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A MATHEMATICAL MODEL ON GENETIC DIHYBRID AND MULTIHYBRID

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Abstract. Human and, in fact, every animal or plant contains many gene oriented traits. This means that the traits depend on chromosomes and are mainly directed by DNA sequence. On the other hand, a particular trait of any species may have much discriminations. Generally, it is known that for dihybrid problem in generation F_2, the phenotype ratio is 9:3:3:1 and the genotype ratio is 1:2:2:4:1:2:1:2:1. Here we consider a mathematical model on dihybrid as well as on multihybrid and analyise the probabilities of phenotype or genotype dissimilarities amongst them. Also the cause of it is shown graphically for dyhybrid.

Keywords: Number of units, dihybrid and multihybrid.

AMS Subject Classification: 92B05.

1. Introduction

Mendel [1], the father of modern genetics, on the basis of his experiments on pea-trees for dihybrid cross, observed that after generation F_2 the phenotype ratio is very close to 9:3:3:1 and concluded that the genotype ratio is 1:2:2:4:1:2:1:2:1. The author also discussed all its causes for pure and hybrid categories. The hybrid may be either dominant or recessive. Till today many researchers are working on gene and genetics from which we obtain a conjecture about the hybrid in more details such as codominant or semidominant. But the work on dihybrid crosses did not get much attention to the researchers.

There are two distinct reasons for making comparisons of genetic variation for quantitative characters. The first one is to compare evoluabilities or ability to respond to selection, and the second is to make inferences about the forces which maintain genetic variability. Houle[2] in 1992, concluded that variation was usually compared in narrow sense heritabilities, but this was almost always an inappropriate comparative measure of evoluability and variability. The author reported that, measures of appropriate variation to a variety of situations might be calculated. Chen et al. [3] studied on characterize fusarium head blight (FHB) resistance in Chinese wheat line W14 of various type. The authors identified quantitative trait loci (QTL) on chromosome 5AS for resistance to initial infection. They determined the extent of allelic variation at the two known FHB QTL for resistance to initial infection (type I), spread (type II), kernel infection etc.

Schork et al. [4] analyzed many two-trait linkage human diseases. They pointed out that most of the familial diseases like diabetes, psoriasis etc. would require very complex model to explain. Considering a model of "two-trait linkage", they compared it with other

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models. Again Dietter et al. [5] also studied on two-trait loci in the multimarker context. However, the authors needed the programs GENEHUNTER-TWOLOCUS, TLINKAGE and SUPERLINK to compare the computation times for two-trait loci.

Cheng-yu et al. [6] worked on a designed directional transfer program. They tried to improve the utilization of the multiple-allele inherited male sterile gene in Chinese cabbage and solved the problems in the transfer process of the gene of male sterile plants.

In our previous paper [7] we have shown that some traits are influenced by social environment or any other situations. Here we study on the dihybrid crossing and more generally on multihybrid crossing for those traits which are gene oriented and show by probabilistic approach, how mutation appears for a species. As every species carries many traits, so multihybrid cross is also applicable to every creature.

2. The model and its analysis

We have already defined the word *number of units* in our previous paper [7]. This is nothing but the number of elements (formed by adenine (A), guanine (G), cytosine (C), thymine (T) etc.) by which the enlightness or obscurity of the gene oriented traits represent. Various exhibitions of a trait of any species are considered by the number of units. On the basis of this concept, we discuss here about dihybrid and also the general case of multihybrid.

Let D^1 and D^2 be two different traits of father and d^1 and d^2 are respectively the same traits (may be dissimilar with D^1 and D^2) of mother. Also let p_i^j and q_i^j (j=1,2) are the number of units corresponding to the traits D^i and d^i (i=1,2) respectively.

Table-1

$D^1_{p_1^1}D^1_{p_1^2}D^2_{p_2^1}D^2_{p_2^2} \times d^1_{q_1^1}d^1_{q_1^2}d^2_{q_2^1}d^2_{q_2^2}$	F_0
$D^1_{x_1}D^2_{x_2}$ (o$^{\nearrow}$)	F_1
$d^1_{y_1}d^2_{y_2}$ (o) + | $D^1_{x_1}D^1_{x_2}d^1_{y_1}d^2_{y_2}$	

Suppose x_i and y_i (i=1,2) are the variables for "number of units" corresponding to the traits D^i and d^i (i=1,2) respectively of the gamete of the parents and $f_i(x_i)$, $g_i(y_i)$ (i=1,2) are the probability mass functions of the variables x_i and y_i (i=1,2) respectively. The functions f_i and g_i are discrete. The offspring formed by the parents is shown in the above table.

Now two cases may arise:

Case-1: The units corresponding to two different traits are contained in the same chromosome.

For this case, due to crossing-over between the non-sister chromatid of the chromosomes, the distributions of D^1, d^1 and D^2, d^2 may be of various kinds because the non-sister chromatid may cross at many loci (shown in Figure 1). Since the units of two traits are contained in the same chromosome, so the probability mass functions of containing the total number of units in the gamete must be of two variables. We may consider that in the case of father's gamete, the mass function will be $f_1(x_1) + f_2(x_2)$ for the variables x_1 and x_2, defined on $0 \le x_1 \le p_1^1 + p_1^2$, $0 \le x_2 \le p_2^1 + p_2^2$. It is also a discrete function

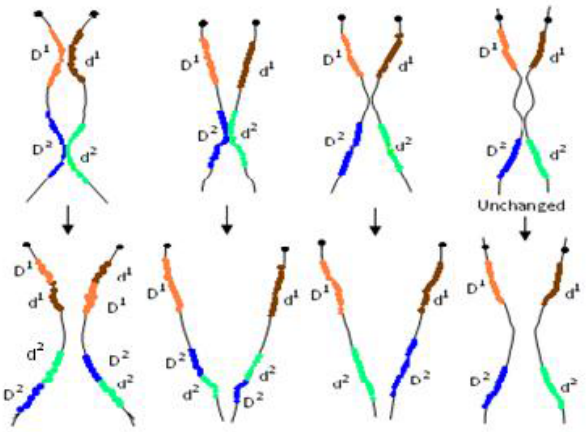

FIGURE 1. Various type of crossing-over

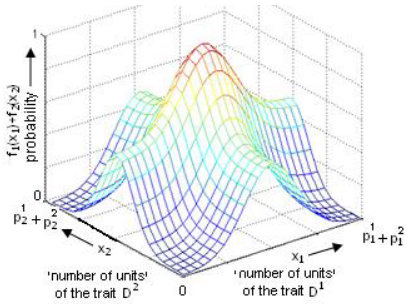

FIGURE 2. The probability function of father's gamete when two traits are contained in the same chromosome.

because x_1, x_2 are integers. Thus

$$\sum_{x_1}\sum_{x_2}[f_1(x_1)+f_2(x_2)]=1$$

$$\text{or}\quad (p_2^1+p_2^2)\sum_{x_1} f_1(x_1)+(p_1^1+p_1^2)\sum_{x_2} f_2(x_2)=1. \tag{1}$$

The graph of the probability function of father's gamete is shown in Figure 2. We see that it is maximum at the centre of its defined region and decreases towards the boundary. On the axes (x_1 or x_2) it is transformed into a single valued function and is maximum near the mid-point so as to its surface looks like "+"sign.

Similarly, the probability mass functions of the mother gamete can be considered as $g_1(y_1)+g_2(y_2)$ for the variables y_1 and y_2 and it is discrete and defined on $0 \le y_1 \le q_1^1+q_1^2$, $0 \le y_2 \le q_2^1+q_2^2$. Its graph is same as in Figure 2. Therefore, for mother gamete we have,

$$\sum_{y_1}\sum_{y_2}[g_1(y_1)+g_2(y_2)]=1$$

$$\text{or}\quad (q_2^1+q_2^2)\sum_{y_1} g_1(y_1)+(q_1^1+q_1^2)\sum_{y_2} g_2(y_2)=1. \tag{2}$$

In particular, if $f_i(x_i) \equiv 0$ for some i, say i=1, and $f_2(x_2) \not\equiv 0$ but $g_i(y_i) \not\equiv 0, \forall i = 1, 2$, then this event indicates that the trait D^1 is absent in father chromosome, but D^2 is present whereas d^1 and d^2 are present in mother chromosome. This implies that either father is abnormal for non-presence of this trait or mother is abnormal for extra-presence of this trait or mother may contain a disease. The offspring formed by them would be either abnormal for both cases or might carry the mother's disease. Thus the mass function for father gamete will be $f_2(x_2)$ with

$$\sum_{x_2} f_2(x_2) = 1 \tag{3}$$

and it remains unchanged for mother gamete. Also if $f_i(x_i) = 0$ at any x_i, for some i, then the gamete does not carry the elements of the trait D^i and if similar case occurs for mother gamete, then the offspring formed by these gametes will not contain the character D^i or d^i (for that i). In this way the above abnormality of non-presence of the trait may come out.

Case-2: The units (elements) corresponding to two different traits contained in different chromosome.

Since any chromosome (any numbered) is paired with same numbered chromosome and then the crossing-over is occurred between the non-sister chromatids of it and so a character's units of any particular chromosome does not interfere with the units of the character of other chromosome by crossing-over at the time of creation of gamete. For this reason, the characters are completely separated and the probability mass functions corresponding to the characters are mutually independent and it will be $f_1(x_1)f_2(x_2)$ in $0 \le x_1 \le p_1^1 + p_1^2$, $0 \le x_2 \le p_2^1 + p_2^2$ so that, for the case of father,

$$\sum_{x_1}\sum_{x_2} f_1(x_1)f_2(x_2) = 1$$

$$\text{i.e.} \quad \sum_{x_1} f_1(x_1) \sum_{x_2} f_2(x_2) = 1. \tag{4}$$

The graph of the probability function of father's gamete is shown in Figure 3. We see

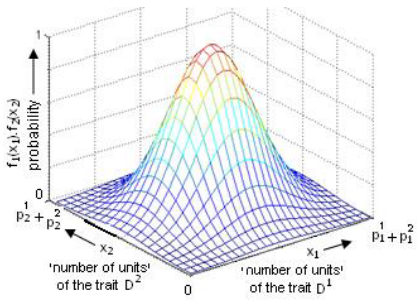

FIGURE 3. The probability function of father's gamete when two different traits are contained in different chromosome.

that it is also maximum at the centre of the defined region and decreases towards the boundary. It is just like a high hill and its cross-section by a plane parallel to x_1-x_2 is an ellipse.

Similarly, for the case of mother, the mass function would be $g_1(y_1)g_2(y_2)$ in $0 \le y_1 \le q_1^1 + q_1^2$, $0 \le y_2 \le q_2^1 + q_2^2$ with

$$\sum_{y_1}\sum_{y_2} g_1(y_1)g_2(y_2) = 1$$

$$\text{i.e.} \quad \sum_{y_1} g_1(y_1) \sum_{y_2} g_2(y_2) = 1. \tag{5}$$

In particular, if $f_1(x_1) \equiv 0$ and $f_2(x_2) \not\equiv 0$, but $g_1(y_1)$ and $g_2(y_2)$ are both non-zero then this event indicates that the trait D^1 is absent, i.e. the units of D^1 does not exist in father's chromosome but D^2 is present whereas d^1 and d^2 are present in mother's chromosome. For this case, the mass function will be $f_2(x_2)$ with

$$\sum_{x_2} f_2(x_2) = 1 \tag{6}$$

which is the same as the equation (3) and the relation (5) remains unchanged.

Generalization:

Let (D^1, d^1),(D^2, d^2), ..., (D^n, d^n) denote the pair of traits with allele of which the first is of father and second is of mother and p_1^i, p_2^i, ...; q_1^i, q_2^i, ...$(i = 1, 2)$ are the number of units corresponding to the traits D^1, D^2, ... ; d^1,d^2, ... respectively. Suppose x_1, x_2, ...; y_1, y_2, ... are the variables of the traits D^1, D^2, ... ; d^1,d^2, ... respectively and $f_1(x_1)$, $f_2(x_2)$, ... ; $g_1(y_1)$,$g_2(y_2)$, ... are corresponding probability mass functions as described previously.

Now if a chromosome carries two or more traits then the mass function for (father's) gamete will be same as in Case-1, the other traits will be possibly as in Case-2. For example if D^{i-1}, D^i, D^{i+1} are contained in a chromosome and D^l, D^{l+1} are contained in another chromosome and all others are presented in a single chromosome, then the discrete mass functions of the gamete will be

$$f_1(x_1)...f_{i-2}(x_{i-2})[f_{i-1}(x_{i-1}) + f_i(x_i) + f_{i+1}(x_{i+1})]...[f_l(x_l) + f_{l+1}(x_{l+1})]...f_n(x_n),$$

in the region defined by the range of each variable.

3. Conclusions

All characters of the species of all creatures may not necessarily satisfy this dihybrid or multihybrid model. Generally, gene oriented traits satisfy this model and distribute it from generation to generation, e.g., quantitative traits like the aspects of morphology (height, weight), physiology (blood pressure), behavior (aggression) etc. Actually a cell is not divided into exactly same daughter cells by cell division (mitosis or meiosis). This is the reason why there exists a distinction among the offsprings of same parents, i.e. the different offsprings are distributed in different ratios of different traits.

It is also observed that for dihybrid problem two cases may arise and if the units of any trait is absent, then both cases coincide. We have considered an ideal idea of the offspring of generation F_1 and concluded that the creatures will form according to this system. The most important factor is that, the allele of a trait and generally, for all traits is mixed and mutation is appeared in the heredity. So a new progeny can communicate with climatic environment.

From Figures 1 and 2 (for both cases), considered above, we see that the probability of creation of normal offspring(s) is maximum but there may form the offspring(s) having more or less units of any trait of various kind. So there form some creatures having an extra-normality of a trait or an abnormality on other side.

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