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Cereals are vulnerable substrates for fungal growth and subsequent mycotoxin contamination. One of the major fungal genera to colonize the ecosystem of stored grain is Penicillium, especially species in the series of Viridicata and Verrucosa. Culturing these species on grains, we hoped to induce the production of relevant secondary metabolites produced by these fungi in the early stage of cereal breakdown. In a multivariate setup six different cereal grains (wheat, rye, barley, oat, rice, and maize), one kind of white beans, and two standard fungal media, Yeast Extract Sucrose agar (YES agar) and Czapek Yeast Autolysate agar (CYA agar), were inoculated with the ten most important cereal-associated species from Penicillium (P. aurantiogriseum, P. cyclopium, P. freii, P. melanoconidium, P. neoechinulatum, P. polonicum, P. tricolor, P. viridicatum, P. hordei, and P. verrucosum). P. nordicum is a meat-associated species, which was included due to its chemical association with P. verrucosum, in addition to see if a substrate change would alter the profile of known chemistry. We found that cereals function very well as substrates for secondary metabolite production, but did not present significantly different secondary metabolite profiles, concerning known chemistry, as compared to standard laboratory agar media. However, white beans altered the semi-quantitative secondary metabolite profiles for several species. Correlations between substrates and certain metabolites were observed, as illuminated by principal component analysis. Many bioactive secondary metabolites were observed for the first time in the analyzed fungal species, including ergot type alkaloids in P. hordei.

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