JMSv1 : A COMPUTER PROGRAM FOR A SIMULATION-BASED EVALUATION OF THE DIAGNOSTIC STATUS OF JUXTAPOSED MICROSATELLITE SYSTEMS

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Forword

Two populations which have diverged from an ancestral population may come back into contact due to human action via stocking or introduction programs. Estoup *et al.* (1999) and Estoup *et al.* (in press) have reported a method to measure genetic admixture in such situations based on juxtaposed microsatellite systems (JMSs). A JMS is composed of two microsatellite repeat arrays separated by a sequence of less than 200 bp and more than 20 bp. The advantage of a JMS stems from the superior genealogical information carried by the two microsatellite sites than would be the case for just one. If five assumptions are fulfilled (see Estoup *et al.* (1999) and Estoup *et al.* in press for details), JMSs provide reliable diagnostic markers which eliminate the need to know the allelic frequencies in the native population in absence of admixture. Historical, biogeographic and genetic structure information are crucial when evaluating the diagnostic status of JMSs. Such information allowed to parameterize

simulations evaluating the validity of the fourth assumption of Estoup *et al* (1999). This assumption stipulates that, prior to admixture, the probability that a JMS haplotype in the native population is composed of shared alleles at both microsatellite sites (SS haplotype) is low. The computer program JMSv1 estimates for two divergent (isolated) populations and for different demographic and marker parameters the expectations and 95% confidence intervals of the fractions of SS, SP (PS), S and P allelic classes as well as Abs[SS,SP,S and P] statistics. A detailed description of the above allelic classes and statistics is given in Estoup *et al.* (1999) and Estoup *et al.* (in press). The mutation model for the simulated JMS is the stepwise mutation model (Kimura & Ohta 1978).

Program specificities: JMSv1 is a PC program. It was written in Pascal. Though JMSv1 was made compatible with Delphi, it runs in a DOS window. There is no APPLE version available.

To run JMSv1

- Put the two files JMSv1.exe (executable file) and Rnd_seed.97 (file used for the generator of random numbers) in the same directory.

- Double click on JMSv1.exe (e.g. using the windows explorer).

- Following the menu, enter the requested population and marker parameters, as well as the name of your output file and the number of iterations. It is worth noting that JMSv1 allows (constant) population size to be different in the alien and the native populations. This is achieved by entering a multiplication factor (MF), so that the population size of the alien

population is equal to MF times the population size of the native population (notice that

MF can be ≥ 1 or ≤ 1). Calculation can be done in a single run for a large range of split

times between the alien and the native populations and a large range of population sizes.

- Use an output file name with a '.xls' extension, so that this file can be opened directly using

    EXCEL, with semicolon as delimiters. Beside statistical results, all population and marker

    parameters chosen for running the simulation are stored in the output file.

References cited

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