Assessment of the impact of tebuconazol (fungicide) on lake and stream bacterial communities using a 16S rRNA pyrosequencing method

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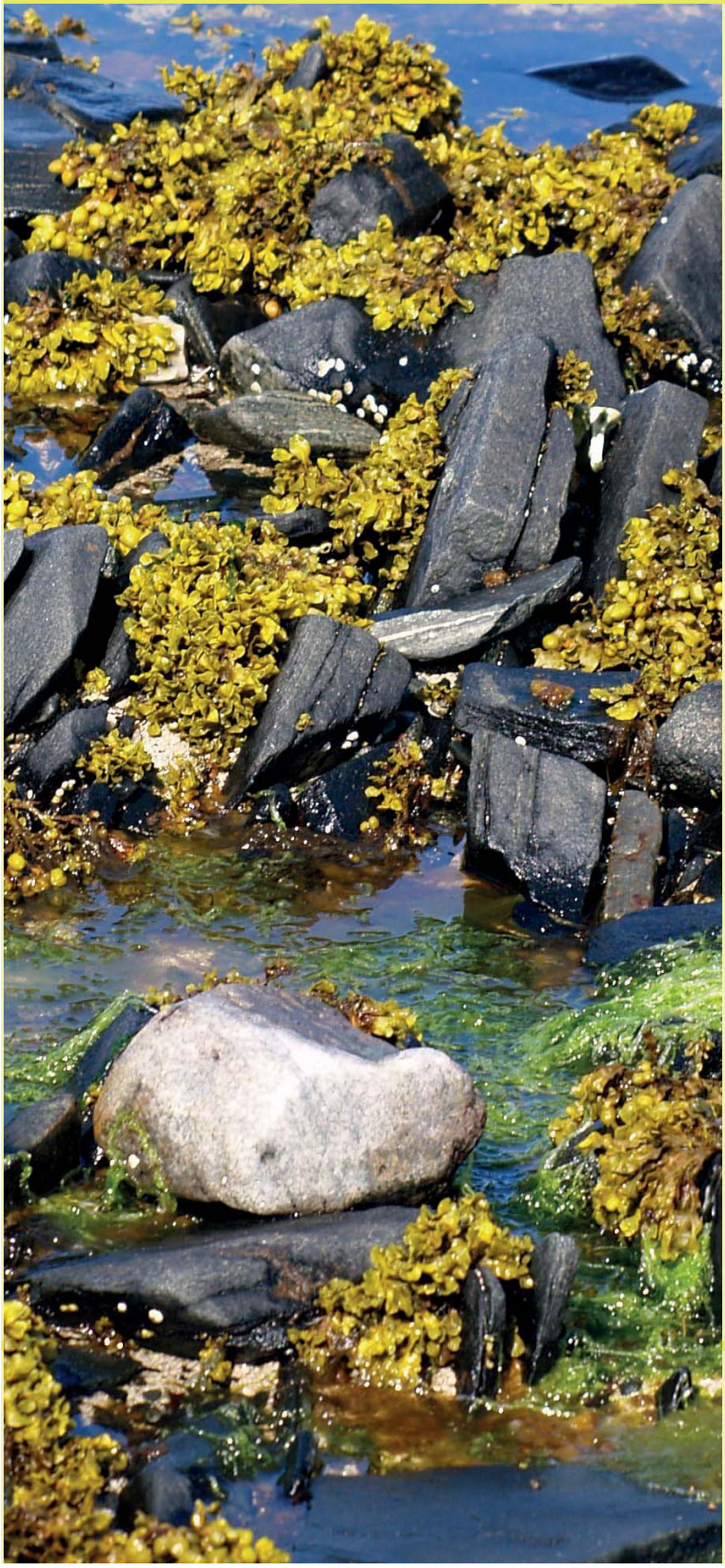

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Assessment of the impact of tebuconazol (fungicide) on lake and stream bacterial communities using a 16S rRNA pyrosequencing method.

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The pollution of lakes and rivers by the agricultural use of pesticides is a growing problem worldwide. As these substances have complex effects on ecosystems, we need to improve our understanding of their fate and their impact on biological communities. With this in mind, we carried out experimental study of the responses of planktonic bacterial communities from lakes and benthic bacterial communities from streams to the fungicide tebuconazol, and of its degradation by these different communities. For each type of ecosystem, communities were collected from pristine environments (Lake Aiguebelette and the upstream segment of the river Morcille, France) and pre-exposed environments (Lake Léman and the downstream segment of the river Morcille, France in which tebuconazol was found). The experiments were carried out in 20L microcosms in which communities from each of the four environments were either not exposed (control), or exposed to a low (2µg/L) or high (20µg/L) concentration of the fungicide, in order to simulate the contamination levels encountered in aquatic ecosystems. Results obtained after three weeks of incubation showed that 60 to 70% of the initial concentration of tebuconazol had been degraded in the stream microcosms, whereas only minor degradation had occurred in the lake microcosms (15-20%). The fungicide had no significant impact on benthic bacterial abundance, although the proportion of dead bacteria increased. The changes observed in planktonic bacterial abundance and dead bacteria were transient and depended on previous exposure. To complete these findings, the bacterial diversity is characterizing by pyrosequencing of the gene coding for 16S rRNA. This high-throughput sequencing technology provides a deep inventory of the diversity in microbial communities. All the resulting findings will be discussed with regard to the fungicide history of the different communities studied, and to the rate at which these communities degrade the fungicide.