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US researchers call for re-evaluation of microbial testing of Cannabis

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A new US study suggests that some of the medicinal benefits of dispensary grade *Cannabis* could be compromised because the flowers host potentially harmful yeasts and toxic molds, which cannot be detected by industry standard culturing techniques.

The report, '*Cannabis* microbiome sequencing reveals several mycotoxic fungi native to dispensary grade *Cannabis* flowers', by Kevin McKernan and a team from Medicinal Genomics Corporation in Massachusetts, has passed peer review http://f1000research.com/articles/4-1422/v2

The authors say that with the availability of medical *Cannabis* in some US states and in other countries, there is an increasing regulatory requirement for the microbial testing of *Cannabis* samples for both medicinal and recreational applications.

However, scientists know relatively little about the nature of all the microbes that may commonly live on the *Cannabis* plant, and whether existing food industry-standard culture techniques can effectively identify potentially harmful organisms in dispensary-grade samples. Moreover, while regulations may require *Cannabis* growers to 'heat kill', or pasteurize *Cannabis* flowers to reduce their microbial content, pasteurization may not eliminate every pathogenic toxin or spore, McKernan's team points out.

The researchers carried out what they claim is the first, next generation sequencing survey of microbes found in dispensary-derived *Cannabis*

flowers, and compared their results with those cultured from the same samples using standard food-industry platforms.

Their results showed that the polymerase chain reaction (qPCR) and next generation sequencing approach identified a range of yeast and mold species in about a third of 17 *Cannabis* samples obtained from dispensaries in the US and the Netherlands. In contrast, three different standard culture platforms failed to detect all of the positive samples.

Kevin McKernan said: "Following the publication of the *Cannabis* genome and many other pathogenic microbial genomes, quantitative PCR tests have been developed that can accurately quantify fungal DNA present in *Cannabis* samples.

"We have detected the DNA of microbes and the genes that synthesize paxilline and citrinin. Further LC-MS/MS assay development is required to detect the presence of these synthesized toxins in the complex background of cannabinoids and terpenoids."

Animal studies have previously shown that citrinin and paxilline can reduce or potentially interfere with the anti-seizure properties of the active *Cannabis* constituent, cannabidiol. Yet existing commercial antibody-based toxin assays are not designed to test for the citrinin and paxilline toxins in *Cannabis*.

The researchers conclude that culture-based techniques currently used for the microbial testing of *Cannabis* should be re-evaluated, and that additional sequencing-based studies need to be carried out to investigate qualitatively and quantitatively the extent of the *Cannabis* microbiome.

The team is particularly keen to examine whether the paxilline toxin is present in *Cannabis* samples, as even very tiny quantities could undermine the effects of the very low levels of cannabidiol that are

commonly used to manage seizures.

Kevin McKernan said: "Based on the political and controversial nature of cannabis, this work would have been very difficult to publish in other journals. We believe the open peer review system at F1000Research is disruptive. It provides such higher quality review that it will be our default journal of choice going forward."

Rebecca Lawrence, Managing Director of F1000, owner of F1000Research, said: "This is a fascinating study, and we are delighted to enable the researchers to quickly bring it into the public domain where its significance can be assessed by the wider scientific community."

More information: Kevin McKernan et al, Cannabis microbiome sequencing reveals several mycotoxic fungi native to dispensary grade Cannabis flowers, *F1000Research* (2016). DOI: 10.12688/f1000research.7507.2

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