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GENETIC STRUCTURE OF POTATO BREEDING GERMPLASM FROM EMBRAPA

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The potato (*Solanum tuberosum* L.) is one of the main staple food in the world. It is cultivated for direct consumption, as well as for processed food products. In potato breeding there is an ongoing challenge to search for cultivars that meet the needs from both markets. Thus, it is essential to potato breeding programs to explore efficiently the genetic variability found in the germplasm available to attend these demands. The objective of this work was to study the genetic structure present in the germplasm from the Embrapa work collection breeding program. One hundred and thirty-one genotypes were characterized with seven microsatellite (SSR) loci. This germplasm comprises cultivars and advanced clones from Brazilian breeding programs, as well as from others countries (Netherlands, Hungary, Argentina, Germany, United States, Peru, Ireland, Canada, India, Chile, France and Italy). In the molecular characterization a total of 28 alleles were identified. The average number of alleles per SSR locus was four, ranging from three to six. The analysis of principal coordinates, based on the dissimilarity matrix generated by the using Jaccard coefficient, showed the two first components explaining 17.03% of the total variation, respectively 10.54% and 6.49%. Although the dispersion of the 131 genotypes in the two first coordinates did not reveal clearly the formation of distinct groups, the cultivars released after 1990 by the Embrapa's potato breeding program were located in the lower portion of the graph, showing a tendency of isolation from the others genotypes. To verify if the genetic variability found in germplasm developed in Brazil is different from that of other countries, an analysis of molecular variance (AMOVA) was performed, which was not significant. It indicates that there is no subdivision in the potato germplasm that was analyzed according to its origin. Based on the results of this study, it can be concluded that although the germplasm of the Embrapa breeding program is not clearly subdivided, considering clustering of the recently released cultivars, there is a trend of narrowing the genetic base that is actually being used by the program.