Laboratory of Plant Molecular Genetics and Cytogenetics
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The prospects for the study of the avirulence genes characteristic for the West Siberian population of wheat stem rust *Puccinia graminis* f. sp. *tritici*

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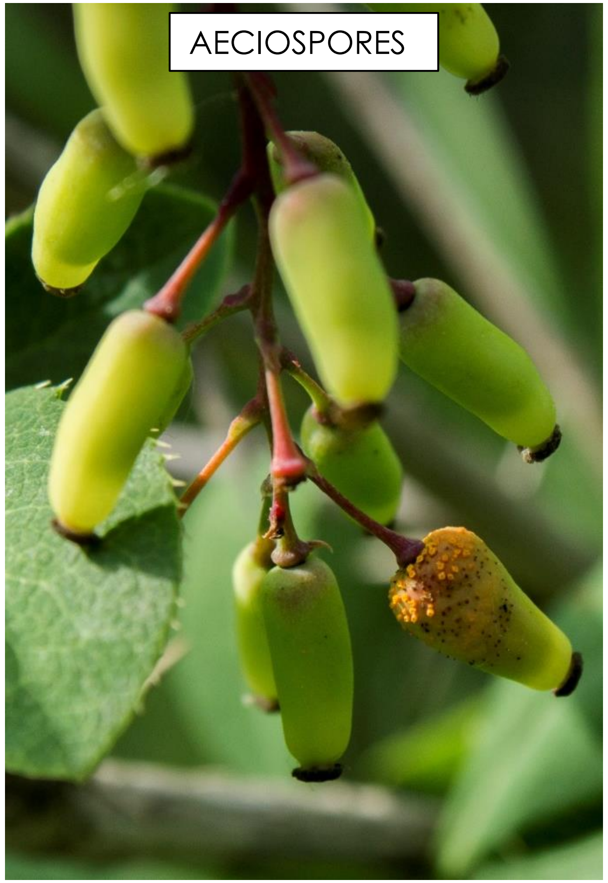
Introduction

- Wheat stem rust is a plant disease caused by pathogenic fungus *Puccinia graminis* f. sp. *tritici* which leads to significant damage of the crop. During the last decade the disease affected the crops in **West Siberia**.

Source: Scolotneva E. ICG SB RAS



Source: Kelbin V. ICG SB RAS

- The plant response to infection is determined by the correspondence of host resistance (**Sr**) and fungus avirulence/virulence (**Avr/vr**) genes.

- **We first characterized the West Siberian population of wheat stem rust**: the probable sources of infection were traced, the race composition and main avirulence genes were defined.

- During the last decade the extensive outbreaks of stem rust occured at the West Siberia region. Plant breeding for immunity to stem rust requires the extensive data on genetic characteristics of pathogen population.

- Our study is dedicated to analysis of West Siberian local population of fungal pathogen *P. graminis* f. sp. *tritici*.

Outbreaks of stem rust in Western Siberia

Year	Region	Reference
2009	Omsk	Шаманин и др., 2015
2010	Novosibirsk	Сочалова и Лихенко, 2015
2011	Novosibirsk	Сочалова и Лихенко, 2015
2014	Omsk	Шаманин и др., 2015
2016	Novosibirsk, Omsk	Шаманин и др., 2015 Сколотнева и др., 2016

Materials and methods

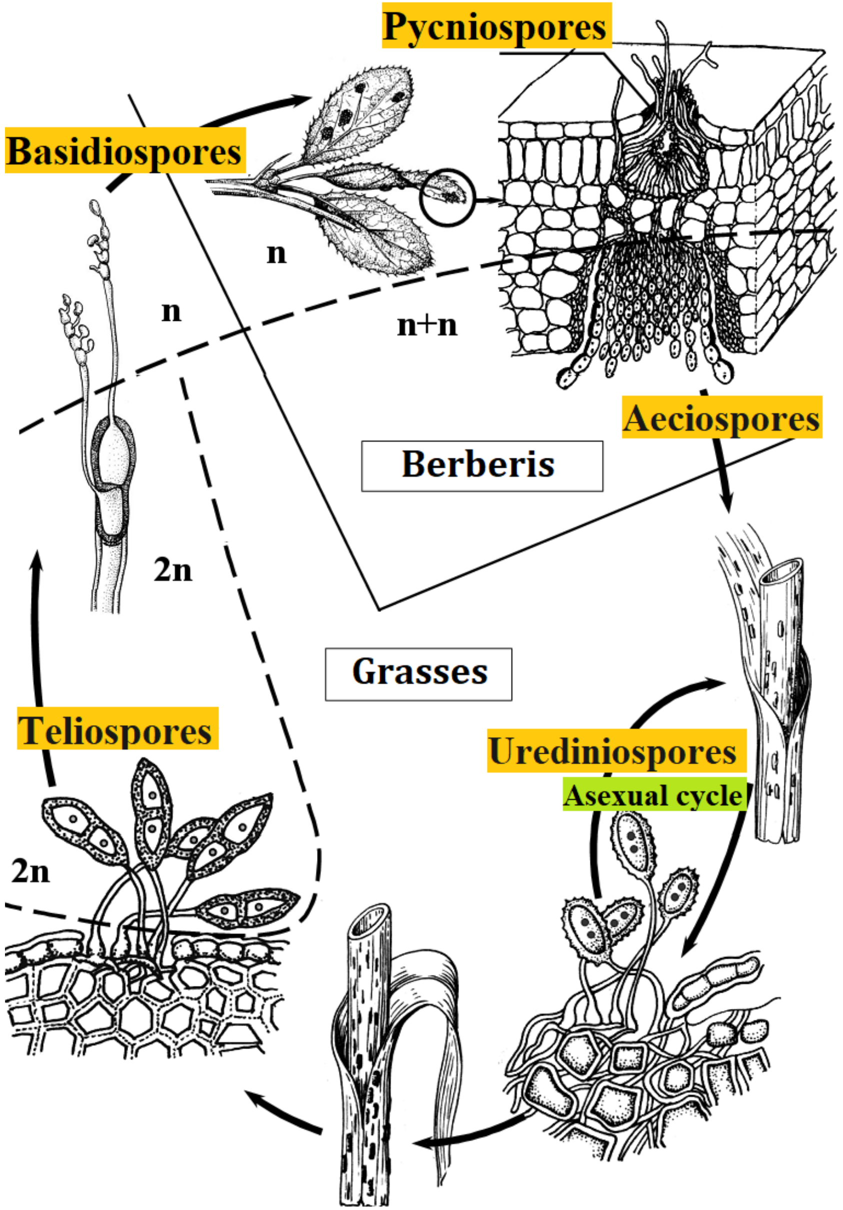
- To describe the population we applied the methods of **phytopathology** and **molecular genetics**.

- Totally we obtained the **94 single pustule isolates** (**2017-2019**) that are maintained in laboratory conditions .

Life Cycle of *Puccinia graminis*

- First, we identified the type of life cycle for the local (**Novosibirsk**) stem rust population. The fungus *P. graminis* can realize complete (**sexual**) or partial (**asexual**) life cycles.

- In case of complete cycle, the barberry (**Berberis**) plant is used as alternate host on which the sexual process is carried out



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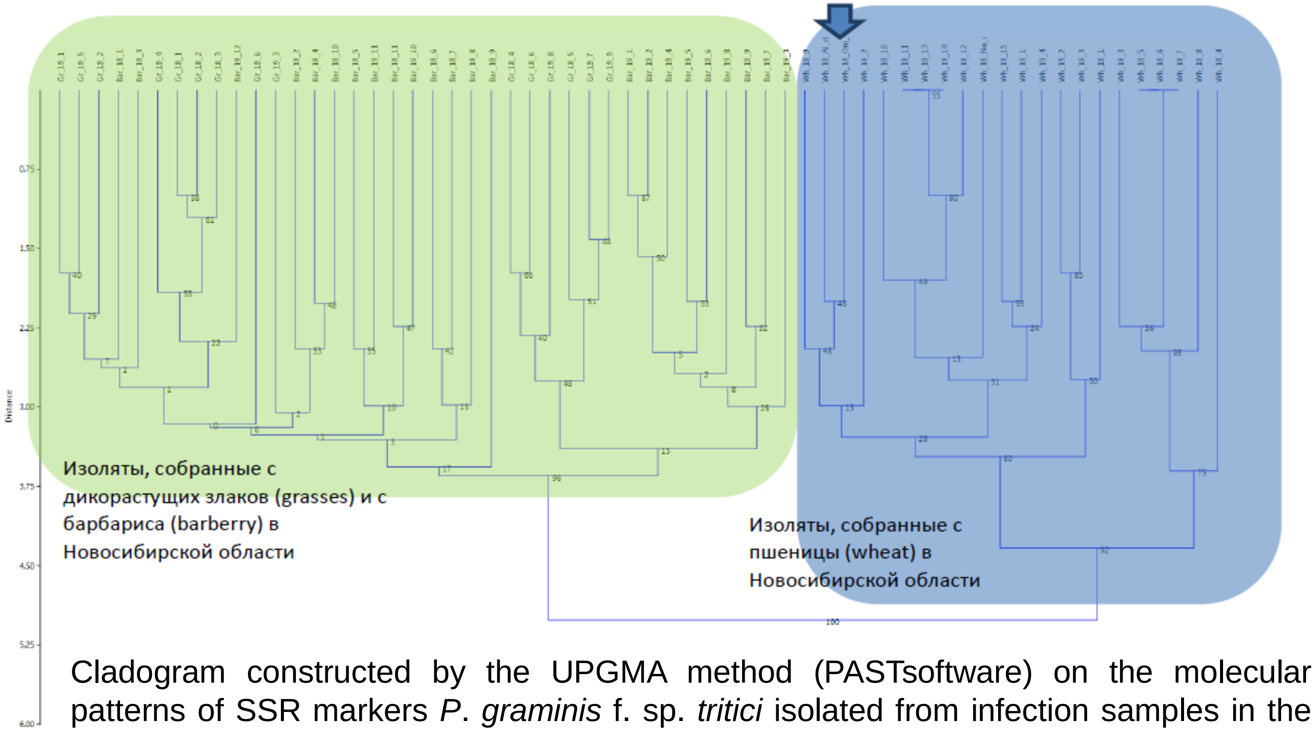
Results and Discussion

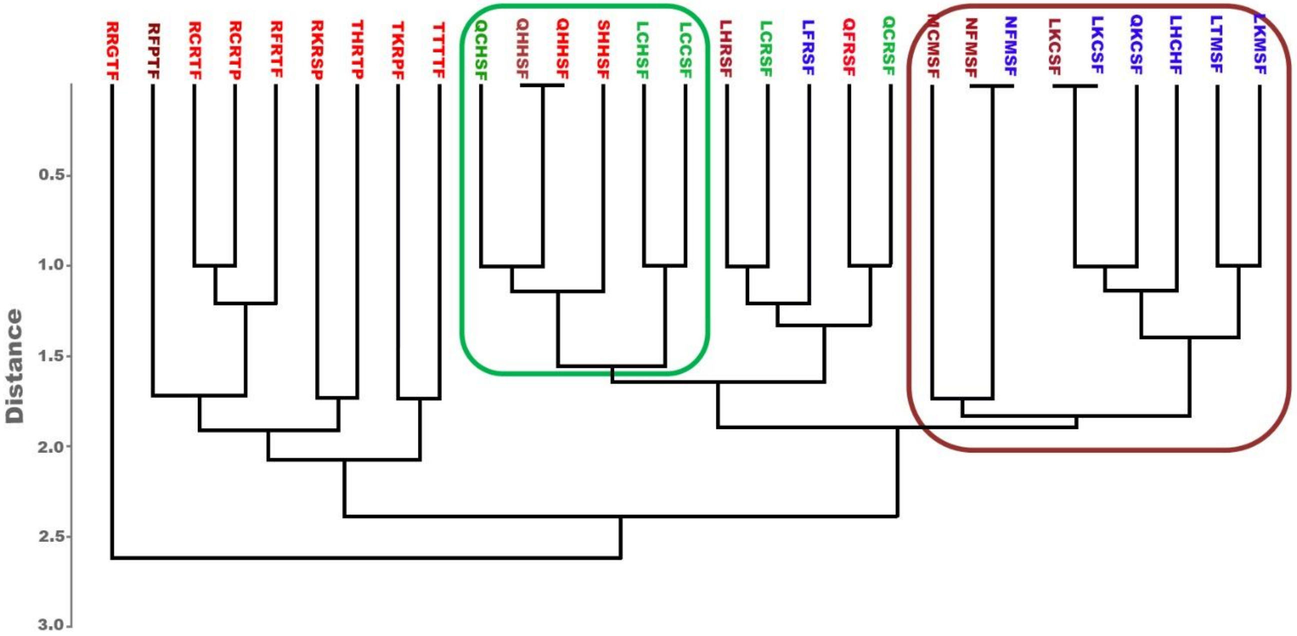
- We compared the genotyping profiles for 11 molecular SSR-markers (simple sequence repeats) of 60 rust samples collected from wheat, barberry and wild grasses.
- Processed using the PAST3 program, SSR profiles obtained from barberry and wild grasses were clustered in the same group and the samples from wheat to distinct one. **Therefore, sexual life for *P. graminis* f. sp. *secalis* through barberries and wild grasses and asexual life cycle for wheat stem rust *P. graminis* f. sp. *tritici* were supposed for local in the Novosibirsk region.**



Cladogram constructed by the UPGMA method (PASTsoftware) on the molecular patterns of SSR markers *P. graminis* f. sp. *tritici* isolated from infection samples in the Novosibirsk region 2018-2019. The arrow indicates the position of infection samples collected in the Altai Territory and Omsk Region from susceptible varieties of wheat (Wh_Al_check, Wh_Om_check).

- In the Novosibirsk region, we identified one predominant race **TKRPF** and the minor races differing for 1-3 genes.

- The cluster analysis (PAST3, Multivariate Software) of the samples originated from **Novosibirsk**, **Omsk** and **Altay regions** demonstrated that there are two independent pathogen subpopulations presented in Omsk and Altay regions sharing the races at the contact area of Novosibirsk region. **Thus, wheat stem rust in the Novosibirsk region is not endemic but carried by wind from both neighboring regions.**

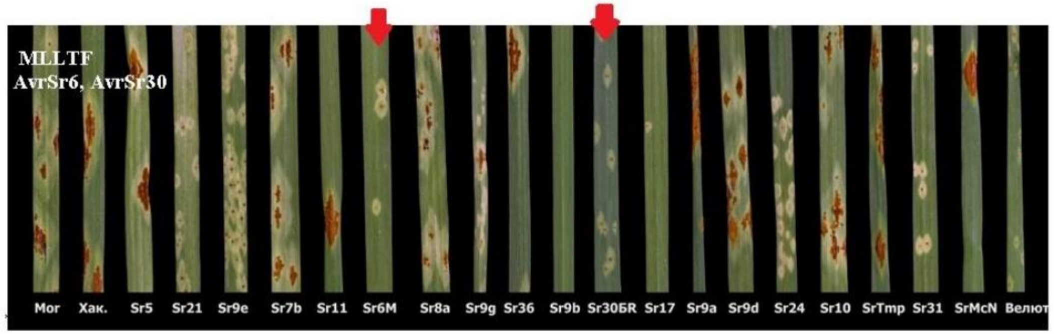


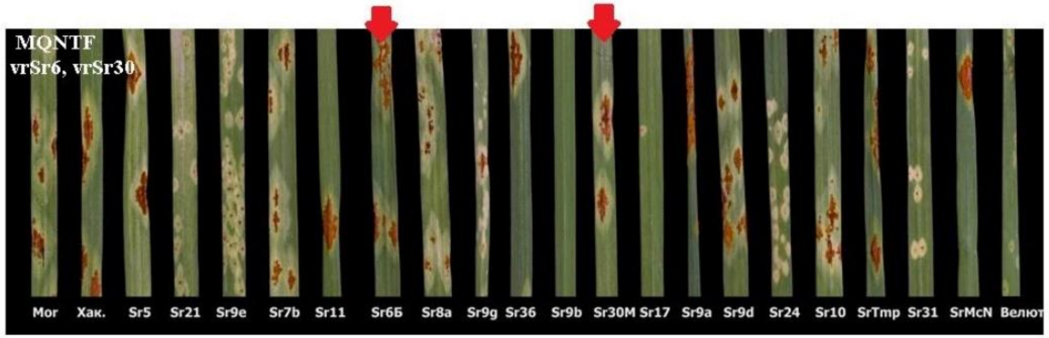
Cladogram constructed by the UPGMA method (PASTsoftware), according to the composition of the virulence genes in the compared races of *P. graminis* f. sp. *tritici* isolated from infection samples in 2017.

Legend: red and blue letters indicate races isolated from samples from the Omsk Region and Altai Territory, respectively (Shamanin et al., 2019); the names of the races isolated from samples of early and late infection in the Novosibirsk region are written in green and brown font.

- The most of *P. graminis* f. sp. *tritici* isolates were virulent to lines with resistance genes *Sr5*, *Sr9a*, *Sr9g*, *Sr10*, *Sr38*, *SrMcN*, and avirulent to lines with *Sr24*, *Sr30*, *Sr31*. Also we found the changes in the frequencies of some reaction types on lines with *Sr6*, *Sr7b*, *Sr8a*, *Sr9b*, *Sr9d*, *Sr9e*, *Sr11*, *Sr17*, *Sr21*, *Sr36*, and SrTmp genes that could be used for tracing the dynamics of virulent/avirulent types in Novosibirsk region.

- That way, we state the presence of the avirulence genes in local *P. graminis* f. sp. *tritici* population: ***AvrSr6***, ***AvrSr7b***, ***AvrSr8a***, ***AvrSr9b***, ***AvrSr9e***, ***AvrSr11***, ***AvrSr17***, ***AvrSr21***, ***AvrSr24***, ***AvrSr30***, ***AvrSr31***, ***AvrSr36***, ***AvrSrTmp***.





Selected as candidates for the genome-sequencing race **MLLTF** (isolate Duet_sp_1) and **MQNTF** (isolate Duet_sp_2) with contrasting types to communicable testernyh liniyh ***Sr6***, ***Sr30*** wheat. The isolates, respectively, carry the alleles ***AvrSr6***, ***AvrSr30*** (Duet_sp_1) and ***vrSr6***, ***vrSr30*** (Duet_sp_2).

- As a result of the foregoing we characterized the West Siberia (**in particular local Novosibirsk population**) for the first time.
- The data obtained in the study let us select the four single pustule isolates with contrasting patterns of Avr genes for further genomic analysis.

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