The Moco riboswitch: the missing metabolite

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Riboswitches are highly structured RNA elements located in mRNA non-coding regions. They regulate the expression of specific genes depending on the cellular concentration of a particular metabolite. In fact, the riboswitch-metabolite interaction induces a structural rearrangement in the RNA causing an alteration in the expression of the proteins encoded by the relative mRNA. About 20 types of riboswitches have been confirmed so far, each one responding to a specific molecule [1]. Bioinformatical studies on several bacterial genomes have recognized the Moco RNA motif (or Moco riboswitch) as a promising riboswitch candidate [2]. If so, Moco itself would be involved in the regulation of its own biosynthetic pathway. The biosynthesis of Moco is well described [3], however, there is no decisive prove that its regulation is indeed based on a riboswitch [4], This lack in evidence is probably due to the instability, high oxygen sensitivity and scarce availability of Moco and its precursors. The goal of our research is to confirm that the Moco riboswitch is actually a riboswitch. In this context, we are exploring for the first time the direct interaction that the Moco RNA motif from *E. coli* might undergo not only with the molybdenum cofactor itself, but also with other metabolites along its biosynthetic pathway. Structural studies on the Moco RNA motif have been performed in order to find the conditions that ensure a stable and uniform three-dimensional structure of the RNA. Moreover, its interaction with each metabolite is detected by footprinting assays [5] e.g. in-line probing, terbium cleavage, hydroxyl radical partial digestion, enzymatic probes and by spectroscopic methods e.g. CD, DLS, UV and fluorescence.

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