

Publications from 2006 to 2017

851	Leinemann, L., Hosius, B., Bergmann, F., Arenhövel, W., Rogge, M., Voth, W. & O. Gailing. 2017. DNS-Genmarker Analysen an Uralteichen in verschiedenen Regionen Deutschlands. <i>Allgemeine Forst- und Jagdzeitung</i> 188:210-221.
850	Müller M, Finkeldey R (2017) Genetic and adaptive trait variation in seedlings of European beech provenances from Northern Germany. <i>Silvae Genetica</i> 65, 65-73. doi: 10.1515/sg-2016-0018
849	Wu, Y., R. Zhang, R., Staton, M., Schlarbaum, S.E., Coggeshall, M.V., Romero-Severson, J., Carlson, J.E., Zembower, N., Liang, H., Xu, Y., Drautz-Moses, D.I., Schuster, S.C & O. Gailing. 2017. Development of genic and genomic microsatellites in <i>Gleditsia triacanthos</i> L. (Fabaceae) using Illumina sequencing. <i>Annals of Forest Research</i> 60:343-350.
848	Harmon, M., Lane, T., Staton, M., Coggeshall, M.V., Best, T., Chen, C.-C., Liang, H., Zembower, N., Drautz-Moses, D.I., Hwee, Y. Z., Schuster, S.C., Schlarbaum, S.E., John E. Carlson, J.E. & O. Gailing. Development of novel genic microsatellite markers from transcriptome sequencing in sugar maple (<i>Acer saccharum</i> Marsh.). <i>BMC Research Notes</i> 10:369
847	Khodwekar, S. & O. Gailing. 2017. Evidence for environment-dependent introgression of adaptive genes between two red oaks species with different drought adaptations. <i>American Journal of Botany</i> 104: 1088-1098.
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844	Semerikov, V.L., S.A. Semerikova, Y.A. Putintseva, V. V. Tarakanov, I. V. Tikhonova, A. I. Vidyakin, N.V. Oreshkova, and K.V. Krutovsky, 2017 Colonization history of Scots pine in Eastern Europe and North Asia based on mitochondrial DNA variation. <i>Tree Genetics and Genomes</i> (accepted)
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842	Moskalev, A. A., A. V. Kudryavtseva, A. S. Grafodatsky, V. R. Beklemisheva, N. A. Serdyukova, K. V. Krutovsky, V. V. Sharov, I. V. Kulakovsky, A. S. Lando, A. S. Kasianov, A. V. Snezhkina ¹ , D. A. Kuzmin, Y. A. Putintseva, S. I. Feranchuk, M. V. Shaposhnikov, V. Fraiefeld ¹ , M. Toren, V. V. Sitnik. 2017. De novo assembling and primary analysis of genome and transcriptome of gray whale <i>Eschrichtius robustus</i> . <i>BMC Evolutionary Biology</i> 17(Suppl 2):258; https://doi.org/10.1186/s12862-017-1103-z
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