ABSTRACT

Pyricularia grisea characterization is a prerequisite for species differentiation and understanding of the pathosystem, evolution and diversity of species. The aim of this study is to determine the morphological variation, pathogen virulence and molecular diversity of P. grisea isolates. Five isolates from infected heads of finger millet were collected from Bomet, Nakuru, Baringo, Busia and Machakos counties in 2019. The samples were cultured in the lab for both characterization and spore suspension preparation. Data on morphological characterization included colony diameter, color and shape of conidia. Pathogenicity test was done in the greenhouse in a randomized complete block design using KNE 741, a susceptible genotype and disease data scored. Molecular characterization involved the use of seven SSR markers. Data analyses included use of softwares such as AUDPC, Power Maker, GeneAlex and Darwin. Results showed that P. grisea isolates had different growth pattern with respect to color, colony diameter and conidia shape. Pathogenicity test revealed that all sites had significant different ($P<0.01$) virulence on the test genotype. Neck blast, scored at physiological maturity was prominent in Koibatek and Bomet strains while leaf blast was severe in Bomet and Alupe strains. Molecular analysis showed that ENA ranged from 1.30 (MGM 437)-1.99 (Pyrm 61-62) with an average of 1.71. PIC varied between 0.20-0.37 for primers MGM 437 and Pyrm 61-62, respectively. Factorial and phylogenetic analysis revealed that P. grisea isolates were diverse with no geographical grouping. AMOVA indicated diversity occurred within populations (87%) as opposed to among populations (13%). The high P. grisea variability found in the study is a clear indication of the high sexual recombination among strains collected in major growing areas of Kenya.