ABSTRACT

The objective this research was identify the fungi associated with the *Chenopodium album* leaf spot. Samplings were carried out at Universidad Autónoma Agraria Antonio Narro in a manner directed towards the weeds (10 plants) that showed signs and symptoms of this disease (pycnidia and a yellow halo on the leaves) and were later taken to the phytopathology laboratory for isolation and identification. The weed identified by morphological criteria. Pathogen was identified by morphocultural of 100 conidia criteria using AxioVision Release 4.5 software. The purification of the isolates was performed by hypha tip in PDA. *Macrophoma* sp. was identified damaging the weed *C. album* whit conidia ellipsoidal to subglobose, of 18.21 µm length and 2.56 µm width. Therefore a future investigation of this pathogen and host is recommended.

**Keywords:** weed; fungi; leaf spot; conidia; mycoherbicide.

RESUMEN

El objetivo de esta investigación fue identificar los hongos asociados con la mancha foliar de *Chenopodium album*. Los muestreos se realizaron en la Universidad Autónoma Agraria Antonio Narro de manera dirigida hacia las malezas (10 plantas) que presentaban signos y síntomas de esta enfermedad (pycnidia y un halo amarillo en las hojas) y posteriormente fueron trasladados al laboratorio de fitopatología para su aislamiento e identificación. La maleza fue identificada por criterios morfológicos. El patógeno se identificó mediante criterios morfoculturales de 100 conidios utilizando el software AxioVision Release 4.5. La purificación de los aislados se realizó mediante punta de hifa en PDA. *Macrophoma* sp. fue identificado en la maleza *C. album* con conidios elipsoidales a subgloso, de 18.21 µm de largo y 2.56 µm de ancho. Por lo tanto, se recomienda una investigación futura de este patógeno y huésped.

**Palabras clave:** maleza; hongo; mancha foliar; conidios; mycoherbicida.
INTRODUCTION

Mycoherbicides are formulations of plant pathogenic fungi that kill unwanted plants (USDA, 2020). Unlike chemical herbicides, which are made in factories, applied to plants and then degraded, mycoherbicides can be considered as living factories of chemicals, always ready to kill and prevent the growth of other plants (Jeremy, 2005). Weed account for more than 30% of total losses caused by all the pests (Gademaier et al., 2014). A considerable number of plant pathogens have been studied for possible use in weed control and some have been shown to be virulent enough to control weed species and compete commercially with chemical herbicides. However, most weed pathogens are not useful in their wild form because they are not sufficiently host specific or virulent (Sands, 2009). C. album is the best example of herbicide resistance, as it has become resistant to synthetic herbicides (Aper et al., 2014; Nawaz et al., 2016) Barton 2005 mentiones such Colletotrichum, Phoma, Sclerotinia, Alternaria, Fusarium and Puccinia as bioherbicide candidates. New groups of phytopathogens are being integrated into the control of weeds such as bacteria and viruses, some are already available in the market (Harding and Raizada, 2015). Dagno et al. (2012) mentioned 15 available mycoherbicides. Aneja et al. (2013) integrates two making a total of 17 mycoherbicides on the market.

Phytopathogenic fungi in C. album are: Cercospora dubia (Riess) Wint., Dothiorella chenopodii Ahmad, Eutyella russels (Berk. & Br.) Berl., Leptosphaeria gallicola Sacc., Metasphaeria ambigua (Dur. & Mont.) Sacc., Peronospora effusa (Grev.) Rabenhorst, Peronospora variabilis (Gaumann) Mittel., Phoma chenopodi Ahmad., and Phoma herbarum West. (Ahmad et al., 1997), Peronospora variabilis (Prinking and Linders, 1986). Ascochyta caulina (Evidente, 2000; Vurro et al., 20 01; Paccolla et al., 2016), Alternaria alternata Nees (Siddiqui, 2009), Alternaria japonica Groves and Skolko (Dutta, 2015), Drechslera rostrata Leonard (Akbar et al., 2017) Fusarium equiseti (Corda) Saccardo (Jiang, 2019). Due to the previously mentioned, the objective this research was identify the fungi associated with the C. album leaf spot.

MATERIAL AND METHODS

Sampling
Sampling was performed on August, 2017 at Universidad Autonoma Agrarian Antonio Narro (25° 21'30.7" N 101° 02'20.8" W). Ten weed plants of the Chenopodiaceae family at the species level was done using the taxonomic keys of Villareal (1983) and Vibrans (2011).

Identification of the weed C. album
The identification of the weed plants of the Chenopodiaceae family at the species level was used. Identification was performed with PDA with 10 replicates, and kept at 25 °C for 168 h. The purification of the isolates was performed by hypha tip in PDA, which were stored at 4 °C.

Identification of Macrophoma
Identification was performed with a microscope using AxioVision Release 4.5 software (ZEISS, 2020), based on the characteristics of the mycelium, color and shape of the colony, color, length and width of 100 conidia, following Barnett and Hunter 2006.

RESULTS AND DISCUSSION

Weed Chenopodium album was identified and the presence of the phytopathogenic genus Macrophoma (Sacc.) Berl. and Voglino, was found. Mycelium brown-brown, septeate, aerial and branched, pycnidia black and subglobose. Microscopically: Conidia, simple, ellipsoidal to subglobose, of 18.21 µm length and 2.56 µm width (Figure 1), results that agree by Barnett and Hunter, 2006 report. Stem black spot is a disease caused by Macrophoma sp. (FAO, 2020) and in severe attacks the incidence percentages can reach 30-100%, in this research the incidence was 100%. This fungus requires certain environmental conditions that favor its development, such as a one to two week dry period before developing (Sánchez et al., 1991, ANAVMP, 2020) and the climate in the study area was warm 35-38 °C. In controlled environment studies Macrophoma sp was pathogenic for the genus Amaranthus and the closely related genus Celosia (Chin, 1995). The impact of plant disease is determined by a tripartite interaction involving the host the pathogen and the environment (Agrios, 1988). Disease development can be constrained by various plant, pathogen and environmental factors with low virulence of the pathogen and fastidious environmental conditions the two major biological constraints (Watson and Wymore, 1990). However, Macrophoma causes diseases in important crops as guava (Psidium guajava L), corn (Zea mays L), tea (Camellia spp.),
Rubus fruticosus L., mango (Mangifera indica L.), berries (Rubus fruticosus L., Rubus idaeus L., Fragaria L.) among other crops. Phoma macrostoma was pathogenic to many dicotyledonous plant species, but nonpathogenic to monocots (Bailey et al., 2011) pathogen has a good potential as mycoherbicide in Parthenium weed. (Kaur and Kumar, 2019). Cimmino et al. (2013) reported that Phoma chenopodcola as bioherbicide in C. album, Cirsium arvense, Setaria viridis, Mercurialis annua and Annual mercury. Qing-yun et al. (2019) reported Aurosbasidium pullulans as mycoherbicide in C. album, pathogen of the class Dothideomycetes, same that Macrophoma. There are numerous Phoma-like phytopathogenic fungi that are phytotoxin-producing. Todero et al. (2018) reported that combining adjuvants with culture filtrate of Phoma sp. showed phytotoxic efficiency against Bidens pilosa L., Amaranthus retroflexus L. and Conyza canadensis L. Brun et al. (2016) reported that metabolites produced by submerged fermentation of Phoma sp. presented activity in pre-emergence, post-emergence, and detached leaves of Cucumis sativus L. and Sorghum bicolor L. Mönch and it could be an alternative in the future for weed control.

**CONCLUSION**

Macrophoma sp. was identified damaging the weed C. album with conidia, ellipsoidal to subglobose, of 18.21 µm length and 2.56 µm width. Therefore a future investigation of this pathogen and host is recommended.

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