Conclusion

The discrepancy between the observed and expected values of phase shifts, by Lissajous method, is now solved. How the measuring device, namely the oscilloscope, plays an important role in this measurement is demonstrated with simple examples.

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Suggested Reading

Any standard text book on basic or advanced Electronics at BSc or MSc level.

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Experiments to Demonstrate Change in Allelic Frequency by Genetic Drift

Populations may show a change in the frequency of alleles due to a number of factors such as migration from or to other populations, mutation, selection and random changes caused by small size of population. Genetic Drift is a random, non-adaptive change in gene frequencies in small populations. Sewall Wright, one of the giants in synthesizing the modern theory of evolution, was the first to introduce the concept of genetic drift, which is also known as 'Sewall–Wright effect'. The changes due to genetic drift are not driven by environmental or adaptive pressures, and may be beneficial, neutral, or detrimental to reproductive success. The statistical effect of sampling error during the reproduction of alleles is much greater in small populations than in large ones. For instance, if a small random sample of individuals is separated from a larger population, the gene frequencies in that sample may differ significantly from those in the population as a whole; this is because of sampling error.

A founder effect is the special case of genetic drift which occurs when a small group in a population splits off from the original

population and forms a new colony. The new colony may have less genetic variation than the original population, and through the random sampling of alleles during reproduction of subsequent generations, continue rapidly towards fixation. This consequence of inbreeding would also makes the colony more vulnerable to extinction because of reduced genetic diversity.

Conducting practical classses using living system to teach evolution in a limited time is very difficult; however, one can design simple models and simulations to overcome this and appreciate the agents causing changes in the allelic frequencies leading to evolution. With respect to this, we have formulated three simple experiments which can be performed within one to four hours in the classroom to get an idea on the role of genetic drift in the change of gene frequency.

Experiment 1. Determination of Effect of Genetic Drift on Population Size

1. Experiment was conducted with two coins which has head and tails. These two coins represented alleles within a population (head and tails = two alleles of a gene).
2. One of the coins was considered as male representative and another coin as female representative.
3. The toss of each coin pair was considered as a mating pair within the population. and the outcome of the toss represents the next generation.
4. For this experiment, an assumption was made that male and female mating pair of each generation could produce only one offspring.
5. With this background, the following experiments were conducted.

Experiment A with a Population of 100 Individuals

a) Experiment was started with a population size of 50 males and 50 females.
b) Both the coins were flipped simultaneously 50 times.
c) For each flip, the allele (heads or tails) that would pass onto the next generation was recorded in *Table* 1.

Experiment B with a Population Size of 10 Individuals

a) Experiment was started with a population of 5 males and 5 females.
b) Both the coins were flipped simultaneously 5 times.
c) For each flip, the allele (heads or tails) that would pass onto the next generation was recorded in *Table* 2.
d) The experiment 'B' was repeated three times and named as experiments C, D and E and the values were recorded in *Tables* 3, 4 and 5 respectively.

Toss (Random Mating)	Coin 1 (Female allele)		Coin 2 (Male allele)		Genotype of offspring
	Head (D)	Tail (R)	Head (D)	Tail (R)	
1	+		+		D
2		+	+		H
3	+			+	H
4		+		+	R
5		+	+		H
6		+		+	R
7		+		+	R
8		+	+		H
9	+			+	H
10	+		+		D
11	+			+	H
12		+	+		H
13		+	+		H
14	+			+	H
15	+		+		D
16	+		+		D
17	+			+	H
18	+			+	H
19		+		+	R
20		+	+		H
21		+		+	R
22		+	+		H
23	+			+	H
24		+	+		H
25	+			+	H
26	+		+		D
27	+		+		D
28		+		+	R
29	+			+	H
30		+		+	R
31	+			+	H
32		+	+		H
33		+		+	R
34		+	+		H
35	+			+	H
36		+		+	R
37		+	+		H
38	+		+		D
39		+	+		H
40	+		+		D
41		+		+	R
42		+	+		H
43	+		+		D
44	+			+	H
45	+			+	H
46	+		+		D
47	+			+	H
48		+		+	R
49	+		+		D
50	+		+		D

Table 1. Experiment A: Alleles and genotypes passed onto next generation by random mating of 50pairs   (D = Dominant allele; H = Heterozygous; R = Recessive).

Toss (Random Mating)	Coin 1 (Female allele)		Coin 2 (Male allele)		Genotype of offspring
	Head (D)	Tail (R)	Head (D)	Tail (R)	
1		+		+	R
2		+		+	R
3		+	+		H
4	+			+	H
5		+	+		H

Table 2. Alleles and genotypes passed onto the next generation by random mating of 5 pairs (Experiment B).

Toss (Random Mating)	Coin 1 (Female allele)		Coin 2 (Male allele)		Genotype of offspring
	Head (D)	Tail (R)	Head (D)	Tail (R)	
1		+		+	R
2		+	+		H
3	+		+		D
4		+		+	R
5	+		+		H

Table 3. Alleles and genotypes passed onto the next generation by random mating of 5 pairs (Experiment C).

Toss (Random Mating)	Coin 1 (Female allele)		Coin 2 (Male allele)		Genotype of offspring
	Head (D)	Tail (R)	Head (D)	Tail (R)	
1	+		+		D
2		+	+		H
3	+		+		D
4		+		+	R
5	+		+		D

Table 4. Alleles and genotypes passed onto the next generation by random mating of 5 pairs (Experiment D.)

Toss (Random Mating)	Coin 1 (Female allele)		Coin 2 (Male allele)		Genotype of offspring
	Head (D)	Tail (R)	Head (D)	Tail (R)	
1	+		+		D
2		+	+		H
3	+			+	H
4	+		+		D
5	+		+		D

Table 5. Alleles and genotypes passed onto the next generation by random mating of 5 pairs (Experiment E).

Analysis of the Data

1. *Frequency of Phenotypes and Genotypes* (*Table* **6**):

Experiments	Population size	Progeny produced in next generation	Phenotypes of the offspring (in %)				Genotypes of the offspring (in %)					
			Head	%	Tails	%	D	%	H	%	R	%
A	100	50	39	78	11	22	12	24	27	54	11	22
B	10	5	3	60	2	40	0	0	3	60	2	40
C	10	5	3	60	2	40	1	20	2	40	2	40
D	10	5	4	80	1	20	3	60	1	20	1	20
E	10	5	5	100	0	0	3	60	2	40	0	0

Table 6. Summary of the percent of phenotypes and genotypes in the offsprings.

2. *Allele Frequency*: The change in the allelic frequency in large and small populations was calculated by using the following formula, where N is total number of offspring and p and q are the frequencies of the two alleles at a locus.

$$p = \frac{2D + H}{2N} \quad \text{and} \quad q = \frac{2R + H}{2N}.$$

A: $p = 0.51$, $q = 0.49$; **B**: $p = 0.30$, $q = 0.70$; **C:** $p = 0.40$, $q = 0.60$;
D: $p = 0.70$, $q = 0.30$; **E:** $p = 0.80$, $q = 0.20$.

3. *Standard Deviation*: The standard deviation in large and small populations was calculated by using the formula $(p \times q)/2N$.

A: 0.05; **B:** 0.15; **C:** 0.16; **D:** 0.15; **E:** 0.13

Inferences

1. The phenotype and genotype frequency varied greatly in small populations than large population
2. In small populations **B** and **E**, there were no genotypes of dominant and recessive respectively.
3. In small populations change in the allele frequency was greater than the large populations.
4. The dominant allele (Head) got fixed in the small population **E**.
5. Similarly, standard deviation was greater in small populations than large population.

Suggested Questions

1. Did you find the fixation of alleles in any of these populations?
2. Did genotype frequency increase/decrease/remained constant in all the four small populations? If not explain.
3. Comment on the role of genetic drift on the population size.

Experiment 2. Determination of Effect of Genetic Drift on Sampling Error

1. Experiments were conducted with four different populations (**A**, **B**, **C** and **D**) having four different alleles, which were represented by color beads.
2. The alleles of each populations were placed in a plastic bowl which represents an island.
3. Population **A** was represented with a large plastic bowl with 100 individuals (25 beads each of four colors).
4. Populations **B**, **C** and **D** were represented by small plastic bowls with 12 individuals (3 beads of each color).
5. From each island half of the alleles were taken randomly and were put into fresh empty bowls. These beads represented the sample of alleles that would pass on to the next generation on their respective islands, the remaining beads were eliminated.
6. Each of the reproducing beads was assumed to replicate one of its own kind and this was done by introducing the same color bead into the respective islands, which brought each island population back to its original number, but with a slightly new proportion of alleles.
7. The respective allele passed onto the next generation by sampling error was recorded in *Table* 7.
8. The steps 5 and 6 were repeated for four more times (generations).

POPULATION	Allele (in color)	IPS	First			Second			Third			Forth			Fifth		
			S	R	T	S	R	T	S	R	T	S	R	T	S	R	T
A (100)	Blue	25	11	11	22	15	15	30	17	17	34	18	18	36	23	23	46
	Green	25	8	8	16	8	8	16	9	9	18	13	13	26	15	15	30
	Pink	25	17	17	34	11	11	22	9	9	18	5	5	10	1	1	2
	White	25	14	14	28	16	16	32	15	15	30	14	14	28	11	11	22
	Total	100	50	50	100	50	50	100	50	50	100	50	50	100	50	50	100
B (12)	Blue	3	3	3	6	3	3	6	5	5	10	6	6	12	6	6	12
	Green	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	Pink	3	1	1	2	0	0	0	0	0	0	0	0	0	0	0	0
	White	3	2	2	4	3	3	6	1	1	2	0	0	0	0	0	0
	Total	12	6	6	12	6	6	12	6	6	12	6	6	12	6	6	12
C (12)	Blue	3	2	2	4	2	2	4	3	3	6	3	3	6	4	4	8
	Green	3	1	1	2	2	2	4	0	0	0	0	0	0	0	0	0
	Pink	3	2	2	4	0	0	0	0	0	0	0	0	0	0	0	0
	White	3	1	1	2	2	2	4	3	3	6	3	3	6	2	2	4
	Total	12	6	6	12	6	6	12	6	6	12	6	6	12	6	6	12
D (12)	Blue	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	Green	3	2	2	4	4	4	8	4	4	8	6	6	12	6	6	12
	Pink	3	1	1	2	0	0	0	0	0	0	0	0	0	0	0	0
	White	3	3	3	6	2	2	4	2	2	4	0	0	0	0	0	0
	Total	12	6	6	12	6	6	12	6	6	12	6	6	12	6	6	12

Table 7. Distribution of four different alleles in a large and three small populations in five generations. IPS = Initial Population Size; S = Sampled number; R = Replicated number; T = Total.

Analysis of the Data (Table 7).

Population	Allele (in color)	Frequency of alleles (in percent) in five generations					
		IPS	1	2	3	4	5
A (100)	Blue	25	22	30	34	36	46
	Green	25	16	16	18	26	30
	Pink	25	34	22	18	10	2
	White	25	28	32	30	28	22
B (12)	Blue	25	50	50	83.3	100	100
	Green	25	0	0	0	0	0
	Pink	25	16.7	0	0	0	0
	White	25	33.3	50	16.7	0	0
C (12)	Blue	25	33.3	33.3	50	50	66.7
	Green	25	16.7	33.3	0	0	0
	Pink	25	33.3	0	0	0	0
	White	25	16.7	33.3	50	50	33.3
D (12)	Blue	25	0	0	0	0	0
	Green	25	33.3	66.7	66.7	100	100
	Pink	25	16.7	0	0	0	0
	White	25	50	33.3	33.3	0	0

Table 8. Analysis of proportion of alleles (colors) changed in percent over five generations in each of the populations studied.

Inferences

1. In large population, all the alleles existed in all the five generations, with varying frequency.
2. In the small population **B**, Green, Pink and White alleles were eliminated in the first, second and fourth generation respectively. The frequency of Blue allele increased and got fixed in the fifth generation.
3. In the small population **C**, Pink and Green alleles were eliminated in the second and third generation respectively, whereas, both Blue and White alleles frequency increased from their initial population.
4. In small population **D**, Blue, Pink and White alleles were eliminated in the first, second and fourth generation respectively. The frequency of Green allele increased and got fixed in the fifth generation.
5. Therefore, sampling error in small populations showed greater changes in allelic frequency and in two small populations, different alleles got fixed.

Suggested Questions

1. Is the change in the proportion of all the alleles in all the small populations different? If so explain why.
2. Did any allele get extinct in any of the populations? If so, explain the consequences in the existing population.
3. Do you accept or reject the working hypothesis? Explain.

Experiment 3. Determination of Bottleneck or Founder Effect

1. The experiment was started with a large population represented by a plastic bowl (island) with 100 individuals, having 4 color beads in an equal proportion representing four different alleles.

2. Four small populations (**A, B, C, D**) were randomly derived from the large population. Each small population was represented by a small plastic bowl with a population size of 12 beads.

3. From each small population half of the alleles (beads) were taken randomly and were put into fresh empty bowls. These beads were represented the sample of alleles that would pass on to the next generation on their respective islands, the remaining beads were eliminated).

4. Each of the reproducing beads was assumed to replicate one of its own kind and this was done by introducing the same color bead into the respective islands which brought each island population back to its original number, but with a slightly new proportion of alleles.

5. The respective allele passed onto the next generation was recorded in *Table* 9.

6. The steps 3 and 4 were repeated four more times (generations).

POPULATION	Allele (in color)	IPS	First			Second			Third			Forth			Fifth		
			S	R	T	S	R	T	S	R	T	S	R	T	S	R	T
A (12)	Blue	1	1	1	2	2	2	4	3	3	6	2	2	4	1	1	2
	Green	1	1	1	2	1	1	2	0	0	0	0	0	0	0	0	0
	Pink	7	3	3	6	1	1	2	0	0	0	0	0	0	0	0	0
	White	3	1	1	2	2	2	4	3	3	6	4	4	8	5	5	10
	Total	12	6	6	12	6	6	12	6	6	12	6	6	12	6	6	12
B (12)	Blue	3	1	1	2	0	0	0	0	0	0	0	0	0	0	0	0
	Green	3	1	1	2	2	2	4	4	4	8	6	6	12	6	6	12
	Pink	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	White	5	4	4	8	4	4	8	2	2	4	0	0	0	0	0	0
	Total	12	6	6	12	6	6	12	6	6	12	6	6	12	6	6	12
C (12)	Blue	2	1	1	2	1	1	2	2	2	4	3	3	6	2	2	4
	Green	2	1	1	2	1	1	2	1	1	2	1	1	2	1	1	2
	Pink	4	1	1	2	1	1	2	2	2	4	2	2	4	3	3	6
	White	4	3	3	6	3	3	6	1	1	2	0	0	0	0	0	0
	Total	12	6	6	12	6	6	12	6	6	12	6	6	12	6	6	12
D (12)	Blue	4	1	1	2	0	0	0	0	0	0	0	0	0	0	0	0
	Green	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	Pink	3	2	2	4	1	1	2	2	2	4	0	0	0	0	0	0
	White	3	3	3	6	5	5	10	4	4	8	6	6	8	6	6	12
	Total	12	6	6	12	6	6	12	6	6	12	6	6	12	6	6	12

Table 9: Distribution of four different alleles in four small populations in five generations.

Inferences

1. In population **A**, Green and Pink alleles were eliminated in the third generation. The frequency of Blue and White alleles increased over generations.
2. In population **B**, Pink, Blue and White alleles were eliminated in the first, second and fourth generations respectively. The allele green increased to maximum and was fixed in the fifth generation.
3. In population **C**, only one allele White was eliminated in the fourth generation.
4. In population **D**, Green, Blue and Pink alleles were eliminated in the first, second and fourth generations respectively. he allele White increased to maximum and was fixed in the fifth generation.
5. Therefore, due to sampling error, certain alleles were extinct and certain alleles were fixed in these small populations.

Questions to be Answered

1. Create Bar Graph for the color alleles of the initial and the final populations for all the groups.
2. Find out the allele which got extinct from first to fifth generation.
3. Is the change in the proportion of all the alleles in all the populations different? If so explain why
4. Comment on the feasibility and the applicability of these experiments to teach evolution in schools and colleges.

Limitations

These simple and rapid experiments were designed based on certain assumptions and models, which can simulate the concept of genetic drift to teach in classroom.

Suggested Reading

[1] D J Futuyma, *Evolution,* Sinauer Associates, Sunderland, USA, pp.225–246, 2005.
[2] http://waynesword.palomar.edu/lmexer6.htm.