Секція 1.
ГЕНЕТИКА, ГЕНОМІКА ТА ІНШІ «ОМІКИ» РОСЛИН

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TA200 MARKER FOR FUSARIUM WILT RACE-1 RESISTANCE IN CHICKPEA (CICER ARIETINUM L.)

Domesticated chickpea with bean and pea are the most important agricultural crops. Chickpea is a popular source of carbohydrates and protein. Chickpea is also an important crop used for fixing atmospheric nitrogen in symbiosis with soil microorganisms. Despite its agronomical importance and international efforts of scientists all over the world, productivity of this crop has not yet been significantly improved. The major difficulty in increasing pathogens is its susceptibility to diseases, such as "vascular disease" caused by *Fusarium oxysporum f. sp. ciceris*.

Eight races of *Fusarium* have been reported worldwide. In the South Asia, races 1 and 2 are the most popular and cause widespread damage, resulting up to 70 % yield loss. Efforts are on to tag molecular markers to loci responsible for resistance against various races of the pathogen. Moreover, the pathogen can survive in soil for up to six years even in the absence of the host, which makes its control very difficult. Hence, using wilt-resistant cultivars is the most effective and eco-friendly strategy to manage the disease.

Fusarium makes chickpea foliage develop a greyish-green chlorosis, typically affecting lower leaves first and extending up the plant. Leaves eventually take on a dull-yellow colour, wilt and the plant collapses and dies. In some cases there may be leaf vein clearing before wilt begins. Internally, the xylem tissues stain dark-brown to almost black. Wilting may initially affect only one side of the plant.

The usage of germplasm resistant to *F. oxysporum f.sp. ciceris* is the primary way of disease control. Losses may also be reduced by fungicide applications, maintaining high levels of organic matter in the soil and avoiding very early planting.

As a step towards understanding the molecular basis of wilt resistance in chickpea, there were researched the transcriptomes of wilt-susceptible and wilt-resistant cultivars under both *Fusarium oxysporum f.sp. ciceris* under challenged and unchallenged conditions. Chickpea consensus map is still low in marker density for mapping as well as for any map based cloning of agronomically important genes. There are large gaps in these maps that need to be filled with new markers. Moreover, to clone important genes, molecular markers are required to be closely linked to the trait of interest.

Marker TA200 can be used in marker assisted selection, introgression of resistance gene (R-gene) into economically important cultivars and finally to clone the candidate gene for *Fusarium*-wilt resistance. Molecular markers are being used as tools for genetic mapping, diversity analysis, tagging genes, marker-assisted selection and map based cloning. TA200 marker has become the choice of molecular marker for chickpea linkage mapping, although new advanced types of molecular markers are being developed.

In our research we have detected polymorphism of Ukrainian and foreign varieties of chickpea by TA200 marker using molecular-genetic methods *in vitro*. Thus, nucleotide sequences of chickpea from National Center for Biotechnology Information and European Molecular Biology Laboratory were analyzed by using bioinformatics methods *in silico*.

As result of molecular-genetic research there were detected the chickpeas varieties with 274 bp, 286 bp, 292 bp and 295 bp alleles. In nucleotide sequences of chickpeas samples from National Center for Biotechnology Information and European Molecular Biology Laboratory there were detected varieties with 274 bp, 286 bp, and 295 bp alleles by TA200 marker for *Fusarium*-wilt resistance.

Key words: chickpea, Fusarium oxysporum, molecular genetics, bioinformatics, TA200 marker, polymorphism.