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IV ВАВИЛОВСКАЯ  
МЕЖДУНАРОДНАЯ  
КОНФЕРЕНЦИЯ

20–24 ноября 2017 г.  
Санкт-Петербург

**ИДЕИ**  
**Н. И. ВАВИЛОВА**  
**В СОВРЕМЕННОМ**  
**МИРЕ**



*.мне не жалко отдать жизнь ради самого малого в науке... »*

*Михаил Васильевич*

*Светлой памяти  
великого русского ученого  
Николая Ивановича Вавилова  
посвящается*



*В науке... »*

A handwritten signature or mark in cursive script, appearing to be the initials 'N.I.' or similar, located at the bottom left of the page.

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**N. I. VAVILOV'S IDEAS  
IN THE MODERN WORLD**

*ABSTRACTS*

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В СОВРЕМЕННОМ МИРЕ**

*ТЕЗИСЫ ДОКЛАДОВ*

САНКТ-ПЕТЕРБУРГ  
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**IDEAS  
WORLD**

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# НАУЧНАЯ ШКОЛА Н. И. ВАВИЛОВА – СОРАТНИКИ И ПОСЛЕДОВАТЕЛИ

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## MINING NATURAL VARIATION TO UNDERSTAND QUANTITATIVE DISEASE RESISTANCES: A CASE STUDY FOR RESISTANCE TO ROOT DISEASE IN MEDICS

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Verticillium wilt causes substantial yield losses in many crops including alfalfa (*Medicago sativa*). The model legume *Medicago truncatula*, a wild species which presents well-established genetic resources and high biodiversity was used as a host for studying resistance and susceptibility to *Verticillium alfalfae*.

Verticillium wilt response in *M. truncatula* is a quantitative disease resistance (QDR), regulated by QTLs that differ across resistant accessions and vary according to the fungus strains, as revealed by a genetic analysis in a multi-cross, multi-strain, multi-site design. This suggests that distinct genetic mechanisms control Verticillium wilt resistance in different *M. truncatula* lines.

To deepen the analysis, we assessed the genetic variability of susceptibility to Verticillium within the *M. truncatula* species, in a collection of 237 lines from around the Mediterranean Basin. Disease parameters and plant colonization by the fungus varied largely among the lines. A whole genome association study (GWAS) allows identifying several loci, that differ for the traits evaluated. A candidate susceptibility gene was identified and experimentally validated.

Despite being very significant, these loci do not explain all of the genetic variance, suggesting that QDR may relies on the cumulative actions of a large number of genes. Such a genetic model for QDR may allows for rapid adaptation of QDR response to new conditions : under selective pressure, the quantitative traits evolve rapidly, via small changes in the population frequencies of a large number of pre-existing polymorphisms. We propose that whole genome admixture components can be used as predictors for phenotypes with polygenic inheritance, accounting for population structure. We test this hypothesis and experimentally confirm it by predicting differences in QDR levels among accessions. We also demonstrate that ancestry explains most of phenotypic variation for several other quantitative functional traits. This method outperform some Genomics Selection (GS) models for predicting quantitative traits in *M. truncatula*.

The capacity of pathogenic fungi to adapt to new environments and hosts is a well-known threat to durability of resistant populations. We tested if moderate increases (+3°C) or decreases (-5°C) of temperature during infection with several strains impacted early plant response and final fitness. We showed a significant impact of temperature on early response to disease and on final fitness of the plants.

We also experimentally adapted a *V. alfalfae* strain to higher temperature (+3°C from optimum) and shows that adaptation of the pathogen to hot conditions is rapid and efficient. Disease responses were modified in *M. truncatula* and *M. sativa*, confirming that global climate change will create mismatch of evolutionary rates between plants and their microbial partners, either pathogenic or mutualistic.

## BIOMIMETICS OF PLANT WAX NANOSTRUCTURES PROVIDING NATURAL IMMUNITY TO HARMFUL ORGANISMS

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Biomimetics is the field of research that investigates living nature by trying to understand its basic principles and transfers them into the development of solutions, products and/or applications. Various plants show natural immunity to harmful organisms, in many cases based on wax micro- and

nano-structures that exhibit specific mechanical and structural properties, such as finely tuned fracture behavior, thereby preventing insect attachment (Borodich et al., 2010). As England and co-workers showed in 2016 surface roughness rather than surface chemistry essentially affects insect adhesion (England et al., 2016). This demonstrates the biomimetic principle that in living nature usually structure is more important than specific materials to achieve a certain functionality. One further example for this principle are structural colors in various butterflies, where periodic, regular nanostructures yield brilliant, non-bleaching colors that can easily be transferred to technological surfaces via stamping (Zobl et al., 2016).

The current presentation aims to illustrate how the research of specific structures that can be transferred from one successful plant species to other can be a non-toxic alternative to chemical pesticides. In that case physics (structure) rather than chemistry (material) can offer a sustainable approach for the protection of crops in modern agriculture against harmful organisms.

### **TRITICUM MILITINAE INTROGRESSIONS INTO BREAD WHEAT AFFECT HOST RESPONSES TO POWDERY MILDEW CHALLENGE**

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Introduction of new sources of disease resistance into breeding stocks is one of the aims of modern plant breeding. Sources of resistance may include modern and old wheat cultivars as well as other species within crop genepool. Breeding for disease resistance is focused on incorporation of single resistance genes or R-genes which are race-specific. This type of resistance can be overcome by a mutation in an avirulence gene of the pathogen and subsequent change race composition of the pathogen populations in the region. One way to broaden the resistance to a range of pathogen races is to use gene pyramiding. Besides R-gene-mediated resistance there is a non-race-specific type of resistance, which mechanism is much less studied. In current work we focused on understanding of the mechanism of non-race specific and quantitative type of resistance conferred to bread wheat cultivar Tähti by an introgression of resistance QTLs from a tetraploid wheat *Triticum militinae*. We used bread wheat lines carrying introgressions from *Triticum militinae* ( $2n = 28$ ) on 1A, 4A, 5A, 5B and 7A chromosomes and two powdery mildew *Blumeria graminis* f. sp. *tritici* isolates to identify the effects of resistance QTLs on powdery mildew development dynamics and host response. Wheat seedling leaves were inoculated by powdery mildew conidia and mycelium development was assessed by measuring rate of primary, secondary penetration of host cells and host cell responses to infection. Wheat line having a combination of all five QTLs exhibits the slowest development of powdery mildew mycelium, wheat line with QTL on 4A chromosome supports the development of powdery mildew mycelium, however in smaller extent than cultivar Tähti. A wheat line with combination of four QTLs on 1A, 5A, 5B, 7A chromosomes shows no difference in powdery mildew development from cultivar Tähti. Introgression of five QTLs on 1A, 4A, 5A, 5B and 7A chromosomes effectively decreases primary and secondary host cell penetration by powdery mildew, QTL on 4A chromosome negatively affects secondary penetration by the fungus, QTLs on 1A, 5A, 5B and 7A chromosomes decrease primary penetration and do not have any significant effect on secondary penetration efficiency. No significant difference between penetration efficiency of two powdery isolates was found. Inability to establish compatible interaction was accompanied by host cell death and hydrogen peroxide production. Data provided by this study contributes to understanding of quantitative disease resistance mechanism.

## **BIOMIMETICS OF PLANT WAX NANOSTRUCTURES PROVIDING NATURAL IMMUNITY TO HARMFUL ORGANISMS**

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