

To evaluate this acid removal efficiency we monitored the O2 class abundance obtained by FT-ICR MS using electrospray ionization (ESI) in negative mode, in which the crude oils and residual oils (2 mg) was previously dissolved in 1 mL of toluene and then diluted with 1 mL of methanol, containing 0.2% of ammonium hydroxide. The samples were analysed before (crude oil) and after the adsorption (residual oil) process to all evaluated adsorbents. From the FT-ICR MS analysis it was detected for both crude oils the heteroatom classes N, NO, NO2, O2, O3 and S, which the O2 compounds was the most abundant class. The relative intensity of O2 compounds present in the C13 and C20 were 50 and 40 %, respectively, analysed before adsorption process. After adsorption process a decrease in the relative abundance of the O2 class was observed for the residual oils, with decreases of ~40%, ~9%, ~4%, ~4% and ~42% for crude oil C13 when using the adsorbents shale, activated charcoal, silica gel, sandstone and sawdust modified, respectively. For crude oil C20 the adsorbents shale, activated charcoal and commercial clay (Bentonita) showed the same results with decreases in the relative abundance of the O2 class of ~6%, ~4% for silica gel modified and ~25% for sandstone and sawdust modified. This result clearly indicates efficiency of all adsorbents evaluated to remove NA from crude oils. For both oils, activated charcoal, commercial clay and silica gel modified were more efficient.

**Keywords:** petroleum, O2 compounds, modified silica gel

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#### References Bibliography:

- [1]Hau, J., 2009. Predicting Sulfidic and Naphthenic Acid Corrosion. *Corrosion*, 65, 831-844.
- [2]Speight, J. G., 2014. High Acid Crudes. In: *Removing Acid Constituents from Crude Oil*. CD&W Inc., Laramie, Wyoming, USA.
- [3]Huang, M. F.; Zhao, S. L.; Li, P.; Huisingh, D. 2006. Removal of naphthenic acid by microwave. *J. Clean. Prod.* 14, 736-739.
- [4]Ding, L.; Rahimi, P.; Hawkins, R.; Bhatt, S.; Shi, Y. 2009. Naphthenic acid removal from heavy oils on alkaline earth-metal oxides and ZnO catalysts. *Appl. Catal. A*. 371, 121-130.
- [5]Hsu, C. S.; Hendrickson, C. L.; Rodgers, R. P.; McKenna, A. M.; Marshall, A. G. 2011. Petroleomics: advanced molecular probe for petroleum heavy ends. *J Mass Spectrom.* 46, 337–343.



#### Identification and classification of Mycobacterium by MALDI-TOF mass spectrometry

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#### Abstract:

Bovine tuberculosis is a zoonotic disease caused by the *Mycobacterium bovis* bacillus, which accounts for significant economic losses in cattle production besides being a public health threat. Our purpose is to establish MALDI-TOF (Matrix Assisted Laser Desorption Ionization – Time-of-Flight) mass spectrometry method to identify and classify mycobacteria species, by means of building a specific biomarker library after solid media culture for these microorganisms. We have identified 26 different protocols employing MALDI-TOF to identify and classify mycobacteria from solid media culture within 58 articles

published since 2010. Four consensus protocols were designed and our results lead to the following cell treatment conditions before MALDI-TOF analysis: heat inactivation at 95°C for 45 minutes, disruption with zirconia beads and MagNA lyser (Roche) and formic acid 70% and acetonitrile protein extraction. Mass spectra were acquired and compared to a library containing 4137 references, including 173 micobacterial isolates, using Biotyper software (Bruker Daltonics). We analysed 8 different isolates from 5 animals positive for tuberculosis and 7 isolates were identified at species level. Four isolates were classified as *Mycobacterium tuberculosis*, two as *Mycobacterium bovis* and one as *Mycobacterium smegmatis*. We conclude that the protocol described here allows mycobacterial identification at species level and represents a significative increment to bovine tuberculosis investigation.

**Keywords:** Mycobacteria, Bovine tuberculosis, MALDI-TOF, Species identification

**Financial support agency:** EMBRAPA

**References Bibliography:**



## **Influence of culture medium in volatile metabolites profile of filamentous fungi from human skin**

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### **Abstract:**

Even residing on the surface of the skin benignly, fungi can occasionally be associated with severe infections, such as onychomycosis, tinea capitis, dermatomycosis, pityriasis versicolor, among other [1,2]. So, it is important to characterize the metabolites produced by these species to learn a little more about these compounds and evaluate this parasite-host interaction [3]. Among the classes of volatile organic compounds produced by them, there are alcohols, aldehydes, esters, fatty acids, terpenes, and others [4]. The profile of secondary metabolites produced by a particular fungus is very sensitive and is modified depending on the culture medium, what is interesting to assess the influence of the metabolites emitted [4]. The use of the technique Solid Phase Microextraction (SPME) for metabolite extraction has been used in several studies in the literature [5,6]. The applicability is due to the fact it is a non-destructive technique, which presents an efficient extraction for volatile metabolites at low concentration and it is also able to limit interferences even in the midst of complex and dynamic arrays [7,8]. In this way, the present work had as objective evaluate the influence of the culture medium potato dextrose agar (PDA), sabouraud (SBA), and malt extract agar (MEA) in the profile volatile metabolites of filamentous fungi using the techniques SPME and gas chromatography coupled to mass spectrometry (GC-MS). The fungal growth occurred in sealed sterile 20 mL vials, containing 4 mL of culture mediums, allowing a headspace analysis of the volatiles. The growth incubation temperature used was 28°C, and samples were analyzed after 10 days of growth. Fungal cultures were submitted to extraction of its volatile metabolites using a Divinylbenzene/Carboxen/polydimethylsiloxane (DVB/CARB/PDMS) fiber at 35°C in thermostatic bath for 3 hours. The volatile metabolites extracted by the fiber were analyzed in a gas chromatograph coupled to a mass spectrometer from Agilent Technologies, operating with a fused silica capillary column (HP-5) with stationary phase (5% diphenyl, 95% dimethylpolysiloxane). The metabolites identified in the three fungi analyzed belong to the most diverse classes of organic