



## Short note [Nota corta]

APPROXIMATION TO THE ORIGIN OF FALSE MILDEW IN SAFFLOWER<sup>†</sup>

[UNA APROXIMACIÓN DEL ORIGEN DE LA FALSA CENICILLA EN CÁRTAMO]

Eber Addí Quintana-Obregón\* and Cesar San Martín-Hernández

CONACYT-CIAD, Centro de Investigación en Alimentación y Desarrollo, A.C.  
 Coordinación Culiacán, Carretera a Eldorado Km 5.5, Col. Campo El Diez,  
 Culiacán, Sinaloa, CP 80110 México. E-mail: cesar.hernandez@ciad.mx;  
 eber.quintana@ciad.mx.  
 \*Corresponding author

## SUMMARY

An approximation of the origin of the “false mildew” in safflower was proposed from a phylogenetic tree obtained by the *Maximum Likelihood* method with the genomic alignment of a nucleotide sequence of *Ramularia cercosporelloides* isolated from safflower lesions. The approximation is the origin of the disease known as “false mildew” in the safflower may be due to new host adaptations of *Mycosphaerella graminicola*.

**Keywords:** Maximum Likelihood; phylogenetic tree.

## RESUMEN

Una aproximación del origen de la “falsa cenicilla” en cártamo fue propuesta a partir de un árbol filogenético obtenido con el método de *Máxima verosimilitud* con el alineamiento genómico de una secuencia de nucleótidos de *Ramularia cercosporelloides* aislada de lesiones de cártamo. La aproximación es que el origen de la enfermedad conocida como “falsa cenicilla” en el cártamo puede deberse a adaptaciones aun nuevo huésped de *Mycosphaerella graminicola*.

**Palabras clave:** Máxima verosimilitud; árbol filogenético.

## INTRODUCTION

The “false mildew” in safflower is a disease that first emerged in the Yaqui Valley, Sonora, in the 2000-2001 agricultural cycle and has since generated problems in safflower production (Montoya 2010; JLSV, 2017). Several studies to identify the species that caused this disease (Huerta-Espino *et al.*, 2006; Montoya-Coronado *et al.*, 2008) coincided with the identification of the fungal genus *Ramularia* species that affected several crops (Videira *et al.*, 2016). In the case of the safflower, there are discrepancies in the taxonomy show with certainty the etiological species of false mildew.

In a previous study, *Ramularia cercosporelloides* was found in safflower leaves collected in the Yaqui Valley (Mexico) as possibly responsible for the “false mildew” disease in safflower (Quintana-Obregón *et al.*, 2013). However, the origin of the disease has not yet been clarified. The aim of this report is to generate an approximation of the origin of the false mildew with phylogenetic analysis, which may help to find the origin of the disease.

## MATERIAL AND METHODS

A nucleotide sequence was obtained beforehand as of pure isolate from safflower leaves infested with false mildew by Quintana-Obregón *et al.* (2013) for make phylogenetic trees. The nucleotide sequence was compared to sequence related species from the National Center for Biotechnology Information (NCBI). The method of *Maximum Likelihood* was completed with the MEGA 5 (Molecular Evolutionary Genetics Analysis) software.

The technique of software used was the None method. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (500 replicates) are shown net to the branches (Felsenstein, 1985). The evolutionary distances were computed using the Jukes-Cantor method (Jukes and Cantor, 1969) and are in the units of the number of base substitutions per site. The analysis involved 30 nucleotide sequences. All ambiguous positions were removed for each sequenced pair. There were a total of 5994 positions in the final dataset. Evolutionary analyses were conducted in MEGA 5 (Neir and Kumar, 2000; Tamura *et al.*, 2011).

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## RESULTS AND DISCUSSION

As a result, and online to the analysis of *Maximum Likelihood* (Figure 1), the isolate obtained in the Yaqui Valley was identified in the phylogenetic tree as *Ramularia* from safflower (Mexico), associated with the nucleotide sequence of *Mycosphaerella graminicola* CBS 100335 (asexual form=*Septoria tritici*) phytopathogenic of *Triticum aestivum* (wheat) (Ponomarenko *et al.*, 2011). *Septoria tritici* is identified in wheat in the Netherlands (Crous *et al.*, 2007; Verkley *et al.*, 2004).

The Yaqui Valley is the major producer of wheat in Mexico. This crop represents one of the main inputs in cereal production (Berber *et al.*, 2014). Before the year 2000, false mildew had not been reported as a problem in safflower, but because of the proximity between the areas for wheat and safflower cultivation in the Yaqui

Valley, it is possible the hypothesis an adaptation in *M. graminicola* that could be favored by a change of reproductive cycle in this crop, severely affecting its production. Adaptation to new host plants of the asexual cycle (*Ramularia*) of *Mycosphaerella labyrinth* been associated with plant diversity as a survival mechanism (Videira *et al.*, 2015). The change from sexual cycle (*Mycosphaerella*) to asexual (*Ramularia*) is an adaptation mechanism that could have developed in the Yaqui Valley. The ancestral specie shown in Figure 1 with *Ramularia* supports the hypothesis presented. Moreover, a study on cotton grown in Brazil where relationships found between sexual and asexual cycles of an isolated of *Ramularia areola* identified as *Mycosphaerella areola*, allowed researchers to visualize a survival mechanism of *Ramularia* (Metha *et al.*, 2016). This approximation opens new windows of investigation that allow full identification of the false mildew.

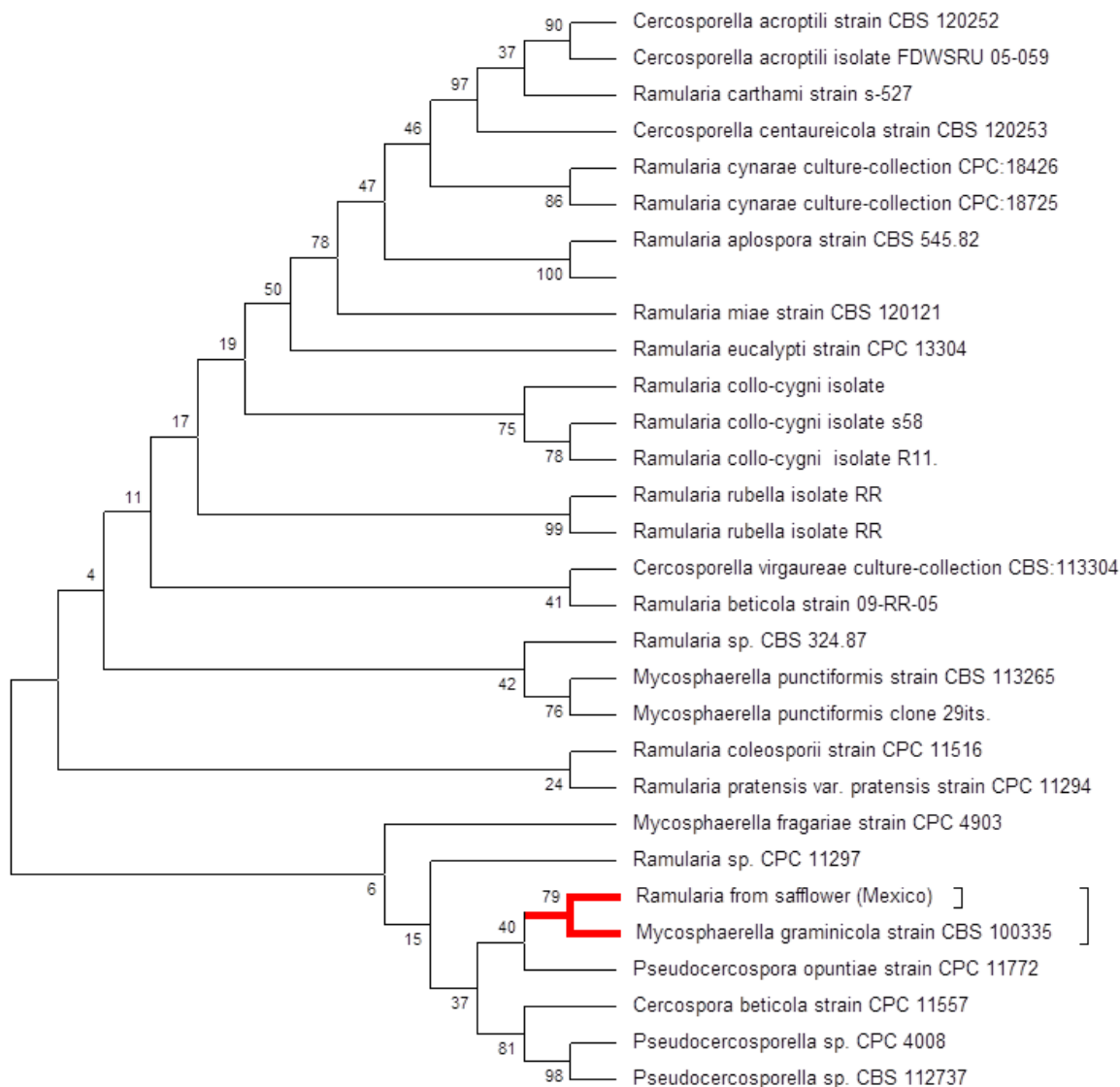


Figure 1. Phylogenetic tree built by the method *Maximum Likelihood*.

## CONCLUSION

Based on the results obtained from this approach, the pathogen that produces false mildew in safflower this related to *Mycosphaerella*. However, more research is needed to study the pathogen and the sexual cycle of *Mycosphaerella graminicola*, to provide a more precise identification, and to explain its association with false mildew. It is important to find the origin of the causative agent of the disease to design control strategies and explain defense and adaptation mechanisms for better control of the pathogen.

## REFERENCES

- Berber, S.R.M., Vargas, G.A., Rindermann, R.S., Garay A.V.A. 2014. *Trigo en Sonora y su contexto nacional e internacional*. Centro de Estudios para el Desarrollo Rural Sustentable y la Soberanía Alimentaria. Honorable Cámara de Diputados LXII Legislatura / Congreso de la Unión. México. [http://biblioteca.diputados.gob.mx/janium/bv/cedrssa/lxii/trig\\_soncon\\_nacint.pdf](http://biblioteca.diputados.gob.mx/janium/bv/cedrssa/lxii/trig_soncon_nacint.pdf)
- Huerta-Espino, J., Constantinescu, O., Velásquez, C., Herrera-Foessel, S.A., Figueroa-López, P. 2006. First report of *Ramularia cercosporelloides* on *Carthamus tinctorius* in Northwestern Mexico. *Plant Disease*. 90: 1552. <https://doi.org/10.1094/PD-90-1552B>
- Crous. P.W., Braun, U., Groenewald, J.Z. 2007. *Mycosphaerella* is polyphyletic. *Studies in Mycology*. 58: 1-32. doi: 10.3114/sim.2007.58.01
- Felsenstein, J. 1985. Confidence limits on phylogenies: An approach using the bootstrap. *Evolution*. 39:783-791. <http://dx.doi.org/10.2307/2408678>
- JLSV (Junta Local de Sanidad Vegetal del Valle del Yaqui). 2017. Falsa cenicilla de cártamo. Report online from JLSV. [http://jlsvyaqui.org.mx/?page\\_id=122](http://jlsvyaqui.org.mx/?page_id=122)
- Jukes, T.H., Cantor, C.R. 1969. Evolution of protein molecules. In Munro HN, editor, *Mammalian Protein Metabolism*, pp. 21-132, Academic Press, New York.
- Mehta, Y.R., Galbieri, R., Marangoni, M.S., Borsato, L.C., Rodrigues, H.P., Pereira, J., Mehta, A. 2016 *Mycosphaerella areola*—The Teleomorph of *Ramularia areola* of Cotton in Brazil, and Its Epidemiological Significance. *American Journal of Plant Sciences*. 7: 1415-1422. <http://dx.doi.org/10.4236/ajps.2016.710135>
- Montoya-Coronado, L., Ochoa-Burgos, F., Wong-Pérez, J., Camarilla-Pulido, M., Macías-Cervantes, J. 2008. CIANO-OL, CIANO-LIN, RC-1002-L, RC-1005-L y RC-1033-L variedades de cártamo altamente tolerantes a falsa cenicilla (*Ramularia carthami*). Folleto técnico número 60. (ed.) Instituto Nacional de Investigaciones Forestales, Agrícolas y Pecuaria, Cd. Obregón, México. <http://biblioteca.inifap.gob.mx:8080/jspui/handle/123456789/1636>
- Montoya, C.L. 2010. El cultivo de cártamo (*Carthamus tinctorius* L.) en México. Editorial SGI. Primera edición. Ciudad. Obregón, Sonora, México. <http://biblioteca.inifap.gob.mx:8080/jspui/bitstream/handle/123456789/1678/EI%20cultivo%20del%20cartamo%20carthamus%20tinctorius%201.%20en%20Mexico.pdf?sequence=1>
- Ponomarenko, A., Goodwin, S.B., Kema G.H. 2011. *Septoria tritici* blotch (STB) of wheat. *Plant Health Instructor*. DOI:10.1094/PHI-I-2011-0407-01
- Quintana-Obregón, E.A., Plascencia-Jatomea, M., Burgos-Hernández, A., Figueroa-López, P., Cortez-Rocha, M.O. 2013. Isolation and identification of fungi from leaves infected with false mildew on safflower crops in the Yaqui Valley, Mexico. *Revista Mexicana de Micología*. 37: 19-27. <http://www.scielo.org.mx/pdf/rmm/v37/v37a4.pdf>
- Tamura, K., Peterson, D., Peterson, N., Stecher, G., Nei, M., Kumar, S. 2011. MEGA 5: molecular evolutionary genetics analysis using *Maximum Likelihood*, evolutionary distance, and *Maximum Parsimony* methods. *Molecular Biology and Evolution*. 28: 2731-2739. DOI: 10.1093/molbev/msr121
- Verkley, G.J., Crous, P.W., Groenewald, J.Z., Braun, U., Aptroot, A. 2004. *Mycosphaerella punctiformis* revisited: morphology, phylogeny, and epitypification of the type species of the genus *Mycosphaerella* (*Dothideales*, *Ascomycota*). *Mycological Research*. 108: 1271-1282. <http://dx.doi.org/10.1017/S0953756204001054>
- Videira, S.I.R., Groenewald, J.Z., Verkley, G.J., Braun, U., Crous, P.W. 2015. The rise of *Ramularia* from the *Mycosphaerella labyrinth*. *Fungal Biology* 119: 823-843. DOI: 10.1016/j.funbio.2015.06.003

Videira, S.I.R., Groenewald, J.Z., Braun, U., Shin, H. D., Crous, P.W. 2016. All that glitters is not Ramularia. *Studies in Mycology*. 83, 49-163. doi: 10.1016/j.simyco.2016.06.001