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POPULATION GENETICS: FACTORS OF HUMAN EVOLUTION

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Introduction

We tend to describe individuals, their morphology and their pathology. In fact, we are not living as individuals, but as social beings, our unity being population. Fossil remains were not always "fossils"; they once belonged to living populations, and prehistoric man did not know they were prehistoric.

The anthropologist is interested in describing the variability of human populations and their origins. However, the definition of a human population is difficult.

The human species is a group of individuals, where all marriages are potentially fertile. However, these unions are limited by numerous barriers of geographical, socioeconomic, ethnical and psychological origin. These barriers would limit isolates if they functioned perfectly: in fact, they are never totally closed and the endogamy is never perfect. Therefore populations have to be defined by their barriers (JACQUARD, 1974, 1977; SUSANNE 1986).

Dimensions of populations

These presence of different barriers results in a limitation of the choice of a partner and thus of the dimension of a population.

We can estimate that throghout evolution the number of individuals in each population was very limited (Table 1). In fact, in our industrial societies, marriage groups (cercles de marriages) are also reduced.

To understand evolution better, the number of individuals is not sufficient information; it is important to know the repartition of sex and age too. If, in a large population, one can estimate that the distribution of sexes is equilibrated, at least at the age of procreation, in limited population the random distribution could in contrast be totally disturbed. Moreover, in wartime, a serious loss of young men can induce an abnormal sex ratio.

Table 1. Estimation of size and of density of populations

Size	
Chimpanzee	20-40
Early Homo	20-50
Veolithicum (village)	50-1000
Amazonia	20-80
Pygmies (camp)	10-100
Australian aborigenes	20-50
Maya (village)	500
New Guinea (village)	100-300
Belgium (marriage group)	300-1000
Density per km^2	
Chimpanzee	0.07-0.09
Omo (Australopithecus)	0.006-0.016
Hunter-gatherer	1
Early agriculture	10
Traditional agriculture	40
Belgium	1000
Hunter-gatherer	
Pygmies	0.2
Eskimo (Caribou)	0.04
(Greenland)	0.06
(Aleut)	0.6
Australian aborigenes	0.03
Primitive agriculture	
New Guinea	4
Maya	20

Therefore, it is necessary to define the effective number of individuals. The probability that two genes of two different individuals come from the same male is 1/4 Nm (with Nm the number of males), and from the same female is 1/4 Nf (with Nf the number of females). The two genes thus come from the same individual with a probability of

$$\frac{1}{4Nm} + \frac{1}{4Nf} = \frac{1}{4Ne}$$

where Ne is the effective dimension of the population.

$$Ne = \frac{4NmNf}{Nm + Nf}$$

This value will in fact depend essentially on the lowest values of Nm or of Nf, and can differ profoundly from the total number of individuals (Table 2).

Table 2. Effective size in function of the number of males (Nm) or females (Nf) for a total N=100.

N	Nm	Nf	Ne
100	1	99	3.96
100	5	95	19
100	10	90	36
100	30	70	84
100	50	50	100
100	70	30	84
100	90	10	36
100	5	95	19
100	1	99	3.96

Law of HARDY and WEINBERG

The theory of population genetics is based on the classical low of HARDY and WEINBERG, defining the situation where the frequency of genes would remain constant (Table 3).

Table 3. Law of Hardy and Weinberg

1) Let us suppose 2 alleles A_1 and A_2
with frequency p_1 and p_2 with $p_1+p_2=1$
The genotypes A_1A_1 A_1A_2 A_2A_2
will have as frequency p_1^2 $2p_1p_2$ p_2^2

In this new generation, the frequency of A_1 is

$$p_1' = \frac{2p_1^2 + 2p_1p_2}{2} = p_1(p_1 + p_2) = p_1$$

and of A_2

$$p_2' = \frac{2p_2^2 + 2p_1p_2}{2} = p_2(p_1 + p_2) = p_2$$

The frequencies of genes are constant.

2) Let us suppose panmictic marriages

	Frequency	Frequency of children		
		A_1A_1	A_1A_2	A_2A_2
$A_1A_1xA_1A_1$	p_1^4	p_1^4		
$A_1A_1xA_1A_2$	$4p_1^3p_2$	$2p_1^3p_2$	$2p_1^3p_2$	
$A_1A_1xA_2A_2$	$2p_1^2p_2^2$		$2p_1^2p_2^2$	
$A_1A_2xA_1A_2$	$4p_1^2p_2^2$	$p_1^2p_2^2$	$2p_1^2p_2^2$	$p_1^2p_2^2$
$A_1A_2xA_2A_2$	$4p_1p_2^3$		$2p_1p_2^3$	$2p_1p_2^3$
$A_2A_2xA_2A_2$	p_2^4			p_2^4
		p_1^2	$2p_1p_2$	p_2^2

The frequencies of genotypes are constant.

The absence of changes in the frequency of genes corresponds to the absence of evolution occurring when no migration, selection or mutation occur, when the

population is large and marriages occur at random (panmixy). This situation is therefore theoretical and the low allows us to study what influence the absence of respect of the conditions could have in terms of evolution.

The study of evolution implies control of the different conditions of the low of HARDY and WEINBERG, but esentially natural selection, mutation and migrations. However, we would like to insist on the random factors linked to the presence of populations of limited dimension.

History of family or history of genes

A family always has a complex history, where each individual has two parents and where, after n generations, each individual can have 2^n ancestors. However, the history of a gene better describes the biological evolution and is easier to follow because of the fact that each gene has only one ancestor gene.

Figure 1 compares an example of genealogy with the history of genes, where we can observe the disappearance of some genes and the multiplication of others.

Genetic drift

As we have seen, an essential part of the history and prehistory of man occurred in populations of limited dimensions, generally around 50 individuals (Table 1). When a population becomes larger, migrants leave the initial group for new territories: this migration results in a random choice of a limited number of genes. The "child" population will have a genetic pool different from the pool of the "mother" population.

Table 4. Probability of absence of transmission

at individual level

a parent to a child	1/2
from a parent to n children	$(1/2)^n$

at population level
probability of absence of transmission

$$p = \sum_1^x \frac{\lambda x}{2^x}$$

with λx the proportion of the population having x children

Examples of 2 populations having average 2 children

A with l2=1

$$p = \frac{1}{2^2} = 0.25$$

B with l0=1/2l4=1/2

$$p = \frac{1}{2} \cdot \frac{1}{2^0} + \frac{1}{2} \cdot \frac{1}{2^4} = 0.53$$

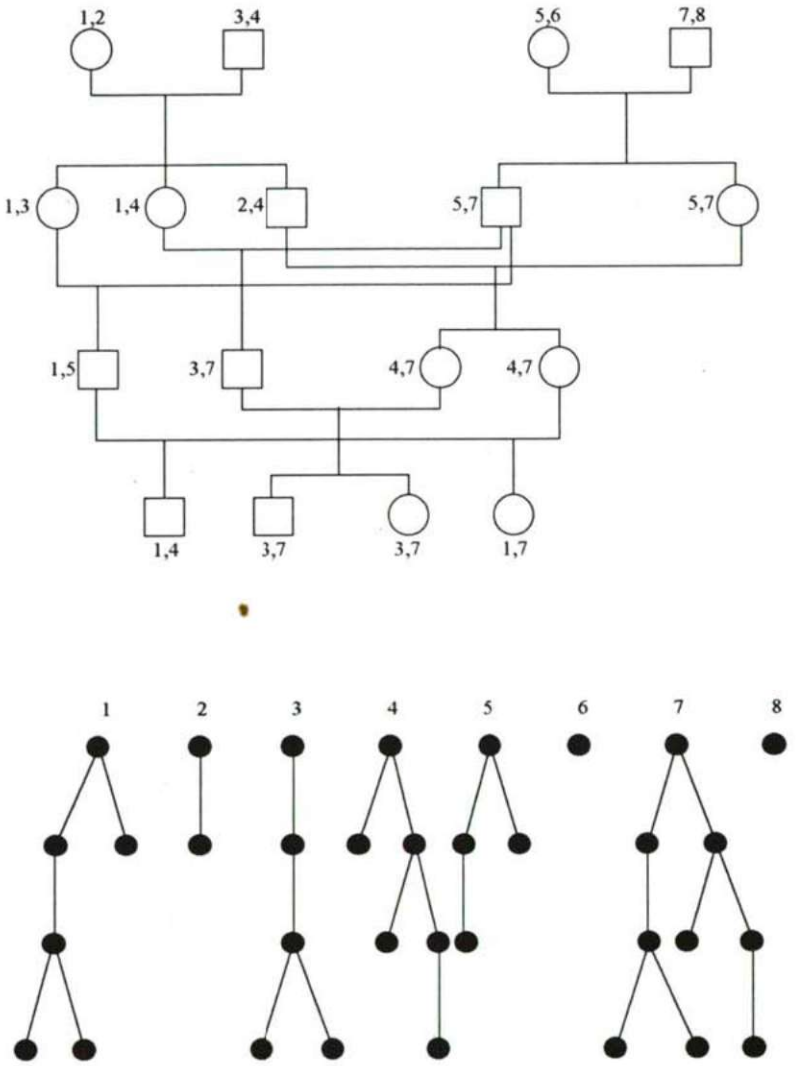

Fig. 1. Above: history of a family, each individual can have 2n ancestors.
Under: history of a gene (represented by numbers), one gene has only one ancestor gene.

A new generation is also always a result of a random choice of the gametes implicated in the fecundation and thus in the new zygotes.

Such a random choice in a very large population will not influence the frequency of genes. However, when the population is very limited, the random factors may result in large fluctuations of frequencies of genes. This situation is known as genetic drift; it corresponds to the random absence of transmission of some genes and to the random fixation of others.

At the limit, it becomes more important to follow the absence of transmission itself. The chance for a gene at a specific locus not to be transmitted to a child is 1/2, and to n children is $(1/2)^n$.

At the level of a population, the probability of absence of transmission is

$$p = \sum_{1}^{x} \frac{L_x}{2^x}$$

where L_x is the proportion of the population having x children. This probability depends on the number of children (x), but also on the variation in the number of children (Table 4).

Table 5. Variance of the frequency p_i of a gene after one generation of reproduction in a population of dimension N.

$$V(p_i) = \frac{p_i(1-p_i)}{2N}$$

Example 1: p_i=1/2 with 95%		Example 2: p_i=1/4 with 95%	
N=5	0.3 à 0.7	N=5	0 à 0.52
N=10	0.32 à 0.68	N=10	0.0 à 6 0.44
N=50	0.42 à 0.58	N=50	0.12 à 0.38
N=100	0.44 à 0.56	N=100	0.17 à 0.33
N=500	0.48 à 0.52	N=500	0.19 à 0.31

Random factors can also influence the frequency of a gene in a population, and this is inversely proportional to the dimension of the population. In a population of dimension N where a gene a_i is present in n_i copies, its frequency is equal to $p_i=n_i/N$.

In the new generation, the probability of frequency of the gene is expected to be equal to the previous frequency, but its variance is a function not only of this frequency, but also of the dimensions of the population (Table 5).:

$$E(p_i)=p_i$$

$$V(p_i) = \frac{p_i(1-p_i)}{2N}$$

If the random fluctuation can be estimated from generation, following the rules of binomial distribution, it becomes more difficult to estimate the evolution of gene

frequencies after many generations. Computer simulations have been used to demonstrate that the final result of genetic drift is fixation of one allele and loss of the other one.

Founder effect

A specific example of genetic drift is the founder effect: our history contains many cases of migrations of limited number of individuals, founding a new population and thus participating in an effect of genetic drift.

The Jicaque population (CHAPMAN et al., 1971) gives a tipical example of the founder effect, but also of a history of genes, where as a function of variation in fecundity and mortality the structure of a population modifies itself.

The Jicaque were founded a century ago by only 7 persons, who isolated themselves and their descendents on a voluntary basis; their genealogy has been reconstructed. Table 6 indicates the number of persons by generation and the level of consanguinity. This consanguinity naturally depends on the low dimension of the population; it is diminishing in the 5th generation under the influence of some migrants. Table 7 is in fact richer in information. It reconstructs the probability of origin of the genes issuing from the 7 founders, and shows that from the 2nd generation the weights of the different founders can fluctuate considerably (with a factor 2.5 in the 2nd generation, and a factor 5 in the 5th generation).

Table 6. Consanguinity and effective size of the Jicaques population.

	Consanguinity	Nm	Nf	Ne	N
1	0	4	3	6.94	7
2	0	19	15	33.5	34
3	0.068	96	80	174.5	176
4	0.092				247
5	0.065+				101

+ This diminution is due to the input of migrants

Table 7. Probability of genes originating from the founders of the Jicaques population.

		Founders								Migrants	
Generation	Nb	Léon	Franc.	Caciana	Juan	Polinaria	Pedro	Petrona	Total	Indians	Hybrids
1	7	143	143	143	143	143	143	143	1000		
2	34	88	74	74	191	176	199	199	1000		
3	176	66	78	78	167	151	208	208	957	43	
4	247	54	68	68	162	146	195	195	888	81	31
5	101	24	31	31	132	126	129	129	602	186	212

The Touaregs Kell Kummer (CHAVENTRÉ, 1972) present a relatively similar example of the founder effect and of genetic drift. At the end of the 17th century, a dominant group of Touaregs (the Kell Tademaket) lived in the South Sahara. A group seceded under the leadership of a man called KARI DENNA. This group (the Kell Kummer) slowly imposed its domination and migrated to the South of Mali. Under the

French occupation at the end of the 19th century, the Kel Kummer resisted and many were killed. In 1970, only 367 individuals (171 men and 196 women) were still living. The whole population is in fact based on 156 founders. Table 8 gives a summary of the origins of the genes of the different founders. The asymmetry is evident, since KARI DENNA contributed to 11-20% of the gene pool, while only 15 founders contributed to 70% of the gene pool and 25 founders to 80%.

Table 8. Touaregs Kel Kummer: Origin of genes (in ‰)

Generation	1 à 5	6-7	8-9	10-11	12-13	14 à 16
Size of the population	126	376	601	653	268	245
Founders						
1093 & 1096	198)	142)	158)	146)	155)	186)
1 & 2	199)571	110)350	116)370	105)357	105)361	116)426
1331 & 1332	174)	98)	106)	106)	101)	124)
1919	30	66	76	64	71	107
1959	47	55	70	60	63	71
2060	16	60	48	33	37	33
2067	16	21	49	45	43	46
1968	29	35	39	34	40	53
2062	0	44	25	24	25	27
1628 & 1629	38	20	19	15	19	24
2063	0	23	23	15	22	20
Whole of the 15 mains	747	674	729	647	681	807
Whole of the 10 following	103	112	102	111	101	78
Whole of the 131 others	150	214	169	242	218	115

1-2 = Kaari Denna and his wife
1331-32 = parents of the wife of Kaari Denna

In fact many other examples of the founder effect are known. The Hutterites, for instance, are a group of anabaptists who migrated from Europe to the United States in 1872. Three colonies were formed, with a large genetic variability from the origin on (STEINBERG et al., 1967). The religious sect of Old Order Amish migrated to Pennsylvania between 1720 and 1770; it created numerous isolated colonies where a recessive pathology is frequently observed (MCKUSICK et al., 1964). The Dunker are another sect who migrated during the 18th century; 55 groups of less than 100 persons were founded, and an important genetic drift explains the genetic variability observed between these groups (GLASS, 1954).

The high frequency of retinitis pigmentosa in the population of Tristan da Cunha (ROBERTS, 1968), of porphyria in the Africaners, and of chorea of Huntington in Tasmanians also result from a founding effect. Porphyria for instance, was introduced into the Africaner population by a migrant couple; GERRIT JANSZ, a Dutch farmer, arrived in Kaapstad in 1688 and married an orphan named ARIAANTJE JACOBS. The chorea of Huntington of the Tasmanians originates from a Huguenot woman who left England in 1848.

The distribution of some blood groups also finds its origin in genetic drift: this is the case with the group O more frequent in Amerindians and rhesus r' and r being absent in the the same Amerindians.

A study of the non-coding DNA situated near the B globin gene shows four variants that are very frequent in human populations: three are present with the same frequency all over the world, while the fourth is only present in Africans. It is possible to estimate that a founder effect was generated by the migration of human populations of *Homo erectus* from Africa. It is even possible to estimate the number of migrants: they were probably about 50 during about 70 years or about 500 during 200 years. These numbers look astonishly low, but are indeed probable (FLINT et al., 1992; ROUHANI et al., 1992).

Migration

If the founder effect corresponds to a history of fissions of populations, the migration corresponds in contrast to a history of fusion. The isolates are never totally closed; exchanges between populations still occur. These migration can temper the genetic effect of gene drift; they have a homogenizing effect.

Conclusion

A population always tends to a balanced situation under the influence of selection, migration and genic drift. However, different populations respond to different balances under the influence of varied effects of selection, migration and genic drift: the random factors are no longer factors of uniformization, but of diversification.

The isolation of a population is never total; some genetic contribution of migrants will always be observed, even if the level of migration is continuously changing. This has the result that no region is sufficiently stable to result in a balanced situation.

The (pre)history of human populations is a history of relatevly isolated populations, of limited dimensions and thus of genetic drift. It is also a history where the culture and socioecological factors result in fissions and fusions: fissions are factors of the breaking-down of endogamy and thus of diversification, while fusions are factors of homogenization.

Our unity is and always has been the population. These populations have never been fossils.

Addendum

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