Marry your Sister: Outbreeding Depression in Penna Ageing Model

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If in the sexual Penna ageing model conditions are applied leading to complementary bit-strings, then marriages between brothers and sisters, or between close cousins, may lead to more offspring than for unrelated couples.

Inbreeding is usually a bad thing for humans and many animals; the Egyptian pharaohs liked marriages between brothers and sisters which led to the city named Philadelphia but did not prevent conquest by the Romans two millennia ago. Also in the Penna ageing model [1], an often used computer simulation model for biological ageing, such inbreeding depression has been found [2]: Too small populations die out because their genomes become too similar, activating many deleterious mutations which in a larger population with more genomic diversity would remain recessive and would not affect the health of the individual.

However, outbreeding depression is also possible [3]: If the genomes are too different, survival becomes difficult. For example, donkey and horses cannot have grand children, and the senior author is the only known homo troglodytes and has no known children [4]. This effect may be connected with the possibility that the two haploid genomes in a species with sexual reproduction are complementary to each other [5], where with few exceptions for each gene one haplotype has one allele (“wild type”) and the other has the opposite allele (“mutant”) and where most mutations are recessive. Thus, even though about half of the genes are mutated, the phenotype is barely affected.

For real humans instead of computer simulations, Helgason et al. [6] checked for all known marriages in Iceland 1800-1965 whether they were cousins and how many offspring they had. They found the greatest reproductive success, measured in the number of grand children, for third and fourth cousins. We now check for similar effects by simulating the Penna ageing model.

Each individual in the Penna model [4] has a genome of two bit-strings of length $L$ each; at age $a$ only the first $a$ bit positions are active. If the two alleles on one position are 00, 01, or 10, they do not affect the health. If one locus at position $a$ is 11 instead, then the individual dies at age $a$. For ages above or at a minimum reproduction age $R = 5L/8$, each surviving female at each iteration randomly tries to find a male of reproductive age and then has $B$ children with him; the two bit-strings within each parent are copied and the copies are crossed-over randomly with a probability $C$ and suffer from one deleterious mutation in each bit-string. Thus the mutations are recessive, irreversible, and lethal if present in both alleles. The population size fluctuates about a value normally somewhat below the carrying capacity $K$ (Verhulst death probability, applied to babies only). 20,000 or 40,0000 iterations (updates of each survivor) are
made for equilibration; then for 1400 iterations we analyse for cousins and their offspring.

For the first half of these 1400 analysis iterations, we check at each marriage five generations back for the first ancestor which is common to husband and wife. Agreement in the $n$-th generation back gives a genealogical distance of $n$; if husband and wife have different $n$, the larger of the two is taken as genealogical distance; this happens if on old man marries his niece, etc. If no common ancestor is found within the investigated five generations back, the genealogical distance is set to 6. Thus second-order cousins have genealogical distance 3.

During the second half (again 700 iterations) of the analysis, we also check how many children (level=1), grand children (level=2) etc, again up to five generations (level=5), couples of genealogical distance $n$ have given birth to. In this way we get a matrix with the two variables level and genealogical distance. (If the levels of the two parents differ, the son adds 1 to the paternal level, and the daughter adds 1 to the maternal level.)

![Figure 1: Number of marriages versus genealogical distance, for $K = 1000$ (curves with maximum) and 10,000 (increasing curves). The recombination rates are $C = 0.001$ (+ and open squares), 1 (stars and circles) and $\times$ ($C = 0.128$, $K = 1000$) and full squares ($C = 0.032$ at $K = 10,000$).](image)

In a small population, our random selection of partners automatically leads
to marriages between close cousins, and relatively few couples have a genealogical distance larger than 5. In a large population, few couples are close cousins, and most have a distance larger than 5. Thus as a function of distance \( n \), a maximum in the number of marriages is expected, shifting to larger \( n \) for larger carrying capacities \( K \). Fig.1 shows this effect: For small \( K = 1000 \) the curves show the maximum, for large \( K = 10,000 \) the maximum is beyond \( n = 6 \). We took \( C = 0.001 \) and 1, as well as an intermediate \( C \) close to the complementarity transition.

In general we found little dependence of the number of offspring on the genealogical distance for large recombination rates \( C \) where the genomic bit-strings are not complementary. With decreasing \( C \) the surviving population first reaches a minimum or dies out and then increases again for lower \( C \), with complementary bit-strings (as shown by analysis of bits set to one and of heterozygous loci; not shown). Then close cousins usually have somewhat more offspring than unrelated couples. Fig.2 shows results per marriage for \( L = 64, B = 2, K = 1000 \) at \( C = 0.032 \); most of the populations died out at \( C = 0.128 \) (\( C \) is increased from 0.001 by factors of two). Each figure part shows the averages over 100 (+), 1000 (×) and 10,000 (*) samples. Thus the stars should be relied upon; their distance from the plus signs is ten times their statistical error. The results are roughly independent of the offspring level. This decrease with increasing genealogical distance also is seen near the complementarity transition, also for larger \( L = 128 \) and smaller \( L = 32 \): Fig.3. The final age distribution showed little dependence on the parental genealogical distance (not shown).

The reproductive fraction is the fraction of survivors at the end of the simulation with an age at or above the minimum reproduction age. Figure 4 shows that it depends little on the genealogical distance \( n \) of the parents or the crossing rate \( C \), except that near the transition to complementarity an upturn is seen towards \( n = 6 \) (meaning again all distances larger than 5).

In summary, we found decreasing numbers of offspring with increasing genealogical distance \( n \) at low \( C \), and little influence of \( n \) at large \( C \). Reality \cite{6} with a maximum at \( n \simeq 4 \) seems to be in between.

References

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Figure 2: Number of children (top part), grand children (central part), and 5th-level offspring (bottom part) versus genealogical distance $n$ where the separate symbols at $n = 6$ refers to couples without known relation ($n > 5$). Averages over 100 (+, open squares), 1000 (×, full squares) and 10,000 (stars, circles) samples at $K = 1000$. 
Figure 3: Top part: Number of children (+, *) and grand children (×, open squares) offspring for $L = 64$, $C = 0.128$ (upper data) and for $L = 128$, $C = 0.064$ (lower data), all at $B = 3$ near the complementarity transition with 10,000 runs. Bottom part: grand children from 10,000 samples for $L = 128$, $C = 0.064(+)$; $L = 64$, $C = 0.128(×)$; $L = 64$, $C = 0.256(*)$, for $B = 4$; in the last case no complementarity was seen. Finally the squares represent $L = 32$, $C = 0.064$, $B = 8$. 

$(L,C) = (128,0.064):+,(64,0.128):×,(64,0.256):∗,(32,0.064):sq.$
Figure 4: Reproductive fractions from 10,000 samples at $K = 1000$, where the sum over all genealogical distances is plotted at zero, and that over all distances above 5 at 6: Top part: $L = 64$, $B = 4$ at: $C = 0.001(+), 0.128(\times), 1(*)$. Bottom part near the transition to complementarity at: $L = 32$, $B = 8$, $C = 0.064(+)$; $L = 64$, $B = 4$, $C = 0.128(\times)$; $L = 128$, $B = 4$, $C = 0.064(*)$. 