**Rates of growth for Y-linked genes through bisexual branching processes**

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The XX/XY sex-determination system is one of the most familiar sex-determination systems and is found in human beings and most other mammals. In this sex-determination system, females have two sex chromosomes of the same kind, while males have two distinct sex chromosomes. Hence, if certain characteristics are due to genes linked to the Y chromosome, then they are only associated to the males. Anyway, females and males in a generation form mating units in order to produce offspring. Each mating unit has a genotype which is formed from the genotype of the male in the unit. Consequently, the offspring will receive its genetic structure following the inheritance rules.

From a practical viewpoint, it is of interest to model and to analyze the evolution of the number of carriers of a Y-linked gene from generation to generation. But first, a sexual reproduction scheme must be developed since we are assuming that offspring are generated by mating units.

A first approach has been provided in [1], where preference of females for males with a specific genetic characteristic determined by an allele of the gene is assumed. However, not always the choice of mate by females is conditioned by the genotype of the males. Most Y-linked characters do not appear in the phenotype of the males. Therefore it seems more realistic to consider a model where females choose their mates without caring the genotype they have. Taking into account this premise, a bisexual branching process with random mating adequate to describe the behavior of genotypes defined by Y-linked genes has been proposed in [2]. Moreover, some conditions for the extinction and/or survival of Y-linked genes in the population have been provided.

In this framework, when a genotype survives in a population, an interesting question is to study its behavior along generations. To this aim, in this work we will determine rates of growth of genotypes associated to Y-linked genes which do not appear in the phenotype of the males. Such rates will depend on the magnitude of the average number of female and male descendants per mating unit. Futhermore, we will illustrate the theoretical results by means of simulated examples.

## Acknowledgements

## References

[1] M. González, D. M. Hull, R. Martínez, M. Mota (2006) Bisexual branching processes in a genetic context: The extinction problem for Y-linked genes. Mathematical Biosciences 202:227-247

[2] M. González, R. Martínez, M. Mota (2007) Y-linked bisexual branching models. Proccedings of the II Conference on Computational and Mathematical Population Dynamics.