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VERIFICATION OF SOME THEORETICAL MODELS FOR BAIDYAS IN REALITY

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ABSTRACT

In this paper we are going to verify the theoretical models in reality for the population of the Baidyas (a caste in India) by calculating the frequency ratios of the five states XY, $\bar{X}Y$, XX, $\bar{X}X$, $\bar{X}\bar{X}$, ($\bar{X}$ denoting the X chromosome containing defective gene). In this connection, the population genetics of some sex-linked characters, the age of these characters and the models for the best population are also discussed.

Key words: Population genetics, frequency ratios, Baidyas, chromosomes.

The frequencies of five states were observed among 500 Baidyas of West Bengal selected at random. Baidyas of Burdwan and 24 Parganas districts were mainly studied. More than 500 Baidyas were studied for some sex-linked disease and observed whether they satisfied the models or not.

FITTING THE MODELS

1) Let $P_1(n)$, $P_2(n)$, $P_3'(n)$, $P_3''(n)$ and $P_4(n)$ be the frequency ratios of the states, XY, $\bar{X}Y$, XX, $\bar{X}X$, $\bar{X}\bar{X}$, (where $\bar{X}$ is the X chromosome containing defective gene for yellow colour blindness) in nth generation among Baidyas. The values of these frequency ratios are 0.494, 0.006, 0.493, 0.002 and 0.005.

In the next generation, the frequency ratios of these five states were 0.492, 0.008, 0.494, 0.004 and 0.002. Let us denote these frequency ratios by $P_1(n+1)$, $P_2(n+1)$, $P_3'(n+1)$, $P_3''(n+1)$ and $P_4(n+1)$. We know from our earlier studies [1, 2] that if $P_1(n) < P_3'(n) + P_3''(n)$, and $P_1(n) > P_3'(n)$, then $P_1(n+1) = P_3'(n) + 1/2\ P_3''(n)$, $P_2(n+1) = P_4(n) + 1/2\ P_3''(n)$, $P_3'(n+1) = 1/2\ P_3'(n) + 1/2\ P_1(n)$, $P_3''(n+1) = 1/2\ P_3''(n)$, and $P_4(n+1) = 1/2\ P_2(n) + 1/2\ P_4(n)$.

For Baidyas, it is found that $P_1(n) < P_3'(n) + P''_3(n)$ (since $0.494 < 0.493 + 0.002$) and $P_1(n) > P_3'(n)$ (since $0.494 > 0.493$). Therefore, according to the model, the expected frequency ratios are $P_1(n+1) = 0.494$, $P_2(n+1) = 0.006$, $P_3'(n+1) = 0.4935$, $P_3''(n+1) = 0.001$, $P_4(n+1) = 0.0055$. The observed frequency ratios are not the same as the expected frequency ratios.

2) Now, let us cosider the case when $\bar{X}$ is the X chromosome containing the defective gene for green colour blindness among Baidyas.

In the preceding generations, the frequency ratios of the five states XY, $\bar{X}Y$, XX, $\bar{X}X$, and $\bar{X}\bar{X}$ are 0.492, 0.008, 0.492, 0.004 and 0.004. In the next generation, the frequency ratios of these five states were 0.474, 0.026, 0.472, 0.002 and 0.026.

According to the model [2] the expected frequency ratios are 0.494, 0.006, 0.492, 0.002 and 0.006, respectively. The observed frequency ratios are not the same as the expected frequency ratios. But if we multiply the frequency ratios of the five states in the nth generation by 0.96, 3.5, 9.6, 1.1 and 6, respectively, we get 0.472, 0.028, 0.472, 0.004 and 0.025. If we take these frequency ratios to be the effective frequency ratios of the five states before selection, then by the model [2] we can say that

$$P_1(n+1) = P_1(n) + \tfrac{1}{2} P_3''(n)$$
$$P_2(n+1) = P_4(n) + \tfrac{1}{2} P_3''(n)$$
$$P_3'(n+1) = P_1(n)$$
$$P_3''(n+1) = \tfrac{1}{2} P_3''(n)$$
$$P_4(n+1) = \tfrac{1}{2} P_4(n) + \tfrac{1}{2} P_3''(n)$$

i.e., the expected frequency ratios in the (n+1)-th generation are 0.474, 0.026, 0.472, 0.002 and 0.026, respectively. Therefore, in the modified form the expected frequency ratios are the same as the observed frequency ratios. If we can maintain this principle for all generations, then the frequency ratios of the five states after nth generation can be calculated by changing the transformation matrix T_1 to T_2. Elements of each column of the previous transformation matrix T_1 should be multiplied by

0.96, 3.5, 0.96, 1.1 and 6, respectively, to get T_2

Then $P(n) = T_2^n P(0)$ ... (1)

The frequency ratios of the five states in the nth generation are obtained from equation (1). Also from these equations we can get n, i.e., age of the character and age of the population. Models for the best population of Baidyas can be constructed in the same way.

3) Now let us consider the case when $\bar{Y}$ is the Y chromosome containing the defective gene responsible for hair growth on the ear among Baidyas. In the preceding generation the frequency ratios of the three states, XY, $X\bar{Y}$ and XX were 0.492, 0.008 and 0.5, respectively. In the next generation, the frequency ratios of the above three states were 0.49, 0.01 and 0.5. From the models [1] and [2], the frequency ratios should be unchanged in the next generation. But here the observed frequency ratios are not the same as the expected frequency ratios. Either the data are wrong, or the statement 'hair on the ear is Y-linked' is wrong, or the effective frequency ratios at the time of selection are not the same. To get proper answer we have to observe the next generation.

4) Now let us consider the case when $\bar{X}$ is the X chromosome containing the defective gene for 'haemophilia' among Baidyas. In the preceding generation the frequency ratios of the five states were 0.5, 0, 0.5, 0 and 0, respectively. In the next generation the frequency ratios of these five states were 0.5, 0, 0.5, 0 and 0, respectively. Therefore, according to the model, the expected frequency ratios should

be 0.5, 0, 0.5, 0 and 0, respectively. The observed frequency ratios are actually the same as the expected frequency ratios.

5) Now let us consider the case when $\bar{X}$ is the X chromosome containing the defective gene for night blindness among Baidyas.

In the preceding generation, the frequency ratios of the five states were 0.497, 0.003, 0.497, 0.001 and 0.002, respectively. In the next generation, the frequency ratios of the above five states were 0.4975, 0.0025, 0.497, 0.0005 and 0.0025, respectively. Therefore, according to the model, the expected frequency ratios should be 0.4975, 0.0025, 0.497, 0.0005 and 0.0025. The observed frequency ratios are actually the same as the expected frequency ratios.

6) Now let us consider the case when $\bar{X}$ is the X chromosome containing the defective gene for red colour blindness among Baidyas. In the preceding generation the frequency ratios of the five states XY, $\bar{X}$Y, XX, $\bar{X}$X, $\bar{X}\bar{X}$ were 0.493, 0.007, 0.493, 0.005 and 0.002, respectively. In the next generation the frequency ratios of these five states were 0.4955, 0.0045, 0.493, 0.0025 and 0.0045. Therefore, according to the model, the expected frequency ratios should be 0.4955, 0.0045, 0.493, 0.0025 and 0.0045. The observed frequency ratios are actually the same as the expected frequency ratios.

DISCUSSION

Thus, in some cases the observed frequency ratios are not equal to expected. In some cases they differ very much and in others only a little. The little difference may also be due to error in data collection. Even when the observed frequency ratios are the same as expected, we cannot say that the population satisfies the conditions of the model, because it is not verified for all generations. Therefore, it cannot be concluded that the Baidyas satisfy the conditions and results of the model for these characters. But it is evident from the behaviour of selection that normal male of type XY will not select as life partner a female of type $\bar{X}\bar{X}$ and normal male of the type XY will not select female of type $\bar{X}$X if a normal male gets female of type XX at the time of selection. But it is very difficult to identify the state $\bar{X}$X. Therefore, some inaccuracy creeps in at the time of selection which is reflected in the results.

Also, the selection pattern is changing continuously. Sometimes the number of males is not equal to the number of females in a population due to abnormal sex chromosomes, although males are generally equal to females. Besides the inaccuracy due to wrong detection of XX will be eliminated after a few generations. Therefore, we may conclude that Baidyas satisfy the results and conditions of the models for these characters. Other conditions are also satisfied more or less by many populations. We may expect that the number of populations satisfying the conditions of the model may increase in future. Of course, the population can be changed at that time.

POPULATION GENETICS OF BAIDYAS

Now we can calculate the frequency ratios of different states in n th generation of these characters for which the results of the models are satisfied.

1) We saw that the results of the models were satisfied for haemophilia among Baidyas. Let $P_1(n+1)$, $P_2(n+1)$, $P_3'(n+1)$, $P_3''(n+1)$ and $P_4(n+1)$ be the frequency ratios of the states XY, $\bar{X}Y$, XX, $\bar{X}X$, and $\bar{X}\bar{X}$, where $\bar{X}$ is the X chromosome containing the defective gene of haemophilia. These frequency ratios are 0.5, 0, 0.5, 0 and 0. Here it is easy to show that $P_1(n) = 0.5$, $P_2(n) = 0$, $P_3'(n) = 0.5$, $P_3''(n) = 0$, $P_4(n) = 0$ for all n.

2) We saw that the results of the models were satisfied for night blindness among Baidyas. Let $P_1(n)$, $P_2(n)$, $P_3'(n)$, $P_3''(n)$ and $P_4(n)$ be the frequency ratios of the five states XY, $\bar{X}Y$, XX, $\bar{X}X$, and $\bar{X}\bar{X}$, where $\bar{X}$ is the X chromosome containing the defective gene for night blindness. These frequency ratios are 0.497, 0.003, 0.497, 0.001 and 0.002.

Let $P_1(0) = P_1(n) = 0.497$, $P_2(0) = P_2(n) = 0.003$, $P_3'(0) = P_3'(n) = 0.497$, $P_3''(0) = P_3''(n) = 0.001$, and $P_4(0) = P_4(n) = 0.002$.

From the model [1, 2] we can write that $P_1(2n) = 0.497 + 1/3\ (1 - 1/3\ (1-2^{1/2n})\ (0.001)$, $P_2(2n) = 0.002 + 2/3\ (1 + 2^{1/2n+1})\ (0.001)$, $P_3'(2n) = 0.497 + 1/3\ (1 - 2^{1/2n})\ (0.001)$, $P_3''(2n) = 2^{1/2n}(0.001)$, $P_3''(2n) = 2^{1/2n}\ (0.001)$; and $P_4(2n) = 0.002 + 2/3\ (1-2^{1/2n})\ (0.001)$; and $P_1(2n+1) = 0.497 + 1/3\ (1 + 2^{1/2n+1})\ (0.001)$, $P_2(2n+1) = 0.002 + 2/3\ (1-2^{1/2n+1})\ (0.001)$, $P_3'(2n+1) = 0.497 + 1/3\ (1 - 2^{1/2n+2})\ (0.001)$, $P_3''(2n+1) = 2^{1/2n+1})\ (0.001)$, and $P_4(2n+1) = 0.002 + 2/3\ (1 - 2^{1/2n+2})\ (0.001)$.

3) We saw that the results of the models were satisfied for red colour blindness among Baidyas. Let $P_1(n)$, $P_2(n)$, $P_3'(n)$, $P_3''(n)$ and $P_4(n)$ be the frequency ratios of the five states XY, $\bar{X}Y$, XX, $\bar{X}X$ and $\bar{X}\bar{X}$, where $\bar{X}$ is the X chromosome containing the defective gene for night blindness among Baidyas. These frequency ratios are 0.493, 0.007, 0.493, 0.005 and 0.002.

Let $P_1(0) = P_1(n) = 0.493$, $P_2(0) = P_2(n) = 0.007$, $P_3'(0) = P_3'(n) = 0.493$, $P_3''(0) = P_3''(n) = 0.005$, and $P_4(0) = P_4(n) = 0.002$.

Here $P_1(0) < P_3'(0) + P_3''(0)$, and $P_1(0) = P_3'(0)$, i.e. $0.493 < 0.493 + 0.005$, and $0.493 = 0.493$), $P_1(2n) = 0.493 + 1/3\ (1 - 2^{1/2n})\ (0.005)$, $P_2(2n) = 0.002 + 2/3\ (1 + 2^{1/2n+1})\ (0.005)$, $P_3'(2n) = 0.493 + 1/3\ (1 - 2^{1/2n})\ (0.005)$, $P_3''(2n) = 2^{1/2n}(0.005)$, and $P_4(2n) = 0.802 + 2/3\ (1 - 2^{1/2n})\ (0.005)$; and $P_1(2n+1) = 0.493 + 1/3\ (1 + 2^{1/2n+1})\ (0.005)$, $P_2(2n+1) = 0.002 + 2/3\ (1 - 2^{1/2n+2})\ (0.005)$, $P_3''(2n+1) = 2^{1/2n+1}\ (0.005)$, and $P_4(2n+1) = 0.002 + 2/3\ (1 - 2^{1/2n+2})\ (0.005)$.

DETERMINATION OF AGE OF DIFFERENT CHARACTERS OF BAIDYAS

We have calculated the frequency ratios of the five states in nth generation of these characters for which the results of the models were satisfied. Now we may calculate the age (No. of generations) of these characters for the Baidyas populations studied.

1) We saw that the results of the previous models were satisfied for haemophilia among Baidyas. It is not possible to calculate the age of this character, since the frequency ratios of all the states remained the same in all generations.

2) We also saw that the results of the models were satisfied for night blindness among Baidyas. We can now calculate the age of this character.

Let $P_1(n)$, $P_2(n)$, $P_3'(n)$, $P_3''(n)$ and $P_4(n)$ be the frequency ratios of the five states XX, $\bar{X}Y$, XX, $\bar{X}X$ and $\bar{X}\bar{X}$ in the nth generation, where $\bar{X}$ is the X chromosome containing the defective gene.

We see that $P_1(n) = 0.4975$, $P_2(n) = 0.0025$, $P_3'(n) = 0.497$, $P_3''(n) = 0.0025$, and $P_4(n) = 0.0025$.

This is the chain $P_1(n) = P_3'(n) + P_3''(n)$ and this is odd generation, say $n = 2m+1$.

We can write from model [1]: $P_1(2m+1) = P_1(0) + 1/3\ (1 + 2^{1/2m+1})\ P_3''(0)$, $P_2(2m+1) = P_4(0) + 2/3\ (1 - 2^{1/2m+1})\ P_3''(0)$, $P_3'(2m+1) = P_1(0) + 1/3\ (1 - 2^{1/2m})\ P_3''(0)$, $P_3''(2m+1) = 2^{1/2m+1})\ P_3''(0)$, and $P_4(2m+1) = P_4(0) + 2/3\ (1 - 2^{1/2m+2})\ P_3''(0)$.

Now, putting the values of $P_1(2m+1)$, $P_2(2m+1)$, $P_3'(2m+1)$, $P_3''(2m+1)$ and $P_4(2m+1)$ in the above equations, it is not possible to get n, because one more independent equation is needed.

3) We saw that the results of the models were satisfied for red colour blindness among Baidyas. But it is not possible to calculate the age of this character, because one more independent equation is required.

MODELS FOR THE BEST POPULATION OF BAIDYAS

Now we can suggest some mathematical models where the states of the sex-linked diseases will be removed, or the frequency ratios of these states will be minimum, or the time from the state of a sex-linked disease to normal state will be minimum, or the time from the normal state to sex-linked disease will be maximum. Also, some models can be suggested where the process for number of generations is maximum in a normal state and minimum in the case of a sex-linked disease.

1) Since $P_2(n)=0$, $P_3''(n)=0$, and $P_4(n)=0$ for haemophilia, it is not necessary to change the frequency ratios. The present population is the best population.

2) Now let us consider the case of night blindness among Baidyas. We have $P_1(0)=0.4975$, $P_2(0)=0.0025$, $P_3'(0)=0.497$, $P_3''(0)=0.0005$, and $P_4(0)=0.0025$ as frequency ratios of the states XY, $\bar{X}Y$, XX, $\bar{X}X$ and $\bar{X}\bar{X}$ at a certain stage; where $\bar{X}$ is the X chromosome containing the defective gene.

For the chain $P_1(0)<P_3'(0)+P_3''(0)$, $P_1(0)=P_3'(0)$, the frequency ratio of affected males and females tends to be $P_4(0)+2/3\ P_3(0)=0.0025+2/3 \times (0.0005)=0.0025 + 0.00033 = 0.00283$.

From the model [1, 2] we can say that for the chain $P_1(0)<P_3'(0) + P_3''(0)$, $P_1(0)>P_3'(0)$, the frequency ratio of affected males and females tends to be $1/3P_2(0) + 2/3\ P_4(0) + 1/3 \times P_3''(0) = 1/3 \times (0.0025) + 2 \times 0.0025 + 0.0005) = 1/3\ (0.008) = 0.00267$.

Now, $1/3P_2(0) + 2/3\ P_4(0) + 1/3P_3''(0) < P_4(0) + 2/3\ P_3''(0)$.

Therefore, the population should be changed to the chain $P_1(0) < P_3'(0) + P_3''(0)$, $P_1(0) > P_3'(0)$ by adjusting initial frequency ratios to get a better population.

Since $P_1(0) = P_3'(0) + P_3''(0)$, the population should be changed to the chain $P_1(0) < P_3'(0) + P_3''(0)$, $P_1(0) > P_3'(0)$.

3) Now, let us consider the case of red colour blindness among Baidyas. Here $P_1(0) = 0.4955$, $P_2(0) = 0.0045$, $P_3'(0) = 0.493$, $P_3''(0) = 0.0025$ and $P_4(0) = 0.0045$ are the frequency ratios of the states XY, $\bar{X}$Y, XX, $\bar{X}$X and $\bar{X}\bar{X}$ at a certain stage, where the $\bar{X}$ chromosome contains the defective gene.

For the chain $P_1(0) < P_3'(0) + P_3''(0)$, $P_1(0) = P_3'(0)$, the frequency ratio of affected males and females tends to be $P_4(0) + 2/3\ P_3''(0) = 0.0045 + 2/3 \times (0.0025) = 0.0045 + 0.00167 = 0.00617$.

From the model [1, 2] we can say that for the chain $P_1(0) < P_3'(0) + P_3''(0)$, $P_1(0) > P_3'(0)$, the frequency ratio of affected males and females tends to be $1/3\ P_2(0) + 2/3P_4(0) + 1/3P_3''(0) = 1/3\ (0.0045 + 2 \times 0.0045 + 0.0025) = 1/3 \times (0.016) = 0.00533$. Since $1/3\ P_2(0) + 2/3\ P_4(0) + 1/3\ P_3''(0) < P_4(0) + 2/3P_3''(0)$, therefore, the population should be changed to the chain $P_1(0) < P_3'(0) + P_3''(0)$, $P_1(0) > P_3'(0)$ by adjusting initial frequency ratios to get a better population.

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