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Nickel-responsive transcriptional repressor of *sodF* coding for Fe- and Zn-containing superoxide dismutase of *Streptomyces griseus* is comprised of two proteins, SrnR and SrnQ, interacting with each other

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Abstract

We previously identified an operator site for nickel-responsive transcriptional repression of *sodF*, which codes for iron- and zinc-containing superoxide dismutase (FeZnSOD) of *Streptomyces griseus*. Nickel-responsive transcriptional repression of *sodF* was mediated through an operator site spanning over the 5' end of the *sodF* transcript. Two open reading frames (ORFs), SrnR (12,343 Da) and SrnQ (12,486 Da) with overlapping stop-start codons, were identified at the downstream of *sodF*, and responsible for the nickel-responsive repression of *sodF*. The deduced amino acid sequence of SrnR revealed a DNA-binding motif and showed homology to the transcriptional regulators of ArsR family, while SrnQ did not show any similarity to any known proteins. When *srnRQ* DNA was maintained in trans in *S. griseus* on a multicopy plasmid, *sodF* transcription was highly repressed by nickel, while neither *srnR* nor *srnQ* alone showed any repressive effect. Nickel-dependent interactions between *sodF* operator DNA and the proteins of SrnR and SrnQ, monitored through a gel-mobility shift assay, were observed only when both SrnR and SrnQ were provided. The maximum protein-DNA interaction was observed in the presence of the two proteins in one-to-one stoichiometric ratio. SrnR directly interacted with SrnQ even in the absence of *sodF* operator. The interaction between the proteins did not require nickel. SrnQ was shown to be a direct sensor of nickel with a ratio of one Ni^{+2} ion per one molecules of the protein.