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Identification of the molecular mechanisms underlying the negative effects of nitrogen fertilizers on resistance to sheath blight in rice

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Motivation and Aim: Rice (*Oryza sativa* L.) is considered the most valuable crop in the world, as half of the world's humanity uses it for food every day. Sheath blight disease, caused by fungus *Rhizoctonia solani* Kühn causes serious damage to rice yields, leading to losses of up to 50 % of the yield [2]. It is well known that the use of fertilizers increases the productivity of agricultural plants. However, in addition to the positive effect, nitrogen fertilization has been shown to worsen the resistance of rice to sheath blight [3]. The molecular mechanisms of this effect are still not understood and require more thorough research.

Methods and Algorithms: Publicly available transcriptomic data (RNA-seq) on the response to nitrogen fertilizers and sheath blight infection were analyzed to identify differentially expressed genes. To reconstruct and analyze gene networks, the SmartSrop cognitive platform, developed by us, was used, which was created to study the genotype-phenotype-environment relationships of agriculturally valuable crops rice and wheat using artificial intelligence methods and text analysis.

Results: We analyzed transcriptomic data on the response of rice to *Rhizoctonia solani* infection, identified a group of differentially expressed genes, and reconstructed the corresponding gene network. Similar work was carried out on publicly available data on the effects of nitrogen fertilizers on the rice transcriptome. Next, the resulting gene networks were analyzed in the SmartSrop cognitive platform to search for mechanisms of the negative effect of nitrogen fertilizers on resistance to sheath blight.

Conclusion: The data obtained allow us to make assumptions about the mechanisms underlying the negative effect of fertilizers on resistance to sheath blight.

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