

## THE MOLECULAR GENETICS OF SUPEROXIDE DISMUTASE IN *E. COLI*

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The biological role and the regulation of superoxide dismutase (SOD) in *E. coli* have been investigated using genetics. Cloning of both *E. coli* SOD genes permitted construction of mutants completely lacking SOD. The conditional oxygen sensitivity of those mutants, together with their increased mutation rate, demonstrated the essential biological role of SOD. SOD-deficient mutants constitute a powerful tool to assess a possible role of  $O_2^-$  or SOD in biological processes. Complementation of their deficiencies by the expression of SOD originating from a different organism is used for screening libraries for SOD genes of other species. Regulation of MnSOD has been studied using protein and operon fusions with the lactose operon, and isolating regulation mutants. These studies reveal multiregulation of MnSOD including response to the superoxide mediated oxidative stress and response to variations of the intracellular redox state induced by metabolic changes.

**KEY WORDS:** Oxidative stress, superoxide dismutase, *E. coli*, mutants, regulation, mutagenesis.

### INTRODUCTION

Cells subjected to oxidative stress protect themselves from the potential damages by several means: — oxidative agents can be eliminated by enzymatic or nonenzymatic processes, — oxidative lesions can be eliminated or repaired, unfaithfully repaired DNA lesions leading to mutagenesis, — alternative pathways to bypass the damaged functions can also be developed.

In *E. coli*, in normal aerobic growth conditions, superoxide radicals ( $O_2^-$ ) produced by cellular metabolism are rapidly eliminated by the dismutation reaction catalysed by superoxide dismutase (SOD), giving rise to hydrogen peroxide ( $H_2O_2$ ) which is eliminated in turn by catalases and peroxidases. Since elimination of  $O_2^-$  produces another toxic oxygen species,  $H_2O_2$ , and since an excess of either  $O_2^-$  or  $H_2O_2$  will favor formation of hydroxyl radicals ( $OH^\cdot$ ), a subtle equilibrium, implying rigorous controls, should be maintained to allow the cells to survive.

Indeed when intracellular flux of  $O_2^-$  increases, MnSOD is induced,<sup>1</sup> resulting in an overproduction of  $H_2O_2$ . The increase of  $H_2O_2$  concentration induces in turn catalases and peroxidases.<sup>2</sup> Together with the SOD or catalase induction, each one being triggered by the oxygen species it eliminates, numerous other functions are induced in response to the stress provoked by an excess of  $O_2^-$  or  $H_2O_2$ . Up to 30 proteins have been shown to be overproduced after  $H_2O_2$  stress.<sup>2</sup> Several of them are controlled by a same transcriptional activator, the *oxyR* gene product.<sup>2</sup> Few of them are identified (catalase hydroperoxidase I, alkyl hydroperoxide reductase). Similarly, it has been shown that several proteins are overexpressed in response to  $O_2^-$  stress.<sup>3,4</sup> Moreover, several of these  $O_2^-$  induced proteins — including MnSOD, endonuclease IV repair

enzyme,<sup>5</sup> glucose-6-phosphate dehydrogenase<sup>4</sup> – are under the control of a same regulatory protein (B. Demple, this issue). Other functions as the catalase hydroperoxide II and the repair enzyme exonuclease III, both positively regulated by the *katF* gene product, are involved in the response to oxidative stress;<sup>6</sup> it is not known which signal triggers it on.

Beside of the direct response to the oxidative stress created by an increase of  $O_2^-$  intracellular flux, it seems to be a response to the redox state of the cells, mediated by iron, as suggested by the anaerobic inductions of MnSOD by iron chelator<sup>7,8</sup> or by growth conditions positively changing the redox potential.<sup>9-11</sup> The above incomplete scheme outlines the need, studying or acting on a particular function to not forget all these interactions. The balance has to be maintained for cells to survive.

## RESULTS AND DISCUSSION

### *SOD in E. coli: Biological Role*

We have used genetics as an approach to understand the biological role and mechanisms which control SOD expression in *E. coli*.<sup>12</sup>

The two *E. coli* SOD genes have been cloned, *sodA* gene for manganese SOD<sup>13</sup> and *sodB* for iron SOD,<sup>14</sup> and they have been further sequenced.<sup>15,16</sup> The cloning permitted construction of mutants devoid of one or both SOD.<sup>17</sup> They were obtained by insertional mutagenesis in the cloned gene, followed by an allele exchange with the corresponding wild-type chromosomal allele. The use of transposons conferring different antibiotic resistances for the insertional mutagenesis, allowed each of the mutation to be readily transferred to a wide variety of genetic backgrounds. This also permit to construct a double mutant completely lacking SOD.

SOD lacking mutant survive aerobically, but shows a conditional sensitivity to oxygen. (i) poor growth in rich medium, (ii) hypersensitivity to oxygen and redox cycling compounds, (iii) no growth on minimal medium unless the 20 amino-acids (aa) are provided. Although all aa are necessary to restore complete growth, some are more effective than others suggesting several targets in the chains of aa biosynthesis with differential sensitivity to superoxide, (iv) spontaneous mutagenesis is increased in strains lacking SOD. It is oxygen dependent, RecA independent, and largely depends on an active exonuclease III, a repair enzyme which recognizes oxidative lesions on DNA.<sup>18</sup> In anaerobiosis, the *E. coli* SOD negative behave as wild-type cell. All these deficiencies are complemented by the introduction of a gene expressing SOD. This complementation is obtained not only with *E. coli* SOD, but also with evolutionary unrelated SOD from other organisms, as human Cu-Zn-SOD.<sup>19</sup>

Mutants lacking SOD recovered the property to grow on minimal medium at a pretty high frequency (unpublished observations). We have not yet identified the secondary mutation(s) which is responsible for the loss of aa autotrophy. Those new mutants, still SOD negative, present a leaky phenotype. Several observations suggest that there is a diminution of the intracellular superoxide flux in these mutants, such that  $O_2^-$  concentration do not reach the critical threshold above which the growth in minimal medium is impaired.

Is superoxide or a derivative responsible for the premutagenic lesions on DNA in SOD lacking cells? We suspect that it is not superoxide, but more likely hydroxyl radical. Indeed challenge with 150 mM  $H_2O_2$  increases mutagenesis above the level

which occurs normally in SOD negative mutant and do not change the mutagenesis level in wild-type cells.<sup>21</sup> This synergistic action of  $O_2^-$  (in absence of SOD) and  $H_2O_2$  to enhance mutagenesis likely results from the formation of hydroxyl radicals. Mutation frequency in SOD lacking mutants both with or without  $H_2O_2$  challenge returns to wild-type level in strains which lack exonuclease III, suggesting that the pre-mutagenic lesions on DNA are the same.

SOD lacking mutants can be, have been, used to test presupposed effects of  $O_2^-$  or SOD in biological processes as long as those can be tested in *E. coli*.<sup>22,23</sup>

Also, their complementation by SOD originating from other organisms constitute a tool to screen libraries for SOD genes of other species (A. Hass *et al.*; W. Van Camp *et al.*; this issue).

### *MnSOD regulation*

Global SOD level in *E. coli* is modulated by MnSOD expression. MnSOD is not usually expressed anaerobically, but is expressed in presence of iron chelators or in growth conditions which positively change the redox potential, as growth on nitrate.<sup>9-11</sup> Aerobically, MnSOD is overproduced in presence of product able to generate endogenous superoxide, as paraquat.<sup>1</sup> To determine at which level, transcriptional, translational or post-translational, the expression of MnSOD was regulated, studies using protein or operon fusions with the lactose operon genes were undertaken.<sup>24,25</sup> We conclude to a multiregulation of MnSOD, including (i) a positive transcriptional control via  $O_2^-$ , (ii) a negative transcriptional control via  $Fe^{++}$ , (iii) an autogenous regulation and (iv) a post-translational activity modulation via metal ion concentration.

Our present approach is to identify the effectors of MnSOD expression and their targets on DNA by isolating regulation mutants. Mutants *cis*-acting (targets) or *trans*-acting (effectors) in which MnSOD is expressed anaerobically have been isolated (with H. Hassan). Preliminary characterization of effector mutants permitted to identify at least two regulators, among which the Fur protein. Both are involved in a negative transcriptional control which need iron to be active. They act synergistically and do not affect significantly the aerobic induction of MnSOD by redox cycling compounds.

Therefore MnSOD appears to be submitted to two types of controls acting at the transcriptional level. One is the response to the oxidative aggression via  $O_2^-$ , and is likely mediated by the *soxR* gene product (B. Demple, this issue). The other seems to have the function of maintaining a steady state of intracellular  $O_2^-$ , and responds to cell metabolism variations which modify the redox potential. In this later control iron might play a role of sensor of the redox state of the cells.

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