LETTER

N-Formylmaleamic acid: An intermediate in nicotinic acid metabolism

Jiménez *et al.* (1) have published a thorough and impressive analysis of the genetic determinants of aerobic nicotinic acid degradation in *Pseudomonas putida.* The chemistry of this pathway has been known for some time (2) with the exception of the formation and hydrolysis of the (up to now) putative intermediate, *N*-formylmaleamic acid. These gaps were due to (*i*) difficulties in the synthesis of this molecule and (*ii*) its exceptional lability to nonenzymatic hydrolysis under both acidic and basic conditions (e.g., $t_{1/2}$ = 100 min, 35 °C, pD 7.9) (3, 4). Jiménez *et al*. (1) have now established both its formation from 5-hydroxy-2-pyridone (2,5-dihydroxypyridine) via an oxygenase and its hydrolysis to formic and maleamic acids by a deformylase. However, they misstate the conclusions of previous work and impugn unnecessarily the work of Gauthier and Rittenberg (5, 6). The misstatement is that ref. 3 agreed with refs. 5 and 6 in attributing deformylase activity to the oxygenase. This was mentioned as a logical possibility, but the evidence presented in ref. 3 strongly suggested that the failure of Gauthier and Rittenberg (5, 6) to detect *N*-formylmaleamic acid as a product of the oxygenase was instead due to its rapid nonenzymatic hydrolysis. My other disagreement is that Jiménez *et al.* (1) state that Gauthier and Rittenberg's (5, 6) oxygenase was not purified sufficiently and that it was contaminated with the deformylase. This may have been true, but it seems improbable in view of the data for homogeneity given by Gauthier and Rittenberg (5, 6) for their crystalline oxygenase and the data given in ref. 3 for the kinetics of the nonenzymatic hydrolysis of *N*-formylmaleamic acid.

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