

Publications

Fischer J, Müller SY, Netzker T, Jäger N, Gacek-Matthews A, Scherlach K, Stroe MC, García-Altares M, Pezzini F, Schoeler H, Reichelt M, Gershenzon, Krespach MK, Shelest E, Schroeckh V, Valiante V, Heinzl T, Hertweck C, Strauss J, Brakhage AA (2018) Chromatin mapping identifies BasR, a key regulator of bacteria-triggered production of fungal secondary metabolites. *eLife* 7, e40969.

Tauber JP, Gallegos-Monterrosa R, Kovacs AT, Shelest E, Hoffmeister D (2018) Dissimilar pigment regulation in *Serpula lacrymans* and *Paxillus involutus* during interkingdom interactions. *Microbiology* 164(1), 65-77.

Blin K, Wolf T, Chevrette M, Lu X, Schwalen C, Kautsar S, Suarez Duran, H, de los Santos E, Kim HU, Nave M, Dickschat J, Mitchell D, Shelest E, Breitling R, Takano E, Lee SY, Weber T, Medema M (2017) antiSMASH 4.0 — Improvements in Chemistry Prediction and Gene Cluster Boundary Identification. *Nucleic Acids Res* 45(W1), W36-W41.

de Vries RP, Riley R, Wiebenga A, Aguilar-Osorio G, Amillis S, Uchima CA, Anderluh G, Asadollahi M, Askin M, Barry K, Battaglia E, Bayram Ö, Benocci T, Braus-Stromeyer SA, Caldana C, Cánovas D, Cerqueira GC, Chen F, Chen W, Choi C, Clum A, Dos Santos RA, Damásio AR, Diallinas G, Emri T, Fekete E, Flipphi M, Freyberg S, Gallo A, Gournas C, Habgood R, Hainaut M, Harispe ML, Henrissat B, Hildén KS, Hope R, Hossain A, Karabika E, Karaffa L, Karányi Z, Kraševac N, Kuo A, Kusch H, LaButti K, Lagendijk EL, Lapidus A, Levasseur A, Lindquist E, Lipzen A, Logrieco AF, MacCabe A, Mäkelä MR, Malavazi I, Melin P, Meyer V, Mielnichuk N, Miskei M, Molnár ÁP, Mulé G, Ngan CY, Orejas M, Orosz E, Ouedraogo JP, Overkamp KM, Park HS, Perrone G, Piumi F, Punt PJ, Ram AF, Ramón A, Rauscher S, Record E, Riaño-Pachón DM, Robert V, Röhrig J, Ruller R, Salamov A, Salih NS, Samson RA, Sándor E, Sanguinetti M, Schütze T, Sepčić K, Shelest E, Sherlock G, Sophianopoulou V, Squina FM, Sun H, Susca A, Todd RB, Tsang A, Unkles SE, van de Wiele N, van Rossen-Uffink D, Oliveira JV, Vesth TC, Visser J, Yu JH, Zhou M, Andersen MR, Archer DB, Baker SE, Benoit I, Brakhage AA, Braus GH, Fischer R, Frisvad JC, Goldman GH, Houbaken J, Oakley B, Pócsi I, Scazzocchio C, Seiboth B, vanKuyk PA, Wortman J, Dyer PS, Grigoriev IV (2017) Comparative genomics reveals high biological diversity and specific adaptations in the industrially and medically important fungal genus *Aspergillus*. *Genome Biol* 18(1), 28.

Shelest E (2017) Transcription Factors in Fungi: TFome Dynamics, Three Major Families, and Dual-Specificity TFs. *Front Genet* 8, 53.

Corrochano LM, Kuo A, Marcet-Houben M, Polaino S, Salamov A, Villalobos-Escobedo JM, Grimwood J, Álvarez MI, Avalos J, Bauer D, Benito EP, Benoit I, Burger G, Camino LP, Cánovas D, Cerdá-Olmedo E, Cheng JF, Domínguez A, Eliáš M, Eslava AP, Glaser F, Gutiérrez G, Heitman J, Henrissat B, Iturriaga EA, Lang BF, Lavín JL, Lee SC, Li W, Lindquist E, López-García S, Luque EM, Marcos AT, Martin J, McCluskey K, Medina HR, Miralles-Durán A, Miyazaki A, Muñoz-Torres E, Oguiza JA, Ohm RA, Olmedo M, Orejas M, Ortiz-Castellanos L, Pisabarro AG, Rodríguez-Romero J, Ruiz-Herrera J, Ruiz-Vázquez R, Sanz C, Schackwitz W, Shahriari M, Shelest E, Silva-Franco F, Soanes D, Syed K, Tagua VG, Talbot NJ, Thon MR, Tice H, de Vries RP, Wiebenga A, Yadav JS, Braun EL, Baker SE, Garre V, Schmutz J, Horwitz BA, Torres-Martínez S, Idnurm A, Herrera-Estrella A, Gabaldón T, Grigoriev IV (2016) Expansion of signal transduction pathways in fungi by extensive genome duplication *Current Biology* 26(12), 1577-1584.

Guthke R, Gerber S, Conrad T, Vlaic S, Durmus S, Cakir T, Sevilgen E, Shelest E, Linde J (2016) Data-based reconstruction of gene regulatory networks of fungal pathogens. *Front Microbiol* 7, 570.

Kröber A, Scherlach K, Hortschansky P, Shelest E, Staib P, Kniemeyer O, Brakhage AA (2016) HapX Mediates Iron Homeostasis in the Pathogenic Dermatophyte *Arthroderma benhamiae* but Is Dispensable for Virulence. *PLOS ONE* 11(3), e0150701.

Kroll K, Shekhova E, Mattern DJ, Thywissen A, Jacobsen ID, Strassburger M, Heinekamp T, Shelest E, Brakhage AA, Kniemeyer O (2016) The hypoxia-induced dehydrogenase HorA is required for coenzyme Q10 biosynthesis, azole sensitivity and virulence of *Aspergillus fumigatus* *Mol Microbiol* 101(1), 92-108.

Penselin D, Münsterkötter M, Kirsten S, Felder M, Taudien S, Platzer M, Asheldford K, Paszkiewicz KH, Harrison R, Hughes DJ, Wolf T, Shelest E, Graap J, Hoffmann J, Wenzel C, Wöltje N, King KM, Fitt BDL, Güldener U, Avrova A, Knogge W (2016) Comparative genomics to explore phylogenetic relationship, cryptic sexual potential and host specificity of *Rhynchosporium* species on grasses *BMC Genomics* 17(1), 953.

Rischer M, Klassen J, Wolf T, Guo H, Shelest E, Clardy J, Beemelmans C (2016) Draft Genome Sequence of *Shewanella* sp. P1-14-1, a Bacterial Inducer of Settlement and Morphogenesis in Larvae of the Marine Hydroid Hydractinia Echinata *Genome Announc* 4(1), e00003-16.

Shelest E, Wingender E (2016) Systems biology of transcription regulation *Front. Genet.* 7, 124. (Review)

Tauber JP, Schroeckh V, Shelest E, Brakhage AA, Hoffmeister D (2016) Bacteria induce pigment formation in the basidiomycete *Serpula lacrymans*. *Environ Microbiol* 18, 5218-5227.

Valiante V, Baldin C, Hortschansky P, Jain R, Thywißen A, Straßburger M, Shelest E, Heinekamp T, Brakhage AA (2016) The *Aspergillus fumigatus* conidial melanin production is regulated by the bifunctional bHLH DevR and MADS-box RlmA transcription factors. *Mol Microbiol* 102(2), 321-335.

Voigt K, Wolf T, Ochsenreiter K, Nagy G, Kaerger K, Shelest E, Papp T (2016) 15 Genetic and metabolic aspects of primary and secondary metabolism of the Zygomycetes In: Hoffmeister D. (eds) *Biochemistry and Molecular Biology* (ed.) The Mycota Vol. III: 3rd edition. III, pp. 361-385. Springer Verlag, Berlin, Heidelberg, New York. (Review)

Klassen JL, Rischer M, Wolf T, Guo H, Shelest E, Clardy J, Beemelmans C (2015) Genome Sequences of Three *Pseudoalteromonas* Strains P1-8, P1-11 and P1-30 Isolated from the Marine Hydroid *Hydractinia echinata* *Genome Announc.* 3(6), e01380-15.

Klassen JL, Wolf T, Rischer M, Guo H, Shelest E, Clardy J, Beemelmans C (2015) Draft Genome Sequences of Six *Pseudoalteromonas* sp. Strains P1-7a, P1-9, P1-13-1a, P1-16-1b, P1-25 and P1-26, which Induce Larval Settlement and Metamorphosis in *Hydractinia echinata* *Genome Announc.* 3(6), e01477-15.

Shelest E, Heimerl N, Fichtner M, Sasso S (2015) Multimodular type I polyketide synthases in algae evolve by module duplications and displacement of AT domains in trans *BMC genomics* 16(1), 1015.

- Vettorazzi S, Bode C, Dejager L, Frappart L, Shelest E, Kläßen C, Tasdogan A, Reichardt HM, Libert C, Schneider M, Weih F, Uhlenhaut H, David J-P, Gräler M, Kleiman A, Tuckermann JP (2015) Glucocorticoids limit acute lung inflammation in concert with inflammatory stimuli by induction of SphK1 *Nature Communications* 6, 7796.
- Wolf T, Shelest V, Nath N, Shelest E (2015) CASSIS and SMIPS: Promoter-based prediction of secondary metabolite gene clusters in eukaryotic genomes *Bioinformatics* 32(8), 1138-1143.
- Sasso S, Shelest E, Hoffmeister D (2014) Comments on the distribution and phylogeny of type I polyketide synthases and nonribosomal peptide synthetases in eukaryotes. *Proc Natl Acad Sci U S A* 111, E3946.
- Schwartz VU, Winter S, Shelest E, Marcet-Houben M, Horn F, Wehner S, Linde J, Valiante V, Sammeth M, Riege K, Nowrousian M, Kaerger K, Jacobsen ID, Marz M, Brakhage AA, Gabaldón T, Böcker S, Voigt K (2014) Gene expansion shapes genome architecture in the human pathogen *Lichtheimia corymbifera*: an evolutionary genomics analysis in the ancient terrestrial Mucorales (Mucoromycotina). *PLOS Genetics* 10(8), e1004496.
- Shelest E, Voigt K (2014) Genomics to study basal lineage fungal biology: phylogenomics suggest a common origin In: Alistair J.B. Brown (ed.) *The Mycota XIII, Fungal Genomics* 2. edition. 13, pp. 31-60. Springer, Berlin, Heidelberg.
- Zaehle C, Gressler M, Shelest E, Geib E, Hertweck C, Brock M (2014) Terrein Biosynthesis in *Aspergillus terreus* and Its Impact on Phytotoxicity. *Chem Biol* 21(6), 719-731.
- Wolf T, Shelest V, Shelest E (2013) Motif-based method for genome-wide prediction of eukaryotic gene clusters In: A. Petrosino, L. Maddalena, P. Pala (eds.) *Lecture Notes in Computer Science (LNCS) 2nd International Workshop on Pattern Recognition in Proteomics, Structural Biology and Bioinformatics*, Naples, Italien, 09/09/2013-09/10/2013, 8158, pp. 389-398. Springer-Verlag, Berlin, Heidelberg.
- Druzhinina IS, Shelest E, Kubicek CP (2012) Novel traits of *Trichoderma* predicted through the analysis of its secretome. *FEMS Microbiol Lett* 337(1), 1-9.
- Gerke J, Bayram O, Feussner K, Landesfeind M, Shelest E, Feussner I, Braus GH (2012) Breaking the silence: protein stabilization uncovers silenced biosynthetic gene clusters in the fungus *Aspergillus nidulans*. *Appl Environ Microbiol* 78(23), 8234-8244.
- Martinez DA, Oliver BG, Gräser Y, Goldberg JM, Li W, Martinez-Rossi NM, Monod M, Shelest E, Barton RC, Birch E, Brakhage AA, Chen Z, Gurr SJ, Heiman D, Heitman J, Kost I, Rossi A, Saif S, Samalova M, Saunders CW, Shea T, Summerbell RC, Xu J, Young S, Zeng Q, Birren BW, Cuomo CA, White TC (2012) Comparative genome analysis of *Trichophyton rubrum* and related dermatophytes reveals candidate genes involved in infection. *MBio* 3(5), e00259.
- Bergmann S, Funk AN, Scherlach K, Schroeckh V, Shelest E, Horn U, Hertweck C, Brakhage AA (2010) Activation of a silent fungal polyketide biosynthesis pathway through regulatory cross talk with a cryptic nonribosomal peptide synthetase gene cluster. *Appl Environ Microbiol* 76(24), 8143-8149.
- Shelest V, Albrecht D, Shelest E (2010) DistanceScan: a tool for promoter modeling. *Bioinformatics* 26(11), 1460-1462.

Schroeckh V, Scherlach K, Nützmann HW, Shelest E, Schmidt-Heck W, Schuemann J, Martin K, Hertweck C, Brakhage AA (2009) Intimate bacterial-fungal interaction triggers biosynthesis of archetypal polyketides in *Aspergillus nidulans*. *Proc Natl Acad Sci U S A* 106(34), 14558-14563.

Shelest E (2008) Transcription factors in fungi. *FEMS Microbiol Lett* 286(2), 145-151.

*equal contribution #corresponding author