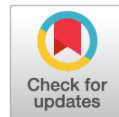


## Basic research in the developmental genetics on the model of tumor growth in higher plants



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Today, thanks to use the modern methods of biotechnology, the molecular mechanism underlying different aspects of plant development are started to open up. Along with the traditional methods of genetic analysis, plant developmental genetics actively uses the technics of genetic engineering and “omics” technologies. One of the problems of plant developmental genetics is the study of tumor growth in plants as a model for revealing the mechanisms of systemic control of cell division. Tumor is a pathological structure emerging as a result of uncontrolled proliferation of a group of cells leaving the systemic control of growth rate, cell differentiation and proliferation. Therefore, the elucidation of the mechanisms of tumor formation may help to identify the key regulators of systemic mechanisms controlling cell proliferation and differentiation. Tumor-like structures are found in almost all multicellular organisms, including higher plants. Pathogen-induced tumors, which make up the majority of neoplasms in higher plants, develop under the influence of infectious agents (bacteria, viruses, fungi, nematodes, insects, etc.) which create a niche for their own habitation in the host plant’s organism mostly by shifting the phytohormonal balance and sometimes activation of the meristematic competence of plant cells or modulation of plant cell cycle. At the same time, much rarer spontaneous tumors of higher plants are formed in plants with certain genotypes (mutants, interspecific hybrids, inbred lines) in the absence of any pathogen, which makes them closer to animal tumors. In particular, in the genetic collection of radish (*Raphanus sativus* L.), the inbred lines that form spontaneous tumors on the taproot during the flowering period were obtained many years ago. The connection between the spontaneous tumor formation in these lines and the altered balance of the main phytohormones, as well as ectopic expression of meristem-specific genes, was previously demonstrated. We have analyzed the differential gene expression in the spontaneous tumors of radish versus the lateral roots using the RNA-seq method. Data were obtained indicating the increased expression of genes associated with cell division and growth (especially genes that regulate G2-M transition and cytokinesis) in the spontaneous tumor. Among genes downregulated in tumor tissue, genes participating in the response to stress and wounding, as well as in the biosynthesis of glucosinolates, were enriched. Subsequently, we also performed whole genome sequencing of two closely related radish lines, contrasting in their ability to spontaneous tumor formation. In the coding genes of tumorous line, we have identified numerous SNPs and InDel which lead to frameshift and are probably associated with the tumor formation trait. Thus, spontaneous tumor formation in inbred lines of radish

is probably under complex polygenic control. Testing of the relationship of these polymorphisms with tumor formation has begun. Our data will help to elucidate the mechanisms of spontaneous tumor development in higher plants.

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