

## Analysis of Pathogen Populations Occurring in Oilseed Rape Using DNA Sequencing Techniques

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**Abstract :** For a few years, the populations of pathogenic fungi occurring in winter oilseed rape in Malyszyn were analyzed. Brassica napus L. in Poland and in the world is a source of energy for both the men (oil), and animals, as post-extraction middling, as well as a motor fuel (oil, biofuel) therefore studies of this type are very important. The species composition of pathogenic fungi can be an indicator of seed yield. The occurrence of oilseed rape pathogens during several years were analyzed using the sequencing method DNA ITS. The results were compared in the gene bank using the program NCBI / BLAST. In field conditions before harvest of oilseed rape presence of pathogens infesting B. napus has been assessed. For example, in 2015, 150 samples have been isolated and applied to PDA medium for the identification of belonging species. From all population has been selected mycelium of 83 isolates which were sequenced. Others (67 isolates) were pathogenic fungi of the genus Alternaria which are easily to recognize. The population of pathogenic species on oilseed rape have been identified after analyzing the DNA ITS and include: Leptosphaeria sp. 38 (L. maculans 25, L. biglobosa 13), Alternaria sp. 29, Fusarium sp. 3, Sclerotinia sclerotiorum 7, heterogeneous 6, total of 83 isolates. The genus Alternaria sp. fungi wear the largest share of B. napus pathogens in particular years. Another dangerous species for oilseed rape was Leptosphaeria sp. Populations of pathogens in each year were different. The number of pathogens occurring in the field and their composition is very important for breeders and farmers because of the possible selection of the most resistant genotypes for sowing in the next growing season.

**Keywords :** B. napus, DNA ITS Sequencing, pathogenic fungi, population

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