Biodegradation of phenol by an indigenous bacterial consortium

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Introduction. The use of microorganisms to remove phenol from the environment is well known, but nowadays, the studies don't focus only on the decrease of the xenobiotic concentration. It is important to know how the microorganisms interact between populations as well as the species that form the consortium.
Thanks to molecular biology techniques, the changes that occur in a microbial community during phenol biodegradation can be evaluated, as well as to know the genes involved during this metabolism of the pollutant. This information can be used later for process optimization.
The aim of this study was to evaluate the biodegradation of phenol by an indigenous bacterial consortium.

Methods. The consortium was acclimatized in a mineral medium (Bushnell-Hass) with phenol as the only carbon source. Five initial concentration of the pollutant were evaluated and the growth rate in each one was calculated using the Gompertz model. The changes in the microbial population where analyzed using denaturing gradient gel electrophoresis of the PCR-amplified DNA samples (1). A DNA sample was pyrosequenced to know the diversity of species interacting in the consortium.

Results. The consortium was incubated during 53 h and was capable of using phenol as carbon source. The kinetic parameters as well as the removal efficiency are showed in Table 1.

Table 1. Removal efficiency and growth rate of the consortium in five different initial phenol concentrations.

Treatment	Initial phenol concentration (mM)	Removal efficiency (%)	Growth rate (μ^{-1})
C1	0.921	53.05	0.031
C2	3.081	71.30	0.086
C3	4.883	81.30	0.110
C4	7.309	84.22	0.126
C5	9.346	87.21	0.054

Similar studies have shown removal efficiencies near to 100%, higher than the reported in this work. The difference may be due to the experimental conditions. A decrease in the activity of the enzymes involved in the aromatic metabolism could occur above 35°C (2).
When the concentration of pollutant was increased an increment in the growth rate of the consortium was observed. Above a concentration of 7 mM the growth rate reduced drastically indicating influence of phenol concentration on bacterial metabolism, since it is well known the inhibitory effect of phenol on the growth of microorganisms (3).

Treatment C4 was selected for the molecular analysis because it presented the highest growth rate. DNA samples were taken during the logarithmic phase in order to observe changes in the population structure.

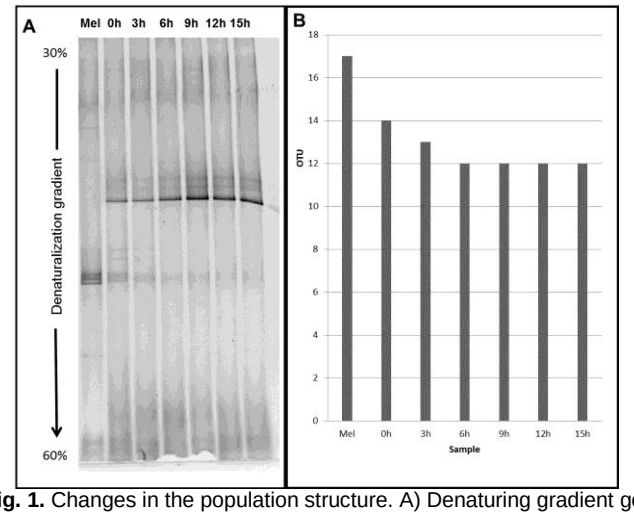

Fig. 1. Changes in the population structure. A) Denaturing gradient gel electrophoresis of PCR-amplified 16S rRNA gene fragmentes from treatment C4. Lane Mel: Control with 1% molasses; lane 0h-15h: sampling times during the logarithmic phase. B) OTU richness graph obtained by gel digitalization.

At the end of the logarithmic phase, it was observed 12 dominant species. The sequencing analysis showed that the most abundant genera were *Sphingomonas, Erytrobacter, Sphingobium, Sphingopyxis, Streptomyces, Novosphingobium, Caulobacter, Methylobacterium, Zymomonas, Burkholderia, Citromicrobium* and *Bradorhizobium.*

Conclusions. The consortium was able of using phenol as a carbon source. The highest growth rate was at 7 mM. Twelve species were dominant comprising over the 50% of total reads.

References.

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