

Genetic and spatial structure of natural populations of *Ziziphus joazeiro* Mart. – strategy for seed collecting.

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Background

Ziziphus joazeiro Mart, known as juazeiro, is a native species of the Biome Caatinga in Brazil, being distributed in several states of the northeast region of the country. It has an economic and ecological importance mainly in Ceará State and due to the overexploitation it has been considered an endangered species. To date, no information is available regarding the genetic diversity for the species and this knowledge would assist the production of seedlings for conservation and reforestation programs of Biome Caatinga Project. This project is part of the Biome Project that has been conducted in Brazil with the aim to extend the use of trees in rural properties to diversify the productive systems with economic and environmental benefits.

Methods

Samples of 31 individuals were collected in a population of *Z. joazeiro* located in an area of natural preservation named “Não me Deixes” (population 1), and 47 individuals were collected in a population located in a farm named Triunfo (population 2). Both populations are located in Ceará State, Brazil. The genetic structure was evaluated with 12 ISSR markers and the attributes polymorphism information content (PIC), marker index, resolution power and optimum number of markers were calculated. The genetic diversity of each population was evaluated using the software POPGENE version 1.32 and the parameters number of observed alleles (n_a), effective number of alleles (n_e), genetic diversity of Nei (H_e), Shannon Index (I), percentage of polymorphic loci (%P) and indirect estimation of gene flow (N_m) were calculated. The genetic diversity inside and between populations was analysed by AMOVA, and Jaccard coefficient, using the software GENES version 2014.6.1, and the individuals were clustered with UPGMA. The spatial structure was analysed with the software SPAGeDi version 1.4, calculating the kinship coefficient for ten distance classes.

Results and Conclusions

In the population 1 was observed 220 loci, in population 2 74 loci and the optimum number of markers for each population was 210 and 65, respectively. There is no appreciable difference between the original number and the optimum number of loci probably due to the dominant character of the ISSR markers. The average PIC for the ISSR set used for populations 1 and 2 was 0.25 and 0.41, respectively, which are of medium informativeness [1]. The markers UBC808, UBC812, UBC815, UBC817 and UBC818 showed the highest values of PIC, marker index, resolution power, being the most informative for both populations. Population 1 showed a low genetic diversity compared to population 2. The number of observed alleles and the number of effective alleles for population 1 were 1.17 and 1.67, and for the population 2 were 2.0 and 1.98. The genetic diversity was high in population 2 ($H_e = 0.38$, $I = 0.56$)

compared to population 1 ($H_e = 0.13$, $I = 0.25$). According to AMOVA results there is a high genetic diversity inside populations, as the species is undomesticated and with outcrossed mating system [2]. Gene flow (Nm) between populations was 2.17 which is considered low [3], insufficient to overcome allele loss and probably due to the distance from each population that was of 26km. The individuals of population 1 were clustered in ten groups and the individuals of population 2 in fourteen groups. In relation to spatial structure, populations 1 and 2 showed positive coancestry values from the distance classes of 196 and 132 meters, respectively (Figure 1). These results indicate that from these distances the individuals are less related and useful for seed collecting for seedlings productions in programs of reforestation and conservation.

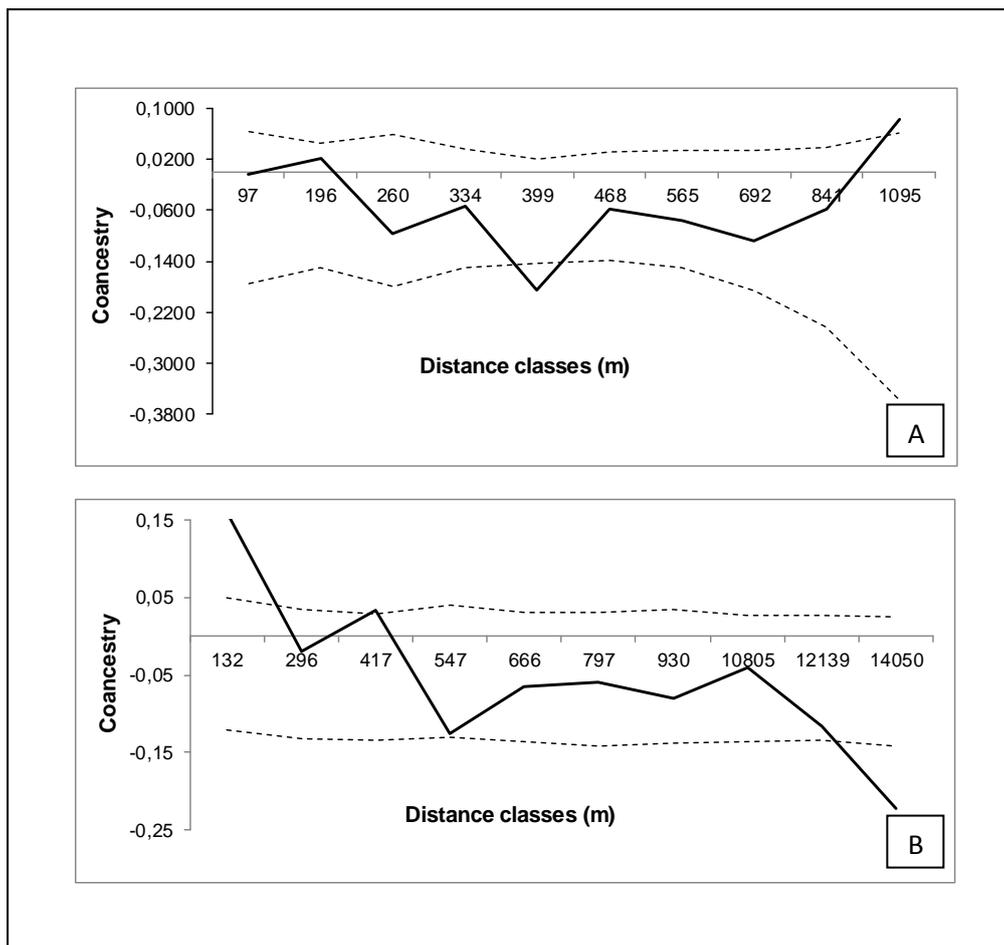


Figure 1 Spatial structure of the populations 1 (area of natural conservation called Não me Deixes – A) and 2 (productive farm called Triunfo - B) calculated using the kinship coefficient and ten classes of distance.

References

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Acknowledgments

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