Justification of Sexual Reproduction by Modified Penna Model of Ageing

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Abstract: We generalize the standard Penna bit-string model of biological ageing by assuming, that each deleterious mutation diminishes the survival probability in every time interval by a small percentage. This effect is added to the usual lethal but age-dependent effect of the same mutation. We then find strong advantages or disadvantages of sexual reproduction (with males and females) compared to asexual cloning, depending on parameters.

Keywords: Monte Carlo, mutation accumulation, population dynamics, pleiotropy

Presently, animals on earth proliferate mainly in two different ways: Sexually with separate males and females (now abbreviated by SX), and asexually with only one gender (abbreviated by AS). Less widespread are intermediate or mixed forms, like hermaphroditism. SX and AS coexist stably since hundreds of million years, with mammals only proliferating sexually and bacteria mostly cloning asexually.

In the Redfield model\(^1,2\), computer simulations have given clear advantages of one or the other way, depending on the parameters (even if we include that males fail to get pregnant and thus reduce the average birthrate per animal by a factor of two). A genomic bitstring model without ageing\(^3\) also justified sexual reproduction; in one case the asexual way of life even died out. No such clear advantage was found until now in the more realistic Penna ageing model\(^4\); there an advantage of AS over SX was seen, which turned into a slight disadvantage for AS if compared to hermaphroditism and meiotic parthenogenesis\(^5,6,7\). Such slight (dis)-advantages can easily be reversed by minor effects not included in the simulated model, like the effort to find a sexual partner. Thus now we present a modification of the Penna model which gives drastic advantages for SX compared with AS, or the opposite result if a single parameter is changed.

In agreement with many earlier models, including\(^4\), we assume that each mutation reduces the survival probability by a small fraction $\epsilon$. Thus at each iteration or “year”, each animal

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\(^1\) Dedicated to E. Müller-Hartmann on the occasion of his 60th birthday
survives with probability $\exp(-m\epsilon)$ if it has $m$ mutations. All mutations are assumed hereditary and detrimental, as is customary in ageing theories \[8\]. In addition, the same mutations have the lethal age-dependent effects of the standard Penna model \[4, 9\], and a Verhulst factor acting on all ages takes into account the limits of food and space. Thus a mutation, realized e.g. by a bit set to one in position $x$ of the bit-string, causes a life-threatening disease at ages $x$ and later, as well as a small additional mortality $\epsilon$ per year for all ages. This possibility of one gene having different effects is known as pleiotropy \[10, 11\]; in contrast to other ageing theories we do not have to assume antagonistic pleiotropy where mutations have both positive and negative effects at different ages.

Figure 1: Advantage of sexual (x) versus asexual (+) reproduction in pleiotropic Penna model. The effect is inverted (squares for SX, stars for AS) if the ten bits corresponding to the oldest ages are ignored in the additional mortality.

The Fortran programs follow the published ones \[9\] and are available from the authors; the birth rate for the females in SX and for all animals in AS was four, while $\epsilon = 0.015$. For SX, mutations count only if they are inherited from both father and mother, or if they happen on a dominant locus and are inherited from one of the two parents; for AS, all mutations count. Our Fig.1 shows that the sexual population is twice as high as the asexual one, in separate
simulations. (In a simultaneous simulation of two populations, the one which in separate simulations with the same parameters gives the higher stationary population \[9\] drives the other to extinction, as we tested in related models.) Unfortunately, the SX mortalities deviate for these parameters stronger than usual \[9\] from the exponential Gompertz increase with age.

The situation changes drastically, in favour of AS, if the mutations in the last 10 of 32 bits (corresponding to the last ten age intervals) are ignored in the mortality \(\exp(-m\epsilon)\). These curves are also shown in our figure. Thus, depending on biological details, either SX or AS can be the clearly preferred choice, in agreement with reality.

![Influence of number d of dominant loci on male (or female) population; \(\epsilon=0.015\), ignore=0](image.png)

**Figure 2**: Variation of male (or female) population as a function of the number \(d\) of dominant loci for SX. Fig.1 uses \(d = 6\) and ten times better statistics. For \(d \geq 23\) the whole population died out.

With no mutations ignored, Fig.2 shows the drastic influence of the number \(d\) of dominant loci on the SX population; in the traditional Penna SX model this influence is much weaker.

In summary, finally also for the Penna ageing model conditions were found where sexual reproduction is clearly preferred over asexual cloning. This may help to explain the origin of sex \(10^9\) years ago, without external effects (questioned in \[8\]) like parasites \[12, 13\] or catastrophes \[14, 15\].
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