

Резюме: Игнатов Александр Николаевич

Адрес

Федеральное государственное бюджетное
учреждение науки Институт биоорганической
химии им. академиков М.М. Шемякина и Ю.А.
Овчинникова Российской академии наук, Москва,
Россия

Контакты

<https://www.ibch.ru/users/1188>

Преподавание

| | | | |
|---------------|--------|------|--------------------------------|
| 2015–наст.вр. | Москва | РУДН | Бактериальные болезни растений |
|---------------|--------|------|--------------------------------|

Работа в ИБХ

| | |
|-----------|---------------------------|
| 2022–2023 | Ведущий научный сотрудник |
| 2021–2021 | Старший научный сотрудник |

Владение языками

русский, английский

Научные интересы

бактериальные болезни растений, систематика бактерий, *Xanthomonas*, *Pseudomonas*, *Curtobacterium*, *Clavibacterium*, *Dickeya*, *Pectobacterium*, *Pantoea*, *Erwinia*

Членство в сообществах

Фитопатологическое общество США

Степени и звания

Доктор наук (Биологические науки, 06.01.11 — Защита растений)

Публикации

1. Tarakanov RI, Evseev PV, Vo HTN, Troshin KS, Gutnik DI, **Ignatov AN**, Toshchakov SV, Miroshnikov KA, Jafarov IH, Dzhaliilov FS (2024). *Xanthomonas* Phage PBR31: Classifying the Unclassifiable. *Viruses* 16 (3), 406, [10.3390/v16030406](https://doi.org/10.3390/v16030406)
2. Tokmakova AD, Tarakanov RI, Lukianova AA, Evseev PV, Dorofeeva LV, **Ignatov AN**, Dzhaliilov FS, Subbotin SA, Miroshnikov KA (2024). Phytopathogenic *Curtobacterium flaccumfaciens* Strains Circulating on Leguminous Plants, Alternative Hosts and Weeds in Russia. *Plants (Basel)* 13 (5), , [10.3390/plants13050667](https://doi.org/10.3390/plants13050667)
3. Evseev P, Lukianova A, Tarakanov R, Tokmakova A, Popova A, Kulikov E, Shneider M, **Ignatov A**, Miroshnikov K (2023). Prophage-Derived Regions in *Curtobacterium* Genomes: Good Things, Small Packages. *Int J Mol Sci* 24 (2), 1586, [10.3390/ijms24021586](https://doi.org/10.3390/ijms24021586)
4. Tarakanov RI, Lukianova AA, Pilik RI, Evseev PV, Miroshnikov KA, Dzhaliilov FS, Tesic S, **Ignatov AN** (2022). First report of *Curtobacterium flaccumfaciens* pv. *flaccumfaciens* causing bacterial tan spot of soybean in Russia. *PLANT DIS* 107 (7), 2211, [10.1094/PDIS-08-22-1778-PDN](https://doi.org/10.1094/PDIS-08-22-1778-PDN)
5. Pilik RI, Tesic S, **Ignatov AN**, Tarakanov RI, Dorofeeva LV, Lukianova AA, Evseev PV, Dzhaliilov FS, Miroshnikov KA (2022). First Report of *Curtobacterium flaccumfaciens* pv. *flaccumfaciens* Causing Bacterial Wilt and Blight on Sunflower in Russia. *PLANT DIS* 107 (5), 1621, [10.1094/PDIS-05-22-1203-PDN](https://doi.org/10.1094/PDIS-05-22-1203-PDN)
6. Lukianova AA, Evseev PV, Shneider MM, Dvoryakova EA, Tokmakova AD, Shpirt AM, Kabilov MR, Obratsova EA, Shashkov AS, **Ignatov AN**, Knirel YA, Dzhaliilov FS, Miroshnikov KA (2022). *Pectobacterium* versatile Bacteriophage Possum: A Complex Polysaccharide-Deacetylating Tail Fiber as a Tool for Host

- Recognition in Pectobacterial Schitoviridae. *Int J Mol Sci* 23 (19), , [10.3390/ijms231911043](https://doi.org/10.3390/ijms231911043)
7. Tarakanov RI, Lukianova AA, Evseev PV, Pilik RI, Tokmakova AD, Kulikov EE, Toshchakov SV, **Ignatov AN**, Dzhaliilov FS, Miroshnikov KA (2022). Ayka, a Novel Curtobacterium Bacteriophage, Provides Protection against Soybean Bacterial Wilt and Tan Spot. *Int J Mol Sci* 23 (18), , [10.3390/ijms231810913](https://doi.org/10.3390/ijms231810913)
 8. Tarakanov RI, Lukianova AA, Evseev PV, Toshchakov SV, Kulikov EE, **Ignatov AN**, Miroshnikov KA, Dzhaliilov FSU (2022). Bacteriophage Control of Pseudomonas savastanoi pv. glycinea in Soybean. *Plants (Basel)* 11 (7), , [10.3390/plants11070938](https://doi.org/10.3390/plants11070938)
 9. Evseev P, Lukianova A, Tarakanov R, Tokmakova A, Shneider M, **Ignatov A**, Miroshnikov K (2022). Curtobacterium spp. and Curtobacterium flaccumfaciens: Phylogeny, Genomics-Based Taxonomy, Pathogenicity, and Diagnostics. *Curr Issues Mol Biol* 44 (2), 889–927, [10.3390/cimb44020060](https://doi.org/10.3390/cimb44020060)
 10. Miroshnikov KA, Evseev PV, Lukianova AA, **Ignatov AN** (2021). Tailed lytic bacteriophages of soft rot pectobacteriaceae. *Microorganisms* 9 (9), , [10.3390/microorganisms9091819](https://doi.org/10.3390/microorganisms9091819)
 11. Lukianova AA, Evseev PV, Stakheev AA, Kotova IB, Zavriev SK, **Ignatov AN**, Miroshnikov KA (2021). Quantitative Real-Time PCR Assay for the Detection of Pectobacterium parmentieri, a Causal Agent of Potato Soft Rot. *Plants (Basel)* 10 (9), , [10.3390/plants10091880](https://doi.org/10.3390/plants10091880)
 12. Bugaeva EN, Voronina MV, Vasiliev DM, Lukianova AA, Landyshev NN, **Ignatov AN**, Miroshnikov KA (2021). Use of a specific phage cocktail for soft rot control on ware potatoes: A case study. *Viruses* 13 (6), , [10.3390/v13061095](https://doi.org/10.3390/v13061095)
 13. **(конференция)** Lukianova A, Evseev P, Tokmakova A, **Ignatov A**, Miroshnikov K (2021). Analysis of updated Pectobacteriaceae sequences highlights the need for taxonomy revisions. , 320–324, [10.1109/CSGB53040.2021.9496039](https://doi.org/10.1109/CSGB53040.2021.9496039)
 14. **(конференция)** Evseev PV, Landysheva YG, Landyshev NN, **Ignatov AN** (2021). Presence of rRNA-like regions in Genbank viral sequences. , 310–314, [10.1109/CSGB53040.2021.9496035](https://doi.org/10.1109/CSGB53040.2021.9496035)
 15. Lukianova AA, Evseev PV, Stakheev AA, Kotova IB, Zavriev SK, **Ignatov AN**, Miroshnikov KA (2021). Development of qPCR Detection Assay for Potato Pathogen Pectobacterium atrosepticum Based on a Unique Target Sequence. *Plants (Basel)* 10 (2), 1–13, [10.3390/plants10020355](https://doi.org/10.3390/plants10020355)
 16. Evseev PV, Lukianova AA, Shneider MM, Korzhenkov AA, Bugaeva EN, Kabanova AP, Miroshnikov KK, Kulikov EE, Toshchakov SV, **Ignatov AN**, Miroshnikov KA (2020). Origin and Evolution of Studiuvirinae Bacteriophages Infecting Pectobacterium: Horizontal Transfer Assists Adaptation to New Niches. *Microorganisms* 8 (11), 1–27, [10.3390/microorganisms8111707](https://doi.org/10.3390/microorganisms8111707)
 17. **(конференция)** Evseev P, **Ignatov A**, Miroshnikov K (2020). Bioinformatic basis to define the species formation within Pectobacterium and Dickeya bacterial genera. , 47–52, [10.1109/CSGB51356.2020.9214693](https://doi.org/10.1109/CSGB51356.2020.9214693)
 18. Shneider MM, Lukianova AA, Evseev PV, Shpirt AM, Kabilov MR, Tokmakova AD, Miroshnikov KK, Obratsova EA, Baturina OA, Shashkov AS, **Ignatov AN**, Knirel YA, Miroshnikov KA (2020). Autographivirinae Bacteriophage Arno 160 Infects Pectobacterium carotovorum via Depolymerization of the Bacterial O-Polysaccharide. *Int J Mol Sci* 21 (9), , [10.3390/ijms21093170](https://doi.org/10.3390/ijms21093170)
 19. Lukianova AA, Shneider MM, Evseev PV, Shpirt AM, Bugaeva EN, Kabanova AP, Obratsova EA, Miroshnikov KK, Senchenkova SN, Shashkov AS, Toshchakov SV, Knirel YA, **Ignatov AN**, Miroshnikov KA (2020). Morphologically Different Pectobacterium brasiliense Bacteriophages PP99 and PP101: Deacetylation of O-Polysaccharide by the Tail Spike Protein of Phage PP99 Accompanies the Infection. *Front Microbiol* 10, 3147, [10.3389/fmicb.2019.03147](https://doi.org/10.3389/fmicb.2019.03147)
 20. Voronina MV, Bugaeva EN, Vasiliev DM, Kabanova AP, Barannik AP, Shneider MM, Kulikov EE, Korzhenkov AA, Toshchakov SV, **Ignatov AN**, Miroshnikov KA (2019). Characterization of Pectobacterium carotovorum subsp. carotovorum Bacteriophage PP16 Prospective for Biocontrol of Potato Soft Rot. *Microbiology* 88 (4), 451–460, [10.1134/S0026261719040118](https://doi.org/10.1134/S0026261719040118)
 21. Voronina MV, Kabanova AP, Shneider MM, Korzhenkov AA, Toshchakov SV, Miroshnikov KK, Miroshnikov KA, **Ignatov AN** (2019). First report of pectobacterium carotovorum subsp. Brasiliense causing blackleg and stem rot disease of potato in Russia. *PLANT DIS* 103 (2), 364, [10.1094/PDIS-03-18-0456-PDN](https://doi.org/10.1094/PDIS-03-18-0456-PDN)
 22. Kabanova AP, Shneider MM, Korzhenkov AA, Bugaeva EN, Miroshnikov KK, Zdorovenko EL, Kulikov EE, Toshchakov SV, **Ignatov AN**, Knirel YA, Miroshnikov KA (2019). Host Specificity of the Bacteriophage PP35 Is Directed by a Tail Spike Interaction With Bacterial -Antigen, Enabling the Infection of Alternative Non-pathogenic Bacterial Host. *Front Microbiol* 9 (JAN), 3288, [10.3389/fmicb.2018.03288](https://doi.org/10.3389/fmicb.2018.03288)

23. **Ignatov AN**, Spechenkova NA, Taliansky M, Kornev KP (2019). First report of *Clavibacter michiganensis* subsp. *Michiganensis* infecting potato in Russia. *PLANT DIS* 103 (1), 147, [10.1094/PDIS-04-18-0691-PDN](https://doi.org/10.1094/PDIS-04-18-0691-PDN)
24. Ngoc Ha VT, Voronina MV, Kabanova AP, Shneider MM, Korzhenkov AA, Toschakov SV, Miroshnikov KK, Miroshnikov KA, **Ignatov AN** (2019). First report of *Pectobacterium parmentieri* causing stem rot disease of potato in Russia. *PLANT DIS* 103 (1), 144, [10.1094/PDIS-11-17-1829-PDN](https://doi.org/10.1094/PDIS-11-17-1829-PDN)
25. Shneider MM, Kabanova AP, Korzhenkov AA, Miroshnikov KK, Vo Thi NH, Toshchakov SV, Miroshnikov KA, **Ignatov AN** (2018). Draft genome sequence of *Pectobacterium atrosepticum* PB72 and complete genome sequence of the specific bacteriophage PP90. *Genome Announc* 6 (27), , [10.1128/genomeA.00473-18](https://doi.org/10.1128/genomeA.00473-18)
26. Kabanova A, Shneider M, Bugaeva E, Ha VTN, Miroshnikov K, Korzhenkov A, Kulikov E, Toschakov S, **Ignatov A**, Miroshnikov K (2018). Genomic characteristics of vB_PpaP_PP74, a T7-like Autographivirinae bacteriophage infecting a potato pathogen of the newly proposed species *Pectobacterium parmentieri*. *Arch Virol* 163 (6), 1691–1694, [10.1007/s00705-018-3766-1](https://doi.org/10.1007/s00705-018-3766-1)
27. **Ignatov AN**, Panycheva JS, Spechenkova N, Taliansky M (2018). First report of *Clavibacter michiganensis* subsp. *sepedonicus* infecting sugar beet in Russia. *PLANT DIS* 102 (12), 2634, [10.1094/PDIS-04-18-0693-PDN](https://doi.org/10.1094/PDIS-04-18-0693-PDN)
28. Shirshikov FV, Korzhenkov AA, Miroshnikov KK, Kabanova AP, Barannik AP, **Ignatov AN**, Miroshnikov KA (2018). Draft genome sequences of new genomospecies. *Genome Announc* 6 (15), e00260–18, [10.1128/genomeA.00260-18](https://doi.org/10.1128/genomeA.00260-18)
29. Sultanov RI, Arapidi GP, Vinogradova SV, Govorun VM, Luster DG, **Ignatov AN** (2016). Comprehensive analysis of draft genomes of two closely related *Pseudomonas syringae* phylogroup 2b strains infecting mono- and dicotyledon host plants. *BMC Genomics* 17 (Suppl 14), 1010, [10.1186/s12864-016-3358-y](https://doi.org/10.1186/s12864-016-3358-y)