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SGC1 Activates Transcription of the Yeast Enolase Gene *ENO2* Indirectly through an Upstream Activation Site

Chang Seo Park^{1,2}, Craig Martens¹, and Michael J. Holland¹

Department of Biological Chemistry, School of Medicine, University of
California, Davis¹ and Doosan Technical Center, Korea²

ABSTRACT

The *GCR1* gene product is required for maximal transcription of yeast glycolytic genes and for growth of yeast strains in media containing glucose as a carbon source. Dominant mutations in the *SGC1* gene were identified as bypass suppressors of the growth and transcriptional defects of a *gcr1* null mutation. The yeast *SGC1* gene encodes a member of the basic-helix-loop-helix family of DNA binding proteins and required for maximal transcription of many yeast glycolytic genes including the enolase genes *ENO1* and *ENO2*. Genetic analyses showed that *SGC1* and *GCR1* function on parallel pathways to activate transcription of glycolytic genes. The *SGC1-1* dominant suppressor contains a single amino acid change at one of the most conserved residues within the basic DNA binding domain (E188Q). Overexpression of the wild-type *SGC1* gene from a multicopy plasmid also partially suppressed the growth and transcriptional defects caused by a *gcr1* null mutation, suggesting that the *SGC1-1* dominant suppressor functions as a superactivator. A 60-bp sequence, previously identified as the minimal *GCR1*-dependent UAS element from the yeast enolase gene *ENO2*, was found to mediate transcriptional activation by *SGC1* when fused to UAS-less *ENO2* or *CYC1* promoter elements. Purified Sgc1 protein failed to bind specifically to the *ENO2* UAS element suggesting the *SGC1* gene product functions indirectly to potentiate the activity of the *ENO2* UAS element. Preliminary results from *in vitro* transcription assay using yeast whole cell transcription extract further support the notion. Possible mechanisms how does *SGC1* activate transcription will be discussed.