

Synmycanthrosium: The Tom Volk Memorial Symposium May 21–22, 2023

La Crosse, WI

May 21, 2023

This event will be held at Myrick Park Center

4:30–7:30p.m.	Myrick Park Center (The Nature Place) - La Crosse Room Reception and Foray Meet-up	La Crosse Room
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May 22, 2023

All events will be in the Student Union, University of Wisconsin-La Crosse

8:30–9 a.m.	Breakfast: <i>Polyeotrophia (state of many dawn food, Greek)</i>	3310
9–9:15 a.m.	Opening Remarks: <i>Logarche (beginning speech, G)</i>	3310
9:15–10 a.m.	KEYNOTE PRESENTATION: Primoratio (<i>first speech, Latin</i>) Fungi, Fun Guys, and What's Keen About Mycology Heather Hallen-Adams, Ph.D. Tom Volk has been an important mentor, colleague, and friend to more people than I can count. This talk will give a necessarily personal and incomplete reflection on Tom and his impact on amateur and professional mycology, with emphasis on the parts where I most interacted with him (Mycological Society of America, Smith Forays, and Edible and Poisonous Mushrooms of Michigan workshops), sharing pictures, anecdotes, and even science.	3310
10–10:10 a.m.	Break: <i>Brevicessor (state of short yield, L)</i>	3310
	Research Presentations: <i>Cerebrofatorium (Place for brains to speak, L)</i>	
10:10–10:30 a.m.	<i>Laetiporus volkii</i>, a new species named in honor of Thomas J. Volk Dan Linder, USDA Forest Service, Center for Forest Mycology Research, Madison, WI A new species in the genus <i>Laetiporus</i> is described using morphological and molecular data. Although morphologically distinct with a white-pore layer, this species was not previously recognized because the ITS region is very similar to a species currently known as <i>L. sulphureus</i> s.s. (species clade E). Tom Volk made many collections of this species in the early 1990s, but work with the species was complicated by the fact that its single spores are extremely difficult to germinate, making mating compatibility tests impossible. With the use of multiple gene regions, this species is now known to form a monophyletic clade distinct from all other species, including <i>L. cincinnatus</i> , a species that occurs in the same geographic region and which also has a white pore layer. This new species, <i>L. volkii</i> , can be distinguished from <i>L. cincinnatus</i> because it does not form a rosette at the base of trees, but instead fruits in a shelving fashion. Tom Volk inspired our work with <i>Laetiporus</i> and loved these brightly colored, edible fungi and we name this	3310

	new species in his honor. Co-authors: Mark T. Banik and Jonathan M. Palmer, USDA Forest Service, Center for Forest Mycology Research, Madison, WI	
10:30–10:50 a.m.	Blastomycosis Diagnosed in a Nonhyperendemic Area Bridget Pfaff, Gundersen Health System Blastomycosis, caused by the dimorphic fungus <i>Blastomyces dermatitidis</i>, is hyperendemic in northern Wisconsin and is unevenly distributed in the rest of the state and contiguous Minnesota. Clinical presentation of this illness has been characterized by localized outbreaks and sporadic cases in endemic areas. Methods: Using ICD-9 CPT codes, we queried our electronic health record system to identify cases of blastomycosis diagnosed at Gundersen Health System over a 32-year period. Gundersen serves a region outside the hyperendemic area of Wisconsin. Records so identified were reviewed for demographic and clinical features. We attempted to interview patients with a blastomycosis diagnosis from 2002 through 2006. Blastomycosis data also were collected from the states of Wisconsin and Minnesota from 2002 through 2006 and assessed for trends. Results: Thirty-six patients had blastomycosis diagnoses at Gundersen Health System during the study period, as identified by ICD-9 code. Of these, 10 were excluded from further review because they were either miscoded or the code indicated a previous diagnosis. The remaining 26 patients were included in the study. Premorbid conditions included diabetes (38%) and smoking (62%). The mean time from onset of symptoms to the first laboratory specimen positive for <i>B dermatitidis</i> was 51 days. Notably, 73% of these patients were treated initially for bacterial pneumonia. The incidence of blastomycosis in Wisconsin in the review period was 2.0 per 100,000, and the rate in Minnesota was 0.5 per 100,000. Based on the census data in Gundersen Health System's 19-county service area, the incidence of blastomycosis is 0.17 cases per 100,000. Conclusion: In this review of blastomycosis cases diagnosed outside the hyperendemic area of northern Wisconsin, diagnosis was often delayed, and 4 patients whose infections might have been treatable died. Although uncommon, blastomycosis needs to be considered in the differential diagnosis in areas outside the hyperendemic area. Co-authors: William A. Agger, M.D., FACP, FIDSA; Thomas J. Volk, Ph.D.	3310
10:50–11:10 a.m.	Making a Mushroom: Expression, Growth, and the Cell Cycle in <i>Flammulina velutipes</i> Development Thomas Roehl, Clark University <i>Flammulina velutipes</i> is a cultivated edible mushroom with two distinct growth forms: highly pigmented and umbrella-shaped in the wild, but pale and thread-like under cultivation conditions. Recent studies on gene expression in <i>F. velutipes</i> have largely ignored tissue-level differences and the normal (wild) growth form. In the work for my masters thesis at UW-La Crosse, I extracted and sequenced <i>F. velutiipes</i> mRNA from four tissues (mycelium, stipe, pileus, and gills) at four growth stages (primordia, young mushrooms, mature cultivated mushrooms, and mature normal mushrooms) to assemble a transcriptome of 20,909 transcripts from 14,416 potential genes. Analyses identified 2,183 differentially expressed genes ($q < 0.05$), 1,456 of which matched named proteins in the UniProtKB Agaricales database. Tissue had a much larger impact on gene expression than did growth stage. Analysis revealed a stipe-specific hydrophobin and tissue-specific cytochrome p450 genes, none of which were previously known to have tissue-specific expression in <i>F. velutipes</i>. Genes previously reported to have been involved	3310

	in the fruiting process (including <i>fds</i>, <i>fvfd16</i>, mitogen-activated protein kinases, heat-shock proteins, and WD40 repeat-containing genes) tended to be most highly expressed in actively growing tissues, suggesting that regulating cell growth is a key mechanism during mushroom formation. The <i>cdc123</i> gene, which functions in controlling the cell cycle at the G1 to S phase transition, was also most highly expressed in actively growing tissues, providing a potential genetic link between mushroom growth and cell cycle regulation. These results augment existing knowledge of developmental genetics of mushroom-forming fungi. Dr. Volk was part of my thesis committee for this work and actively supported my research by providing resources and advice for mushroom cultivation, in addition to all the normal tasks of a committee member.	
11:10–11:30 a.m.	Greek and Latin Roots in Scientific Terminology Christine Schwartz, UW-La Crosse Many terms used in science come from Latin and Greek. Understanding and appreciating the roots of these words can provide insight into the appearance, function, and other characteristics associated with the subject of the term. This is particularly evident in scientific names, like <i>Megaptera</i>, which comes from Greek words meaning “big wing”. This is a genus containing just one species, the humpback whale, which has long, wing-like flippers. This is also noticeable in medical and anatomical terms, like <i>cauda equina</i>, which comes from Latin and translates to “horse tail”. The <i>cauda equina</i> is a collection of spinal nerves at the base of the spinal cord that resembles its namesake. Dr. Tom Volk was passionate about this subject and created a course at UWL called <i>Latin and Greek Roots in Scientific Terminology</i> to help students make these connections between terms and their meanings. One of the ways that he helped students learn was to have them become neologists (one who makes new words), inspiring them to be creative with his own examples. This presentation will serve as a window into some of his creativity and the foundation of his course, along with some classic examples of how Greek and Latin helped shape many scientific terms.	3310
11:30-11:40	Break: Brevicessor (<i>state of short yield, L</i>)	
11:40 a.m.–Noon.	Group Photo of Participants: Polyprosopography (<i>to write many faces, G</i>)	TBD
Noon–12:40 p.m.	Lunch: Edegastria (<i>state of swollen stomach, G</i>)	3310
12:40–1 p.m.	Spores Galore: Tom Volk's Teaching and Mentorship Caleb Kasper Tom Volk's students worked on an amazing breadth of fungus-related research, from the fungi of Chernobyl to the fungal degradation of bowling balls. This talk will highlight some of the most noteworthy accomplishments of Tom Volk's students and mentees.	3310
1–1:20 p.m.	Vaccine Development and Efficacy Testing for Avian Respiratory Aspergillosis Cord Brundage, D.V.M., Ph.D., UW-La Crosse Avian respiratory diseases, including the fungal infection aspergillosis, accounts for >3% of estimated poultry losses. This medical mycology project was based out of Cal Poly Pomona. Based on Tom Volk's passion for the breadth mycology and medical mycology specifically. I would like to present on this veterinary mycology project I worked on. A candidate <i>Aspergillus</i> vaccine was developed by Dr. Jill Adler-Moore using a unique, potent	3310

	liposomal carrier system (VesiVax®). This <i>Aspergillus</i> vaccine provided protective immunity to pulmonary aspergillosis in Swiss Webster mice and SPF chickens. Based on these findings the next stage of development was to investigate methods for minimizing the cost and maximizing the efficacy of this liposomal <i>Aspergillus</i> vaccine for use in the poultry industry. We were able to develop a biosafety level-2 where specific pathogen free (SPF) chicken eggs can be incubated and raised to reliably induce aspergillosis by 24 days of age. This was accomplished through glucocorticoid induced immunosuppression (8mg/kg dexamethsone SP IM twice daily on day 19-23, with day 20 mucosal (mu) challenge with 5.4X10⁸ <i>Aspergillus fumigatus</i> conidia; ATCC 13.073). Birds were vaccinated with 5ug Aspf3 protein/dose and 5ug Aspf9 protein/dose with 5ug/dose of the adjuvant lipidated tucareol. Administrative routes tested included mu and subcutaneously (sq) vaccinations on post-hatching day 4 (+/- day 10) and day 17. Birds were monitored for disease signs until day 24, when lungs and tracheas were collected for fungal burden (CFU/g tissue). Mu vaccine routes produced the greatest level of immunity which was equivalently effective following one booster (day 17) as it was with two (day 10 and 17). These results indicate that we can reduce the number of vaccinations needed for protection from aspergillosis, while decreasing the cost of the vaccine and the amount of chicken handling. Co-authors: Nickolas Holzhecht, Ondieki Gekara, Jill Abler,	
1:20–1:40 p.m.	Demographics of Gray Wolf (<i>Canis lupus</i>) Packs Recolonizing Variable Habitat Types in Central Wisconsin Theresa Simpson, M.S. Though a nontraditional student, Dr. Volk offered me the opportunity to achieve my life-long goal of completing scientific research from conception to publication. Tom accepted me into the master' program without hesitation and encouraged me even through the extended time it took me to complete the degree. His courses in oral presentation were invaluable. Tom was always available for a conversation, free with his advice, and never hesitant to provide me with opportunities to expand my skills (like subbing for him in his Latin class). I offer my abstract and presentation in his honor: Some gray wolves (<i>Canis lupus</i>) live in disjunct populations including Wisconsin's Central Forest Region (CFR), recolonizing there in the early 1990s. We examined how habitat factors and period of initial recolonization facilitated successful re-establishment of wolves to this region. We divided this event into 3 periods: Early (1994–1999), Mid (2000–2005), and Late (2006–2012). We defined habitat classes of individual pack territories as Optimal, Mixed, and Marginal, based on: (1) percent public land, (2) percent agricultural land, and (3) road density within territories. We analyzed the influence of time and habitat classes on pack territory size, winter pack size, pup presence, wolf-human conflicts, human-caused wolf mortalities, territory persistence, and reproductive performance. Pack demographics were similar across time, except pup presence was slightly lower during the Mid period. Wolf-human conflicts increased over time and were correlated with population growth. Packs in Marginal habitat were smaller in winter, exhibited lower reproductive performance, had more conflicts with humans, and experienced human-caused mortalities at rates 4 and 7 times higher than Mixed and Optimal habitats, respectively. We demonstrate that wolves tolerate some level of human-altered landscapes and identify demographic parameters that impact the wolves' ability to survive in human-dominated lands. Co-authors: Richard P. Thiel, Derrick T. Sailer, David M. Reineke; Meredith Thomsen, Ph.D.	3310

1:40-2 PM	Population Genomic Insights Into the Establishment of Non-Native Golden Oyster Mushrooms (<i>Pleurotus citrinopileatus</i>) in the United States Andi Bruce The naturalization of non-native golden oyster mushrooms in midwest and eastern parts of the U.S. (<i>Pleurotus citrinopileatus</i>) represents the first known case of a cultivated mushroom spreading quickly and widely outside of its native range, exhibiting characteristics of invasiveness. The first observations of wild fruitings in American woodlands occurred approximately 11 years ago, and citizen scientist observations have increased significantly over the last six years. To gain insights into the mechanisms behind this species' introduction and spread, I used population genomic data to test the hypothesis that naturalized golden oyster populations are the result of multiple introductions from cultivation operations. I analyzed genome-wide single-nucleotide polymorphisms (SNPs) from 29 wild mushroom specimens collected in six states, plus 6 commercially cultivated isolates. Clustering patterns revealed by the SNP data are consistent with a larger gene pool of commercial strains from which a limited number of strains differentiated via recombination or mutation. High genetic similarity was found between all wild samples plus two of the commercial isolates examined, suggesting possible source strains linked to wild establishment. Genotypic subdivision of the wild samples does not closely correlate with geographic location, suggesting multiple introductions and human-mediated spread.	
2–2:15 p.m.	Break: Brevicessor (<i>state of short yield, L</i>)	3310
2:15–3:15 p.m.	Poster Session: Potentomentatrium (<i>Room of powerful minds, L</i>)	3310
	Analysis of Plant and Fungal Lead Contamination in the La Crosse River Marsh Cara Senn, UW-La Crosse It was Dr. Volk that first introduced me to mycoremediation, the process of using fungi to degrade environmental contaminants, in February 2020. I could not wait to take his Mycology class that fall, and Medical Mycology the next spring. Then he graciously expected that I would TA for those classes without asking me first (which I did, enthusiastically, in '21 and '22). In the time off between fall and spring break, a peer was kind enough to ask me to shovel Dr. Volk's driveway while they were on vacation. From that day on, Tom and I spent a lot of time together as I became his "personal assistant", both on and off campus. One week, in the summer of '22, he asked if I had applied for grad school. I said no; I wanted to work for a while first. The next week, he said there was a grad position waiting for me at UWL- it wasn't a choice. So, I put together a project that lays the groundwork for mycoremediation right at home, next to campus: Analysis of plant and fungal lead contamination in the La Crosse River Marsh. Legacy lead contamination remains from a shooting range that existed over the marsh from 1929–1963, dumping hundreds of millions of lead shot pellets into the sediment. This study will analyze lead levels in local plants and fungi to determine their capacity to accumulate toxins and compare fungal communities across sites with high, low, medium, and no lead contamination. This study will allow us to identify locally adapted organisms to aid in ecologically and economically viable cleanup of lead using native organisms in the La Crosse River Marsh.	
	Ectomycorrhizal Diversity in the Kickapoo Valley Wisconsin, U.S.A. Jacob Hansel, UW-La Crosse Ectomycorrhizal (ECM) trees and fungi form a unique symbiotic relationship.	

	ECM trees provide timber, food, habitat, and feeds its fungal partner with sugars it produces. ECM fungi increase the tree's capacity for nutrient and water absorption, recycle nutrients in the soil making them useable by other organisms in the soil. ECM fungi also increase the carbon sequestration of forest biomes. ECM fungi and trees serve a vital role in their ecosystems yet are often understudied. This lack of scientific inquiry has left the ECM fungi in the unique Kickapoo valley. To provide a thorough examination of the ECM fungal diversity and provide data for forestry management and conservation I will conduct a survey of the ECM capable trees and their root symbionts along a 16-mile stretch of the Kickapoo river from Ontario WI, to south of La Farge WI. I will collect and soil cores from 60, (30 on each side of the river) 25-meter plots. The soil cores will be sifted to separate ECM root tips from the soil and debris. The root tips will then be lyophilized and crushed from sodium hydroxide-based DNA extraction. The DNA will then undergo PCR amplification with two primer types, the fungal ribosomal internal transcribed spacer (ITS), and one to amplify copies of the plant rbcL locus. The samples will then be dual tagged in preparation for DNA sequence analysis via Illumina sequencing technology by the University of Wisconsin Biotechnology Center. This data will fill in the void of ECM tree and fungal associates within the Kickapoo Valley and may provide species new to science. Tom inspired my journey into mycology and through my time together with him I became interested in understanding the many symbiotic relationships between plants and fungi. Under Tom's mentorship I learned a plethora about plants, fungi, and life.	
	Soil Remediation Potential of Cannabis sativa (hemp) Inoculated with Fungal Root Endophytes Caleb Kasper An estimated 20 million ha of land is currently contaminated by heavy metals. Two of the most common of these contaminants being arsenic and lead. The expense of physical removal of these contaminants results in many contaminated properties simply being left vacant. Phytoremediation- the removal of contaminants from soil via absorption by plants- causes less disturbance to the environment and concentrates toxins into more manageable volumes compared to physical removal; however, plants must be selected that can tolerate high levels of heavy metals by absorbing and immobilizing, rather than excluding them. Hemp (Cannabis sativa) is a promising phytoremediator: in addition to being tolerant of poor soils, it produces commercially valuable aboveground tissues that could offset operational costs. Hemp has been shown to hyperaccumulate heavy metals from the soil, but knowledge of the specific mechanisms involved is lacking. One hypothesis is that heavy metal accumulation can be attributed to the plant's fungal symbionts (endophytes). Endophyte inoculation has been shown to increase metal chelation and sequestration in other plants, but has not been studied in hemp. In this experiment endophytes isolated from wild hemp roots were screened for arsenic and lead tolerance. Isolates displaying exceptional tolerance were then inoculated into the roots of hemp seedlings which were then introduced to soil contaminated with arsenic and lead. Inoculated and uninoculated plants will be compared to assess the effects of fungal endophytes on overall health, and the arsenic and lead accumulation potential of hemp cultivars currently being tested in a separate phytoremediation study. Co-Authors: Todd Osmundson, Ph.D.; Brian Barringer, Ph.D.; Ann Impullitti, Ph.D.	
	A Study that Doesn't Overlook the Role of Fungi in Microbial Freshwater Marsh Sediments	

	Cedar Sekorski, UW-L Crosse To be a great scientist, you have to understand how your system is integrated into the larger environment—to see the forest AND the trees. This is the greatest lesson that Dr. Tom Volk taught me during my undergraduate and masters work at UW-La Crosse. Thanks to Tom, I will never see myself as a specialist, but instead always pay attention to the broader issues surrounding my work. The research for my thesis focuses on sediment microbes. But it is not a thesis in microbiology, rather it describes one piece of the larger puzzle that is the freshwater marsh. Freshwater marshes are poorly studied, even though they are important diverse ecosystems. Freshwater marshes cycle nutrients and are centers of primary productivity. Microbial sediment communities are vital to nutrient cycling and healthy functioning of the marsh. Within this broad context of the marsh ecosystem, my research examines microbial (bacteria, fungi, etc.) community structure. But—as Tom taught—me no organisms live independently. All require a community. Therefore, I am also investigating connections between microbes and the plants and invertebrates of the marsh. For this project, I collected sediment samples and recorded site-level variables at five sites for six time points spanning three seasons. Ribosomal ITS Illumina metabarcoding was used to characterize the community in each sample. The connections between community composition, site-level variables, and seasonality were analyzed. The results of this study will allow a deeper understanding of the freshwater marsh sediment communities—not just the composition and diversity of those communities, but also how they connect to and impact marsh health on a larger scale. I will always be looking for these connections—in my work and in my life more broadly—thanks to how Dr. Volk expanded my worldview. Co-Authors: Todd Osmundson, Ph.D.; Anita Davelos, Ph.D.	
	Using <i>Saccharomyces cerevisiae</i> to analyze antimicrobial compound Anne Galbraith Resistance to antimicrobials is a major threat to public health, making it imperative to develop more classes of antimicrobials to combat infectious agents. Researchers at the University of Wisconsin-La Crosse and Milwaukee have developed a library of antimicrobials derived from a stilbenoid compound purified from the sweet fern <i>Comptonia peregrina</i>. We have been using the single-celled fungus <i>Saccharomyces cerevisiae</i> to learn more about the mechanism of action of one of the lead compounds from this antimicrobial library. Results from some of this work will be presented.	
	The Midas Mushroom: Ecological Impacts of the Invasive Golden Oyster Fungus Aishwarya Veerabahu The Golden Oyster Mushroom (GOM; <i>Pleurotus citrinopileatus</i>) is an invasive, edible wood decay fungus found throughout the Midwestern and Northeastern United States. This fungus is native to northeastern Asia and was introduced near southern Wisconsin via commercial strains sold for home cultivation. GOM continues to <i>rapidly</i> spread, with sightings growing exponentially. GOM fruits prolifically from April to November and is highly concentrated in forested areas between the 40 - 45th parallels, from the East Coast to just past the Mississippi River. Though there are few documented examples of invasive decay fungi, there are likely many undocumented invasions. Invasive wood decay fungi spreading in a new habitat may become competitively dominant, displacing native fungi. Our broad objective is to document how GOM affects the ecology in its invaded range, and use	

	this information to inform the management of GOM and model the risks of invasive wood decay fungi. We predict that the presence of GOM is associated with a drastic shift in fungal community composition and function. To test this, drilled wood samples from pairs of GOM and non-GOM trees from Dane County, Wisconsin were collected and their ITS regions were sequenced using high-throughput amplicon sequencing. Samples taken from different heights within each tree were also compared to examine differences in colonization and communities throughout trees. Because wood decomposition is driven by the community of wood-decaying organisms in the wood, disruption or displacement of the community by an invasive will impact the original carbon cycling regime, with significant implications for climate change. Co-Authors: Mark T. Banik⁽²⁾USDA Forest Service, Northern Research Station, Center for Forest Mycology Research, Madison, WI, USA, mark.t.banik@usda.gov Daniel L. Lindner⁽³⁾USDA Forest Service, Northern Research Station, Center for Forest Mycology Research, Madison, WI, USA, daniel.l.lindner@usda.gov Anne Pringle⁽⁴⁾University of Wisconsin-Madison, Department of Botany, Madison, WI, USA, apringle2@wisc.edu Michelle A. Jusino⁽⁵⁾USDA Forest Service, Northern Research Station, Center for Forest Mycology Research, Madison, WI, USA, michelle.jusino@usda.gov	
3:15–3:30	Break	
3:30–4:15 p.m.	Panel Session: Mycomania (<i>madness for fungi</i>, G) • Todd Osmundson, Ph.D., UW-La Crosse • Dan Lindner, Ph.D:USDA Forest Service, Center for Forest Mycology Research • Heather Hallen-Adams • Bridget Pfaff Join us for reminiscences and stories about working with Tom Volk as a scientist and having him as a friend. Bring your questions and your own anecdotes to share! We anticipate that this will be a fun interactive chance for us to remember Tom the human as well as Tom the scientist.	3310
4:15 p.m.–5 p.m.	Closing Reception: Trophidium (<i>little food</i>, G)	3310