

Inbreeding Lifts Recessive Fixation Most, and at Inbreeding Coefficient 1 Dominance Stops Mattering

— with the inbreeding coefficient in the genotype frequencies and the transition matrix solved, the lift is smaller in the order recessive, additive, dominant, and at coefficient 1 all three take the haploid value for the same number of copies —the separator is whether a mutant copy sits in a heterozygote or a homozygote — [Paper 984]

Yuuki YAMAGISHI (山岸 勇輝)

Yamagishi Complexity Torus Lab, Japan

September 2026

YOI: <https://www.yamagishiyuuki.com/yoi/984>

— *From thinking to syncing.* —

Abstract

Dominance divides the fixation of favourable mutations in diploids, and additive ones come near half the haploid value (Paper 982). Only random mating was treated there, and inbreeding was not included. In the diploid model of Paper 982, this paper puts an inbreeding coefficient F into the genotype frequencies, keeps the chance fluctuation of $2N$ copies unchanged, and finds exactly by the transition matrix the probability that a favourable mutation fixes from one copy. No new theorem or law is claimed. First, inbreeding raises the fixation probability for all three degrees of dominance: for $N = 50$, $s = 0.05$, raising F from 0 to 1 took recessive from 0.025104 to 0.093550, and additive from 0.048439 and dominant from 0.080208 to 0.093550, never falling across the six values of F (Section 2). Second, the lift is largest for recessive mutations: at $F = 0.25$ the factor over $F = 0$ was **1.557627** recessive, **1.235492** additive and **1.054607** dominant. For $N = 200$, $s = 0.01$ it was 1.490977, 1.233643 and 1.067726, in the same order (Section 2). Third, dominant over recessive falls to 1 with inbreeding: for $N = 50$ it was **3.194988**, **2.936526**, **2.707644**, **2.163198**, **1.578236** and **1.000000** at $F = 0, 0.05, 0.1, 0.25, 0.5$ and 1 (Section 3). Fourth, at inbreeding coefficient 1, all three take the value for $2N$ haploid copies: the three values at $F = 1$ were **0.093550** for $N = 50$ and 0.019735 for $N = 200$, agreeing within 10^{-10} with the transition matrix for $2N$ haploid copies (Section 3). Fifth, the separator is whether a mutant copy sits in a heterozygote or a homozygote: inbreeding raises the share of copies in homozygotes by F . The smaller the heterozygote advantage hs , the larger the effect of sitting in homozygotes (Section 4). **Keywords:** inbreeding, inbreeding coefficient, dominance, fixation probability, diploid, population genetics.

Scope of this paper (scope note): No new theorem or law is claimed: that inbreeding raises the share of homozygotes and exposes recessive mutations to selection, writing the inbreeding coefficient into genotype frequencies, and that strong inbreeding weakens the effect of dominance, are known in population genetics. No real values are claimed: population sizes of 50 and 200, advantages of 0.05 and 0.01, degrees of dominance 0, 0.5 and 1, and inbreeding coefficients from 0 to 1 are model values and correspond to no plant or livestock. Chance fluctuation is not changed: the inbreeding coefficient enters only the genotype frequencies, and the binomial draw of $2N$ copies is kept. The fall in effective population size under inbreeding is not included, so $F = 1$ is not the same as a fully selfing population. The mechanism is not extended: how inbreeding builds up over generations, inbreeding depression, sex ratio and overlapping generations are not included. Relation to earlier papers: Paper 982, in its scope note, did not extend the model, taking randomly mating diploids with non-overlapping generations and leaving out inbreeding, sex ratio, overlapping generations, linkage between genes and the mechanism of dominance; this paper sits in the seat of inbreeding (no earlier occupant). Paper 982 showed that dominance divides the fixation of favourable mutations in diploids, and that additive ones come near half the haploid value. Here the narrowing of that division when inbreeding is added to the same model is counted. What is added: finding fixation probabilities exactly for six inbreeding coefficients and three degrees of dominance in two settings, measuring that the lift is largest for recessive mutations, confirming that at coefficient 1 all three match the haploid value, reproducing the values of Paper 982 at coefficient 0, and placing the separator on “heterozygote, or homozygote”.

1. Notation and the Question

Model: as in Paper 982, a diploid population of N individuals ($2N$ copies) with genotype fitnesses AA $1 + s$, Aa $1 + hs$ and aa 1. With mutant copy frequency p , $q = 1 - p$ and inbreeding coefficient F , the genotype frequencies are

$$AA = p^2 + Fpq, \quad Aa = 2pq(1 - F), \quad aa = q^2 + Fpq$$

and $2N$ copies are redrawn binomially with the post-selection frequency $p' = (AA(1 + s) + Aa(1 + hs))/2\bar{w}$.

Starting from one copy, the fixation probability was solved with the transition matrix over copy numbers 0 to $2N$.

$F = 0, 0.05, 0.1, 0.25, 0.5, 1$; $h = 0$ (recessive), 0.5 (additive), 1 (dominant); settings $N = 50$, $s = 0.05$ and $N = 200$, $s = 0.01$.

Question: how does inbreeding change the way dominance divides the fixation probability?

2. Inbreeding Coefficient and Fixation Probability

Computation 2.1: $N = 50$, $s = 0.05$.

F	recessive	additive	dominant	dominant over recessive
0	0.025104	0.048439	0.080208	3.194988
0.05	0.027646	0.050716	0.081183	2.936526
0.1	0.030323	0.052996	0.082103	2.707644
0.25	0.039103	0.059846	0.084588	2.163198
0.5	0.055794	0.071218	0.088057	1.578236
1	0.093550	0.093550	0.093550	1.000000

Computation 2.2: $N = 200$, $s = 0.01$.

F	recessive	additive	dominant	dominant over recessive
0	0.005660	0.010107	0.016338	2.886501
0.05	0.006165	0.010574	0.016582	2.689655
0.1	0.006696	0.011044	0.016813	2.510977
0.25	0.008439	0.012469	0.017445	2.067096
0.5	0.011797	0.014877	0.018336	1.554186
1	0.019735	0.019735	0.019735	1.000000

For all three degrees of dominance in both settings, the fixation probability rose with F . The values at $F = 0$ matched the exact solutions of Paper 982 to six decimal places.

Observation 2.3

the lift is largest for recessive mutations. Factors over $F = 0$ at $F = 0.25$ were recessive 1.557627, additive 1.235492, dominant 1.054607 ($N = 50$) and 1.490977, 1.233643, 1.067726 ($N = 200$): at $F = 1$ they were 3.726468, 1.931289, 1.166348 ($N = 50$) and 3.486577, 1.952565, 1.207891 ($N = 200$).

3. Inbreeding Coefficient 1

Computation 3.1: at $F = 1$ there are no heterozygotes, $AA = p$ and $aa = q$, so the post-selection frequency becomes $p(1 + s)/(1 + ps)$ and h disappears. Solving the transition matrix for $2N$ haploid copies gave 0.093550 for $N = 50$ and 0.019735 for $N = 200$, agreeing within 10^{-10} with the three values at $F = 1$.

Observation 3.2

dominant over recessive fell to 1 with inbreeding. For $N = 50$ from 3.194988 through 1.578236 ($F = 0.5$) to 1.000000, and for $N = 200$ from 2.886501 through 1.554186 to 1.000000: the value at $F = 1$ is for haploids that keep the chance fluctuation of $2N$ copies, not for a fully selfing population, where the effective number of copies falls.

4. The Separator

Observation 4.1

the separator is whether a mutant copy sits in a heterozygote or a homozygote. The share of mutant copies in homozygotes at frequency p is $p + Fq$, and inbreeding raises it by Fq : the homozygote advantage s is the same for all three degrees of dominance, and only the heterozygote advantage hs differs. The lift was largest for recessive mutations, with no heterozygote advantage (1.557627 at $F = 0.25$), and smallest for dominant ones, with advantage s (1.054607).

Observation 4.2

what is not said. The fall in effective population size under inbreeding, how inbreeding builds up over generations, inbreeding depression, sex ratio, overlapping generations, and real plants or livestock are not treated. What is shown is that, in a model with the inbreeding coefficient in the genotype frequencies, the division of fixation probabilities by dominance narrows with inbreeding.

5. Roll Call and Closing

1. inbreeding coefficient in genotype frequencies (Section 1): fluctuation of $2N$ copies unchanged.
2. factors at $F = 0.25$: recessive **1.557627**, dominant **1.054607** (Observation 2.3): largest for recessive.

3. **dominant over recessive 3.194988 to 1.000000** (Computation 2.1): **falls to 1 with inbreeding.**
4. **0.093550 at $F = 1$** (Computation 3.1): **matches $2N$ haploid copies.**
5. **reproduces Paper 982 at $F = 0$** (Computation 2.1): **the same model.**
6. **heterozygote, or homozygote** (Observation 4.1): **the separator; the scope note of Paper 982.**

Closing: Inbreeding lifts recessive fixation most, and at inbreeding coefficient 1 dominance stops mattering. With the inbreeding coefficient in the genotype frequencies of the diploid model of Paper 982, the factors at $F = 0.25$ for $N = 50$, $s = 0.05$ were recessive 1.557627, additive 1.235492 and dominant 1.054607, and dominant over recessive fell from 3.194988 to 1.000000 at $F = 1$: the three values at $F = 1$, 0.093550, matched the value for $2N$ haploid copies. The separator is whether a mutant copy sits in a heterozygote or a homozygote. Placed among the earlier papers: to the division by dominance that Paper 982 counted under random mating, the inbreeding Paper 982 did not include was added. To be honest. This counts with the inbreeding coefficient in the genotype frequencies only and chance fluctuation unchanged. How inbreeding narrows the division by dominance, and no further.

References

1. Hartl, D. L., & Clark, A. G. (2007). *Principles of Population Genetics* (4th ed.). Sinauer.
 2. Kimura, M. (1962). On the probability of fixation of mutant genes in a population. *Genetics*.
 3. Yamagishi, Y. (2026). *Dominance Divides the Fixation of Favourable Mutations in Diploids, and Additive Ones Come Near Half the Haploid Value* [Paper 982]. YOI: <https://www.yamagishiyuuki.com/yoi/982>
-

— *From thinking to syncing.* —

Yuuki YAMAGISHI (山岸 勇輝)

© 2026 Yamagishi Complexity Torus Lab, Japan · Licensed under Creative Commons Attribution 4.0 International (CC BY 4.0)