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## Morphological and molecular characterizations of *Fusarium sp.* causing wilt disease in ginger (*Zingiber officinale* Roscoe)

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inger (Zingiber officinae Roscoe) a member of the family Zingiberaceae, is a globally popular tropical herbaceous perennial  ${f J}$  plant with its rhizome merited for its culinary and medicinal properties. Ginger serves as a cash crop for household in the southern and southwestern parts of Ethiopia and also exported for foreign currency from these areas where it is largely cultivated. However ginger production in those areas is constrained by the onset of vascular wilt disease. This study has been undertaken to isolate, identify and to evaluate the pathogenicity of the fungal pathogens in vitro and also to see the molecular variability between the pathogenic isolates. Ginger rhizome, pseudo-stem, leaf and soil samples were collected from ginger growing areas of southwestern Ethiopia. Fungal pathogens were isolated from ginger parts showing vascular browning symptoms and from soil following standard methods. Cultural and morphological characters of pathogenic Fusarium isolates on PDA medium were studied. The pathogenic Fusarium isolates were also examined for molecular variability using PCR-RFL technique. Isolation revealed fungal isolates belonging to four genera: Fusarium, Penicillium, Aspergillus and Trichoderma. Out of 24 fungal isolates 14 isolates were Fusarium species. In vitro pathogenicity test resulted in pathogenicity index (PI) values ranging from 10.96±1.55% to 45.35±11.57%. Cultures of Fusarium species on PDA showed white, creamy white, dull pink and pink coloration. They imparted dull white, orange, light reddish purple, intense reddish purple and dark reddish purple pigmentations on the reverse side. Canoe shaped macroconidia, ovoid microconidia and short phialides were pertinent to all of the Fusarium isolates. Based on their cultural and morphological characters, the isolates were identified as Fusarium oxysporum. The ability of the isolates to induce rhizome rot indicated the forma specials rank of the isolates as F. oxysporum f. sp. zingiberi. PCR- RFLP profile of the ITS1 rDNA region indicated genetic variation between the pathogenic Fusarium isolates.

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