Oilseed rape, *Brassica napus* ssp. *oleracea* (DC.) Metzger, is grown worldwide for the production of vegetable oil for human consumption, animal feed, and biodiesel. In Korea, this crop has also been used as an important vegetable by harvesting the leaves in late winter or early spring or by picking the main flowering shoots just before the first flowers open. Since May 2004, typical symptoms of white blister rust disease on oilseed rape have been continuously found in several localities of Korea. Leaves of infected plants had whitish sori mostly on the lower surfaces and reddish violet blotches on the corresponding upper leaf surfaces (Fig. 1A-C). Representative samples were deposited in the herbarium (KUS-F20204, F22717, F24893).

Microscopic examination of the sori from fresh materials was performed under a DIC-light microscope (Zeiss AX10). The sporangia were arranged in basipetal chains, hyaline, globose to subglobose, with uniform wall thickness and measured 15–22 × 12–19 μm (Fig. 1F). The primary sporangia were similar to the secondary sporangia, although the former exhibit a slightly thicker wall than the latter. No resting organs were observed. Up to now, the white blister rust pathogen on oilseed rape has been considered *Albugo candida* or *A. cruciferarum* (cf. Farr and Rossman, 2010). *Albugo cruciferarum* is regarded as a synonym of *A. candida* (cf. Choi et al., 2007). Based on the morphological characteristics and the specific host plant, the causal agent of this disease was identified as *A. candida* (Pers.) Kuntze (Choi et al., 2007).

The amplification and sequencing of *cox2* mtDNA and ITS rDNA were performed according to a method of Choi et al. (2006), and the resulting sequences were deposited in GenBank (Acc. No. DQ409817 and DQ409816, respectively). In *cox2* mtDNA-based phylogenetic analysis with *Albugo* s.s.r. sequences from GenBank (Fig. 2), the present causal agent formed a well-supported group with *A. candida* from *Brassica juncea* (AY927046) as well as various brassicaceous plants, among which no sequence difference was found. The sequence of ITS region was also identical to those of *A. candida* from *B. oleracea* (AF241767) and *B. juncea* (AY929828). Therefore, the sequence analysis verified the pathogen to be *A. candida*.

**Fig. 1.** White blister rust of oilseed rape associated with *Albugo candida*. (A) A typical symptom of white blister rust on a leaf. Close-up of reddish violet discolorations on the upper surface (B) and concentric sori on the lower surface (C). Sporangioles without sporangium (D) and with sporangium (E), and also sporangia (F) of *A. candida*. Scale bar=20 μm.

**Fig. 2.** Phylogenetic tree of *Albugo* s.s.r. inferred by Minimum Evolution analysis using the partial *cox2* mtDNA. Bootstrap values above 50% are given above the branches. The number of nucleotide changes between taxa is represented by branch length and the scale bar equals the number of nucleotide substitutions per site. *Albugo* specimens from *Brassica* spp. are in bold.

In Korea, it has been reported that *A. candida* attacks *B. juncea* and *B. campestris* subsp. *pekinensis* (Korean Society of Plant Pathology, 2009), but to our knowledge this is the first record of *A. candida* on oilseed rape. As the white blister rust pathogen caused by *A. candida* is one of the most devastating diseases of oilseed rape in many countries where the crop is cultivated, the occurrence of this disease poses a significant threat for the commercial large-scale cultivation of oilseed rape in Korea.

**References**


*Corresponding author (hdshin@korea.ac.kr)