POPULATION SIZE

Census Population
$$N = N_m + N_f$$

Effective Population
$$Ne = 4 N_m N_f / (N_m + N_f)$$

GENE SUBSTITUTION

FIXATION PROBABILITY

P(mutant allele fixation)

A_1A_1	A_1A_2	A_2A_2
w_{11}	w_{12}	w_{22}
1	1 + s	1 + 2s
p^2	2pq	q^2

$$P = (1 - e^{-4Nesq}) / (1 - e^{-4Nes})$$

$$P = 1 / (2N)$$

$$P = 2s / (1 - e^{-4Ns})$$

$$P \approx 2s$$

FIXATION TIME

$t = 4N$	10^6
$t = 2 \, Log[2N] / s$	5800

GENE SUBSTITUTION RATE

$$K = 2Nu (1 / 2N) = u$$

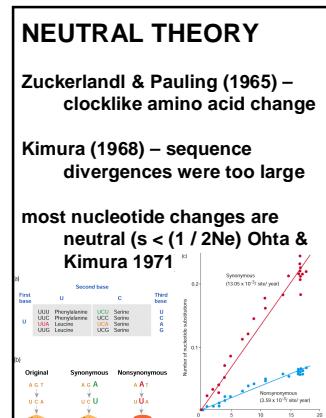$$K = 2Nu (2s) = 4Nsu$$

$$1 / K$$

GENE DIVERSITY

$$h = \Sigma (1 - x_i^2)$$

$$H = (\Sigma h_i) / n$$

GAGGTGCAACAG GAGGTGCAACAG
GCGGTGCAACAG GAGGACCAACAG
GTGGTGCAACAG GAGGTGCATCAA
GGGGTGCAACAG GGGGTGGAACAG
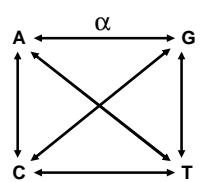
$$\Pi = \Sigma x_i x_j \pi_{ij}$$

NEUTRAL THEORY

**Zuckerlandl & Pauling (1965) –
clocklike amino acid change**

**Kimura (1968) – sequence
divergences were too large**

**most nucleotide changes are
neutral (s < (1 / 2Ne) Ohta &
Kimura 1971**

NUCLEOTIDE SUBSTITUTIONS

**population   molecular
genetics   evolution**

alleles   sequence

Jukes-Cantor 1-Parameter Model

Jukes-Cantor 1-Parameter Model

$P_{A(t)}$ = P(site A, time t)

$P_{A(0)}$ = 1
$P_{A(1)}$ = 1 - 3α
$P_{A(2)}$ = $P_{A(1)}$ (1 - 3α) + (1 - $P_{A(1)}$) α

$P_{A(t + 1)}$ = $P_{A(t)}$ (1 - 3α) + (1 - $P_{A(t)}$) α

$\Delta P_{A(t)}$ = -4α $P_{A(t)}$ + α

$P_{ii(t)}$ = (1 + 3 $e^{-4\alpha t}$) / 4
$P_{ij(t)}$ = (1 - $e^{-4\alpha t}$) / 4

$P_{A(t)}$ = f(A in sequence, time t)

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