

Identification of SNPs and InDels probably associated with the development of spontaneous tumors in radish (*Raphanus sativus* L.)

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Radish (*Raphanus sativus* L.) is an agronomically important root crop belonging to the *Brassicaceae* family. A genetic collection of inbred radish lines, which was based on contrasting genetically determined traits including trait “ability to develop tumors”, was created at St. Petersburg State University in the middle of the 20th century [1]. Full genetics network controlling this trait still remains unclear [2], and elucidation of its mechanisms can help reveal the key regulators of systemic mechanisms that control cell proliferation and differentiation.

The purpose of this work is to identify single nucleotide polymorphisms (SNPs) and InDels in genes which are candidates for participation in the tumor development process within in the tumor-forming radish line compared to the non-tumor radish line.

We have assembled the genomes of two lines contrasting in the ability to tumorigenesis, annotated them, aligned sequences per assembly, identified candidate genes and differences in the structure of these genes in contrasting radish lines using bioinformatics tools. Bioinformatics data were confirmed by the sequencing by Sanger method.

As a result, in the tumor-forming radish line we identified 151 genes with InDels in their coding regions, which led to various variants of frameshift. Moreover, we detected 39 genes with single nucleotide substitutions (SNPs). According to the gene pathway enrichment analysis, the corresponding genes were classified into the several groups.

Thus, the data obtained will allow us to clarify in more detail the genetic control mechanisms of the tumor development in radish.

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