

## Publications 2022

1	Kuchma O., J. Rebola-Lichtenberg, D. Janz, K. V. Krutovsky, C. Ammer, A. Polle, O. Gailing. 2022. Response of poplar leaf transcriptome to changed management and environmental conditions in pure and mixed with black locust stands. <i>Forests</i> 13(2), 147. <a href="https://doi.org/10.3390/f13020147">https://doi.org/10.3390/f13020147</a> .
2	Shevchenko G. V., K. V. Krutovsky. 2022. Mechanical stress effects on transcriptional regulation of genes encoding microtubule- and actin-associated proteins. <i>Physiology and Molecular Biology of Plants</i> 28: 17-30. <a href="https://doi.org/10.1007/s12298-021-01123-x">https://doi.org/10.1007/s12298-021-01123-x</a> Published: 21 January 2022 online first.
3	Biriukov V.V., Pavlov I.N., Litovka Yu.A., Oreshkova N.V., Sharov V.V., Simonov E.P., Kuzmin D.A., Krutovsky K.V. 2022. De novo transcriptome assembly and annotation of a new plant pathogenic <i>Corinectria</i> sp. strain in Siberia. <i>Mikologiya i Fitopatologiya (Mycology and Phytopathology)</i> 56(2) : 114–126. <a href="https://doi.org/10.31857/S0026364822020052">https://doi.org/10.31857/S0026364822020052</a> .
4	Wati, R., Amandita, F.Y., Brambach, F., Siregar, I.Z., Gailing, O. & C.C. de Melo Moura. 2022. Filling gaps of reference DNA barcodes in <i>Syzygium</i> from rainforest fragments in Sumatra. <i>Tree Genetics and Genomes</i> 18:6. <a href="https://doi.org/10.1007/s11295-022-01536-z">https://doi.org/10.1007/s11295-022-01536-z</a> .
5	Müller, M., Niesar, M., Berens, I. & O. Gailing. 2022. Genotyping by sequencing reveals lack of local genetic structure between two German <i>Ips typographus</i> L. populations. <i>Forestry Research</i> 2: 1. <a href="https://doi.org/10.48130/FR-2022-0001">https://doi.org/10.48130/FR-2022-0001</a> .
6	de Melo Moura, C.C., Setyaningsih, C.A., Li, K., Merk, M.S., Schröck, S., Raffiudin, R., Grass, I., H., Tscharnke, T., Westphal, C. & O. Gailing. 2022. Biomonitoring via DNA metabarcoding and light microscopy of bee pollen in rainforest transformation landscapes of Sumatra. <i>BMC Ecology and Evolution</i> 22:51. <a href="https://doi.org/10.1186/s12862-022-02004-x">https://doi.org/10.1186/s12862-022-02004-x</a> .
7	Götz, J., Rajora, O.P. & O. Gailing. 2022. Genetic structure of natural northern range-margin mainland, peninsular, and island populations of northern red oak ( <i>Quercus rubra</i> L.). <i>Frontiers in Ecology and Evolution</i> 10:907414. <a href="https://doi.org/10.3389/fevo.2022.907414">https://doi.org/10.3389/fevo.2022.907414</a> .
8	Sayed Jalal Moosavi, S.J., Budde, K.B., Mueller, M. & O. Gailing. 2022. Genetic diversity and fine-scale spatial genetic structure of the near-threatened <i>Pinus gerardiana</i> in Gardiz, Afghanistan. <i>Plant Ecology and Evolution</i> 155 (3): 363–378. <a href="https://doi.org/10.5091/plecevo.95754">https://doi.org/10.5091/plecevo.95754</a> .
9	Stein, F., Wagner, S., Bräsicke, N., Moura, C., Gailing, O. & M. Götz. 2022. A non-destructive high-speed procedure to obtain DNA barcodes from soft-bodied insect samples with a focus on the dipteran section of Schizophora. <i>Insects</i> 13: 679. <a href="https://doi.org/10.3390/insects13080679">https://doi.org/10.3390/insects13080679</a> .
10	Burger, K. & O. Gailing. 2022. Genetic variability of indigenous ( <i>Quercus robur</i> L.) and late flushing oak ( <i>Quercus robur</i> L. subsp. <i>slavonica</i> (Gáyer) Mátyás) in adult stands compared with their natural regeneration. <i>European Journal of Forest Research</i> 141: 1073–1088 <a href="https://doi.org/10.1007/s10342-022-01491-3">https://doi.org/10.1007/s10342-022-01491-3</a> .
11	Götz, J., & O. Gailing. 2022. A novel set of polymorphic chloroplast microsatellite markers for northern red oak ( <i>Q. rubra</i> L.). <i>Plant Genetic Resources: Characterization and Utilization</i> 20: 174-177. <a href="https://doi.org/10.1017/S1479262122000156">https://doi.org/10.1017/S1479262122000156</a>

12	Borthakur, D., Busov, V., Cao, X.H., Du, Q., Gailing, O., Isik, F., Ko, J.-H., Li, C., Li, Q., Niu, S., Qu, Q., Vu, T.H.G., Wang, X.-R., Wei, Z., Lin Zhang, L. & H. Wei. 2022. Current status and trends of forest genomics. <i>Forestry Research</i> 2:11. <a href="https://doi.org/10.48130/FR-2022-0011">https://doi.org/10.48130/FR-2022-0011</a> .
13	Hartung, T., Budde, K.B., & O. Gailing. 2022. Characterisation of nuclear microsatellite (SSR) markers for European ash ( <i>Fraxinus excelsior</i> L.) and their transferability across six related species. <i>Silvae Genetica</i> 71: 65 -71. <a href="https://doi.org/10.2478/sg-2022-0008">https://doi.org/10.2478/sg-2022-0008</a> .
14	Mehdi Youneesi-Hamzekhanlu, M. & O. Gailing. 2022. Genome-wide SNP markers accelerate perennial forest tree breeding rate for disease resistance through marker-assisted selection and genome-wide selection. <i>International Journal of Molecular Sciences</i> 23: 12315. <a href="https://doi.org/10.3390/ijms232012315">https://doi.org/10.3390/ijms232012315</a> .
15	Halmschlag, C.B., Carneiro de Melo Moura, C., Brambach, F., Siregar, I.Z. & O. Gailing. 2022. Molecular and morphological survey of Lamiaceae species in converted landscapes in Sumatra. <i>PLOSone</i> 17 (12): e0277749. <a href="https://doi.org/10.1371/journal.pone.0277749">https://doi.org/10.1371/journal.pone.0277749</a> .
16	Moosavi SJ, Budde KB, Müller M, Gailing O (2022) Genetic diversity and fine-scale spatial genetic structure of the near-threatened <i>Pinus gerardiana</i> in Gardiz, Afghanistan. <i>Plant Ecology and Evolution</i> , 155, 363-378, <a href="https://doi.org/10.5091/plecevo.95754">https://doi.org/10.5091/plecevo.95754</a> .
17	Santos-del-Blanco L, Olsson S, Budde KB, Grivet D, González-Martínez SC, Alía R, Robledo-Arnuncio JJ (2022) On the feasibility of estimating contemporary effective population size (Ne) for genetic conservation and monitoring of forest trees. <i>Biological Conservation</i> , 273, 109704, <a href="https://doi.org/10.1016/j.biocon.2022.109704">https://doi.org/10.1016/j.biocon.2022.109704</a> .
18	Sterck L, María N, Cañas RA, Miguel M, Perdiguero P, Raffin A, Budde KB, López-Hinojosa M et al. (2022) Maritime pine genomics in Focus. In: De La Torre AR (ed.) <i>The Pine Genomes</i> , pp. 67-123 Springer, Cham.
19	Gailing O, Budde KB, Müller M (2022) Veränderung genetischer Variationsmuster von Waldbäumen unter Gesichtspunkten des Klimawandels. <i>AFJZ</i> , 192, 93-105.
20	Cao, H.X. Giang Thi Ha Vu, G.T.H. & O. Gailing. 2022. From genome sequencing to CRISPR-based genome editing for climate-resilient forest trees. <i>International Journal of Molecular Sciences</i> 23, 966. <a href="https://doi.org/10.3390/ijms23020966">https://doi.org/10.3390/ijms23020966</a> .
21	Müller, M., Niesar, M., Berens, I. & O. Gailing. 2022. Genotyping by sequencing reveals lack of local genetic structure between two German <i>Ips typographus</i> L. populations. <i>Forestry Research</i> 2: 1. <a href="https://doi.org/10.48130/FR-2022-0001">https://doi.org/10.48130/FR-2022-0001</a> .
22	Bondar, E. I., M. Troukhan, K. V. Krutovsky, T. V. Tatarinova. 2022. Genome-wide prediction of transcription start sites in conifers. <i>International Journal of Molecular Sciences</i> 23(3): 1735. <a href="https://doi.org/10.3390/ijms23031735">https://doi.org/10.3390/ijms23031735</a> .
23	Kirichenko, A. D., A. A. Poroshina, D. Yu. Sherbakov, M. G. Sadovsky, K. V. Krutovsky. 2022. Comparative analysis of alignment-free genome clustering and whole genome alignment-based phylogenomic relationship of coronaviruses. <i>PLoS One</i> 17(3): e0264640. <a href="https://doi.org/10.1371/journal.pone.0264640">https://doi.org/10.1371/journal.pone.0264640</a> .
24	Popov, V. N., M. Yu. Syromyatnikov, C. Franceschi, A. A. Moskalev, K. V. Krutovsky. 2022. Genetic mechanisms of aging in plants: What can we learn from them? <i>Ageing Research Reviews</i> 77: 101601. <a href="https://doi.org/10.1016/j.arr.2022.101601">https://doi.org/10.1016/j.arr.2022.101601</a>
25	Batalova, A. Y., Y. A. Putintseva, M. G. Sadovsky, K. V. Krutovsky. 2022. Comparative genomics of seasonal senescence in forest trees. <i>International Journal of Molecular Sciences</i> 23(7): 3761. <a href="https://doi.org/10.3390/ijms23073761">https://doi.org/10.3390/ijms23073761</a> .

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27	Schulte L., S. Meucci, K. Stoof-Leichsenring, T. Heitkam, N. Schmidt, B. von Hippel, A. A. Andreev, B. Diekmann, B. K. Biskaborn, B. Wagner, M. Melles, L. A. Pestryakova, I. G. Alsos, C. Clarke, K. V. Krutovsky, U. Herzschuh. 2022. <i>Larix</i> species range dynamics in Siberia since the Last Glacial captured from sedimentary ancient DNA. <i>Communications Biology</i> 5: 570. <a href="https://doi.org/10.1038/s42003-022-03455-0">https://doi.org/10.1038/s42003-022-03455-0</a> .
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29	Bondar, E. I., S. I. Feranchuk, K. A. Miroshnikova, V. V. Sharov, D. A. Kuzmin, N. V. Oreshkova, K. V. Krutovsky. 2022. Annotation of Siberian larch ( <i>Larix sibirica</i> Ledeb.) nuclear genome – one of the most cold resistant tree species in the only seasonal senescence Genus in Pinaceae. <i>Plants</i> 11(15): 2062. <a href="https://doi.org/10.3390/plants11152062">https://doi.org/10.3390/plants11152062</a> .
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32	Zhirnova D.F., Belokopytova L.V., Krutovsky K.V., Kholdaenko Y.A., Babushkina E.A., Vaganov E.A. 2022 Spatial-coherent dynamics and climatic signal in radial growth of Siberian stone pine ( <i>Pinus sibirica</i> Du Tour) in subalpine stands along the Western Sayan Mountains. <i>Forests</i> 13(12): 1994. <a href="https://doi.org/10.3390/f13121994">https://doi.org/10.3390/f13121994</a> .