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## Highly transferable microsatellite markers for the genera *Lasiodiplodia* and *Neofusicoccum*



Jan H. Nagel <sup>a</sup>, Elsie M. Cruywagen <sup>a, b</sup>, Joseph Machua <sup>a</sup>, Michael J. Wingfield <sup>a</sup>, Bernard Slippers <sup>a, \*</sup>

- <sup>a</sup> Department of Biochemistry, Genetics and Microbiology, Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria, Pretoria, 0001, South Africa
- b Agricultural Research Council, Vegetable and Ornamental Plants, Crop Protection Division, Roodeplaat, Pretoria, 0001, South Africa

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## ABSTRACT

Population genetic studies play an integral role in understanding the ecology and management of fungal plant pathogens. Such studies for species of Botryosphaeriaceae are hampered by a lack of available markers. Genomic sequences are available for multiple species in this family and they provide excellent resources for the development of population genetic markers. Here we describe highly transferable microsatellite or simple sequence repeat (SSR) markers for species in Lasiodiplodia and Neofusicoccum; two important and globally distributed members of the Botryosphaeriaceae. These were developed by extracting SSR-containing sequences from available genomes. Seventy-seven markers were developed for Lasiodiplodia and 32 markers were developed for Neofusicoccum. Most of these markers were transferable between species within a genus. Twelve markers tested for fragment length polymorphism in 20 isolates of Lasiodiplodia mahajangana identified between two and nine alleles and gene diversities between 0.18 and 0.83. Eleven markers indicated between two and five alleles for 20 isolates of Neofusicoccum parvum and gene diversities between 0.26 and 0.57. The large number and high transferability of the developed markers will facilitate population studies of a wide range of Lasiodiplodia and Neofusicoccum species associated with tree diseases globally.

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