	0	0	0	0	0	0

Table 3 shows that if approached with $n = 1, 2, …, 30,$, then for a_n, it will close the value 1 in the 25th to nth generation, it will have the genotype AaBbCc. For b_n, c_n and e_n in the 22nd generation to the nth generation, there are no more descendants with genotypes AaBbcc, Aabbcc, and aaBbCc. For d_n, f_n and g_n in the 11th generation to the nth generation, there are no more descendants with genotypes Aabbcc, aaBbcc, and aaBbCc. For h_n, in the 7th generation to the nth generation, there are no more descendants of the aabbcc genotype.

The implementation for Table 3 can be seen that in the first generation for a_n of 0.5787037 or 57%, in the second generation a_n of 0.7702546 or 77% is obtained, in the third generation a_n is obtained of 0.880136 or 88%, in the fourth generation, it is obtained a_n of 0.938793 or 93%. So it shows that the cross between AABBCC and AoBoCo in the fourth generation has reached a 93% confidence level. This indicates that by doing four crosses, superior offspring can be obtained, namely offspring with the AABBCC genotype with a confidence level of 93%. For more details, the cross between AABBCC and AoBoCo can be seen in Figure 2 below.
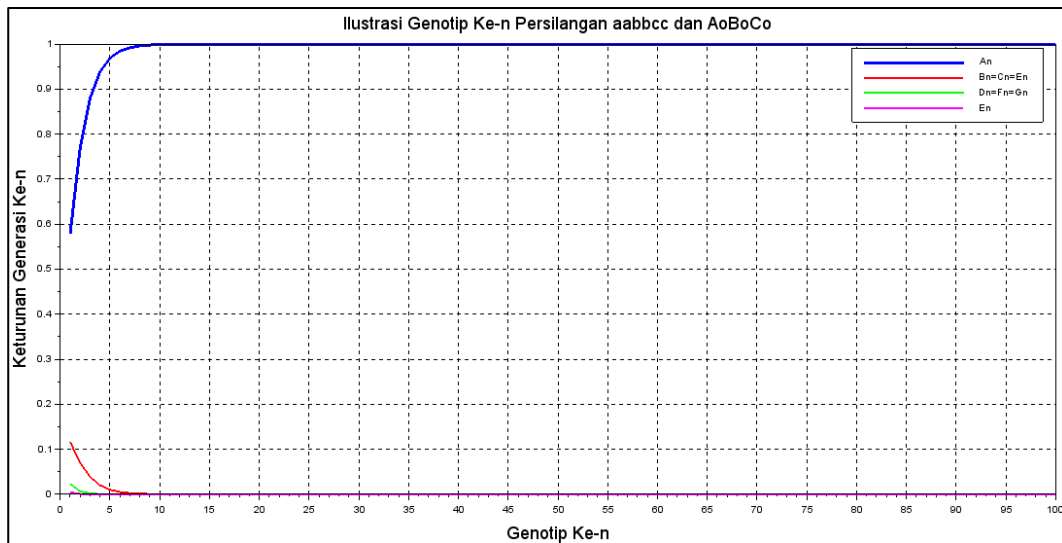
Figure 2. Illustration of the nth genotype Cross of aabbcc and AoBoCo

Figure 2 above shows that a_n will be stable or convergent at numbers 1 to infinity. This figure shows that the offspring of the AaBbCc genotype will always exist in every iteration. Thus, the genotype of a cross between aabbcc and AoBoCo in the nth generation will produce offspring with the genotype of AaBbCc. Meanwhile, $b_n, c_n, d_n, e_n, f_n, g_n, h_n$, and h_n will be stable from 0 to infinity. This figure shows the offspring with genotype AaBbcc, AabbCc, Aabbcc, aaBbCc, aaBbcc, aabbCc, and aabbcc will not appear in every iteration. This indicates that in aabbcc crosses with AoBoCo in the nth generation, there are no more descendants of AaBbcc, AabbCc, Aabbcc, aaBbCc, aaBbcc, aabbCc, aabbcc. Produce offspring with the AaBbCc genotype (normal heterozygous).

CONCLUSION

The following conclusions can be obtained based on the discussion and analysis in the previous chapter.

1. Inheritance of traits with three distinct characteristics meets the Linear Equation. In general, the formulation of the distribution of genotypes is as follows.

$x^n = Ax^{n-1}$,   n = 1,2,3, …

Where table 4.2 can be made in the form of a matrix model, namely:

$$x^n = \begin{bmatrix} a_n \\ b_n \\ c_n \\ d_n \\ e_n \\ f_n \\ g_n \\ h_n \end{bmatrix}, x^{n-1} = \begin{bmatrix} a_{n-1} \\ b_{n-1} \\ c_{n-1} \\ d_{n-1} \\ e_{n-1} \\ f_{n-1} \\ g_{n-1} \\ h_{n-1} \end{bmatrix}, A = \begin{bmatrix} 1 & 1/2 & 1/2 & 1/2 & 1/4 & 1/4 & 1/4 & 1/8 \\ 0 & 1/2 & 0 & 0 & 1/4 & 1/4 & 0 & 1/8 \\ 0 & 0 & 1/2 & 0 & 1/4 & 0 & 1/4 & 1/8 \\ 0 & 0 & 0 & 1/2 & 0 & 1/4 & 1/4 & 1/8 \\ 0 & 0 & 0 & 0 & 1/4 & 0 & 0 & 1/8 \\ 0 & 0 & 0 & 0 & 0 & 1/4 & 0 & 1/8 \\ 0 & 0 & 0 & 0 & 0 & 0 & 1/4 & 1/8 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1/8 \end{bmatrix}$$

Where table 4.3 can be made a matrix model, that is.

$$x^n = \begin{bmatrix} a_n \\ b_n \\ c_n \\ d_n \\ e_n \\ f_n \\ g_n \\ h_n \end{bmatrix}, x^{n-1} = \begin{bmatrix} a_{n-1} \\ b_{n-1} \\ c_{n-1} \\ d_{n-1} \\ e_{n-1} \\ f_{n-1} \\ g_{n-1} \\ h_{n-1} \end{bmatrix}, A = \begin{bmatrix} 1 & 1/2 & 1/2 & 1/4 & 1/2 & 1/4 & 1/4 & 1/8 \\ 0 & 1/2 & 0 & 1/4 & 0 & 1/4 & 0 & 1/8 \\ 0 & 0 & 1/2 & 1/4 & 0 & 0 & 1/4 & 1/8 \\ 0 & 0 & 0 & 1/4 & 0 & 0 & 0 & 1/8 \\ 0 & 0 & 0 & 0 & 1/2 & 1/4 & 1/4 & 1/8 \\ 0 & 0 & 0 & 0 & 0 & 1/4 & 0 & 1/8 \\ 0 & 0 & 0 & 0 & 0 & 0 & 1/4 & 1/8 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1/8 \end{bmatrix}$$

The finished behavior of the result of the crossover is in the form of an explicit equation formulated as follows.

$x^n = A^n x^0 = P^{-1} D^n P x^0$ where $n = 1, 2, 3, …$

with,

$$D^n = \begin{bmatrix} \lambda_1 & 0 & \cdots & 0 \\ 0 & \lambda_2 & \cdots & 0 \\ 0 & 0 & \ddots & 0 \\ 0 & 0 & \cdots & \lambda_k \end{bmatrix}^n = \begin{bmatrix} \lambda_1{}^n & 0 & \cdots & 0 \\ 0 & \lambda_2{}^n & \cdots & 0 \\ 0 & 0 & \ddots & 0 \\ 0 & 0 & \cdots & \lambda_k{}^n \end{bmatrix}$$

2. The explicit equations for the fractions of the eight genotypes in the nth generation of backcrosses between AABBCC and AoBoCo are as follows.

$$a_n = a_0 + \left(1 - \left(\frac{1}{2}\right)^n\right)b_0 + \left(1 - \left(\frac{1}{2}\right)^n\right)c_0 + \left(1 - \left(\frac{1}{2}\right)^n\right)d_0 + \left(1 - 2\left(\frac{1}{2}\right)^n + \left(\frac{1}{4}\right)^n\right)e_0$$
$$+ \left(1 - 2\left(\frac{1}{2}\right)^n + \left(\frac{1}{4}\right)^n\right)f_0 + \left(1 - 2\left(\frac{1}{2}\right)^n + \left(\frac{1}{4}\right)^n\right)g_0$$
$$+ \left(1 - 3\left(\frac{1}{2}\right)^n + 3\left(\frac{1}{4}\right)^n - \left(\frac{1}{8}\right)^n\right)h_0$$

$$b_n = \left(\frac{1}{2}\right)^n b_0 + \left(\left(\frac{1}{2}\right)^n - \left(\frac{1}{4}\right)^n\right)e_0 + \left(\left(\frac{1}{2}\right)^n - \left(\frac{1}{4}\right)^n\right)f_0 + \left(\left(\frac{1}{2}\right)^n - 2\left(\frac{1}{4}\right)^n + \left(\frac{1}{8}\right)^n\right)h_0$$

$$c_n = \left(\frac{1}{2}\right)^n c_0 + \left(\left(\frac{1}{2}\right)^n - \left(\frac{1}{4}\right)^n\right)e_0 + \left(\left(\frac{1}{2}\right)^n - \left(\frac{1}{4}\right)^n\right)g_0 + \left(\left(\frac{1}{2}\right)^n - 2\left(\frac{1}{4}\right)^n + \left(\frac{1}{8}\right)^n\right)h_0$$

$$d_n = \left(\frac{1}{2}\right)^n d_0 + \left(\left(\frac{1}{2}\right)^n - \left(\frac{1}{4}\right)^n\right)f_0 + \left(\left(\frac{1}{2}\right)^n - \left(\frac{1}{4}\right)^n\right)g_0 + \left(\left(\frac{1}{2}\right)^n - 2\left(\frac{1}{4}\right)^n + \left(\frac{1}{8}\right)^n\right)h_0$$

$$e_n = \left(\frac{1}{4}\right)^n e_0 + \left(\left(\frac{1}{4}\right)^n - \left(\frac{1}{8}\right)^n\right)h_0$$

$$f_n = \left(\frac{1}{4}\right)^n f_0 + \left(\left(\frac{1}{4}\right)^n - \left(\frac{1}{8}\right)^n\right)h_0$$

$$g_n = \left(\frac{1}{4}\right)^n g_0 + \left(\left(\frac{1}{4}\right)^n - \left(\frac{1}{8}\right)^n\right)h_0$$

$$h_n = \left(\frac{1}{8}\right)^n h_0 \qquad\qquad \text{where n} = 1,2,\dots$$

If the above explicit equation is approximated by the limit for $\left(\frac{1}{2}\right)^n$ and tends to approach 0 for n towards infinity $n \rightarrow \infty$ then the limit of the above equation is as follows.

$a_n = a_0 + b_0 + c_0 + d_0 + e_0 + f_0 + g_0 + h_0 = 1$
$b_n = c_n = d_n = e_n = f_n = g_n = h_n = 0$

From the approach of the limit above to n go towards infinity obtained the value $a_n = 1$ dan $b_n = 0$, $c_n = 0$, $d_n = 0$, $e_0 = 0$, $f_0 = 0$, $g_0 = 0$, $h_0 = 0$, so that at that limit all descendants in the population will have a genotype AABBCC

3. The explicit equations for the fractions of the eight genotypes in the nth generation of backcrosses between AABBCC and AoBoCo are as follows.

$$a_n = a_0 + \left(1 - \left(\frac{1}{2}\right)^n\right)b_0 + \left(1 - \left(\frac{1}{2}\right)^n\right)c_0 + \left(1 - 2\left(\frac{1}{2}\right)^n + \left(\frac{1}{4}\right)^n\right)d_0 + \left(1 - \left(\frac{1}{2}\right)^n\right)e_0$$
$$+ \left(1 - 2\left(\frac{1}{2}\right)^n + \left(\frac{1}{4}\right)^n\right)f_0 + \left(1 - 2\left(\frac{1}{2}\right)^n + \left(\frac{1}{4}\right)^n\right)g_0$$
$$+ \left(1 - 3\left(\frac{1}{2}\right)^n + 3\left(\frac{1}{4}\right)^n - \left(\frac{1}{8}\right)^n\right)h_0$$

$$b_n = \left(\frac{1}{2}\right)^n b_0 + \left(\left(\frac{1}{2}\right)^n - \left(\frac{1}{4}\right)^n\right)d_0 + \left(\left(\frac{1}{2}\right)^n - \left(\frac{1}{4}\right)^n\right)f_0 + \left(\left(\frac{1}{2}\right)^n - 2\left(\frac{1}{4}\right)^n + \left(\frac{1}{8}\right)^n\right)h_0$$

$$c_n = \left(\frac{1}{2}\right)^n c_0 + \left(\left(\frac{1}{2}\right)^n - \left(\frac{1}{4}\right)^n\right)d_0 + \left(\left(\frac{1}{2}\right)^n - \left(\frac{1}{4}\right)^n\right)g_0 + \left(\left(\frac{1}{2}\right)^n - 2\left(\frac{1}{4}\right)^n + \left(\frac{1}{8}\right)^n\right)h_0$$

$$d_n = \left(\frac{1}{4}\right)^n d_0 + \left(\left(\frac{1}{4}\right)^n - \left(\frac{1}{8}\right)^n\right)h_0$$

$$e_n = \left(\frac{1}{2}\right)^n e_0 + \left(\left(\frac{1}{2}\right)^n - \left(\frac{1}{4}\right)^n\right)f_0 + \left(\left(\frac{1}{2}\right)^n - \left(\frac{1}{4}\right)^n\right)g_0 + \left(\left(\frac{1}{2}\right)^n - 2\left(\frac{1}{4}\right)^n + \left(\frac{1}{8}\right)^n\right)h_0$$

$$f_n = \left(\frac{1}{4}\right)^n f_0 + \left(\left(\frac{1}{4}\right)^n - \left(\frac{1}{8}\right)^n\right)h_0$$

$$g_n = \left(\frac{1}{4}\right)^n g_0 + \left(\left(\frac{1}{4}\right)^n - \left(\frac{1}{8}\right)^n\right)h_0$$

$$h_n = \left(\frac{1}{8}\right)^n h_0 \qquad \text{where n = 1,2, ...}$$

If the above explicit equation is approximated by the limit for $\left(\frac{1}{2}\right)^n$ and tends to approach 0 for n towards infinity $n \longrightarrow \infty$ then the limit of the above equation is as follows.

$$a_n = a_0 + b_0 + c_0 + d_0 + e_0 + f_0 + g_0 + h_0 = 1$$
$$b_n = c_n = d_n = e_n = f_n = g_n = h_n = 0$$

From the above limit approach to n go towards infinity obtained values $a_n = 1$ and $b_n = 0$, $c_n = 0$, $d_n = 0$, $e_0 = 0$, $f_0 = 0$, $g_0 = 0$, $h_0 = 0$, so that at that limit all descendants in the population will have a genotype AABBCC.

4. The results of the numerical analysis of backcrosses between AABBCC and AABBCC parents with offspring with the AoBoCo genotype showed that in the fourth generation, the best offspring were obtained with a 93% confidence level.

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