

FixJ family regulator AcfR of *Azorhizobium caulinodans* is involved in symbiosis with the host plant

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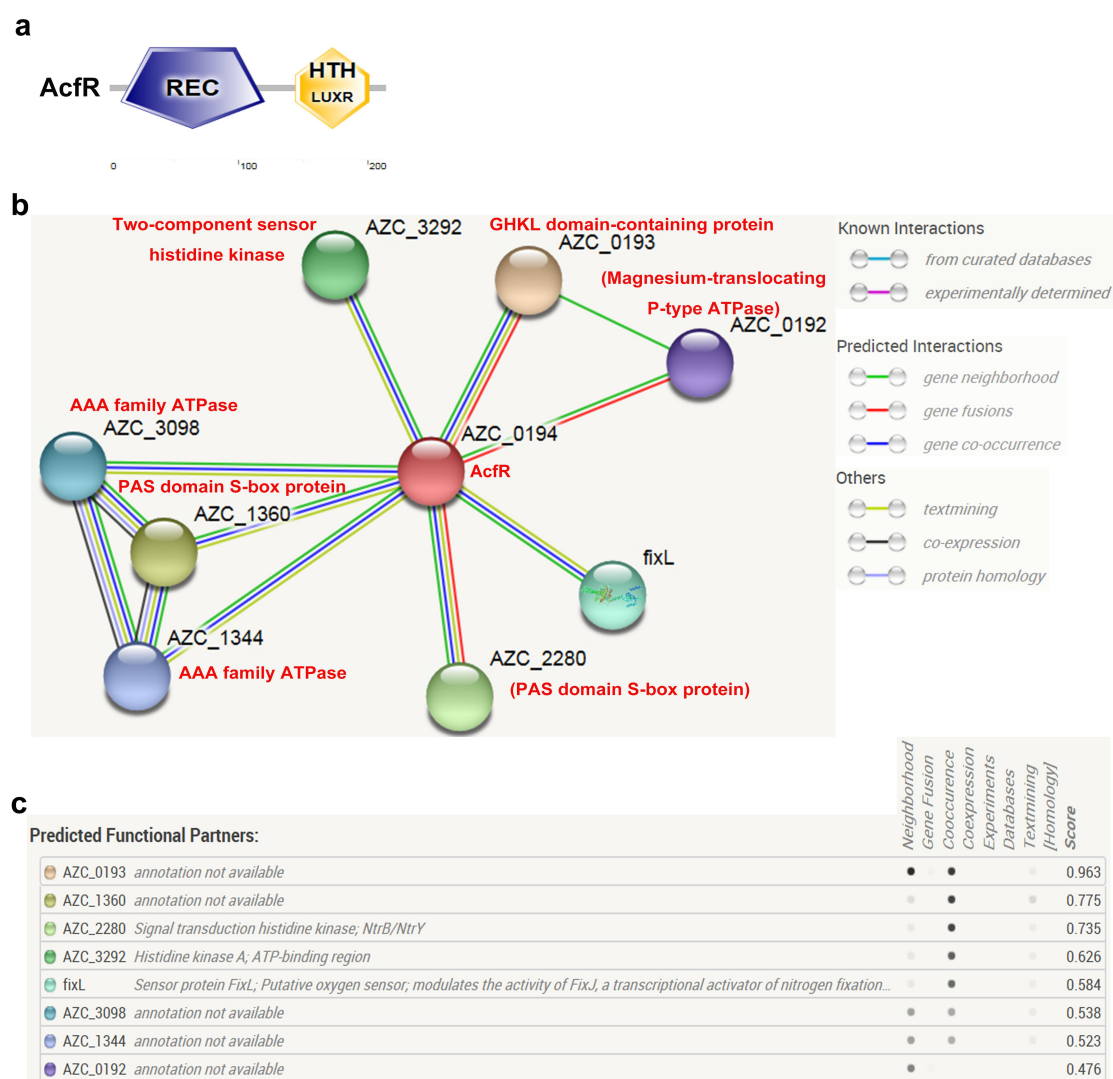


Fig. S1 Domain architecture and interaction network of AcfR. (a) Domain architecture of AcfR predicted by SMART. AcfR was identified encoding a protein of 214 amino acids that containing a REC domain and a HTH_LuxR domain. (b) The interactive protein network of the AcfR predicted by STRING. Eight proteins (containing two AAA family ATPase, two PAS domain S-box, FixL, etc.) predicted to interact with *A. caulinodans* AcfR. (c) The predicted functional partners based on the neighborhood evidence, cooccurrence evidence, and text-mining evidence.

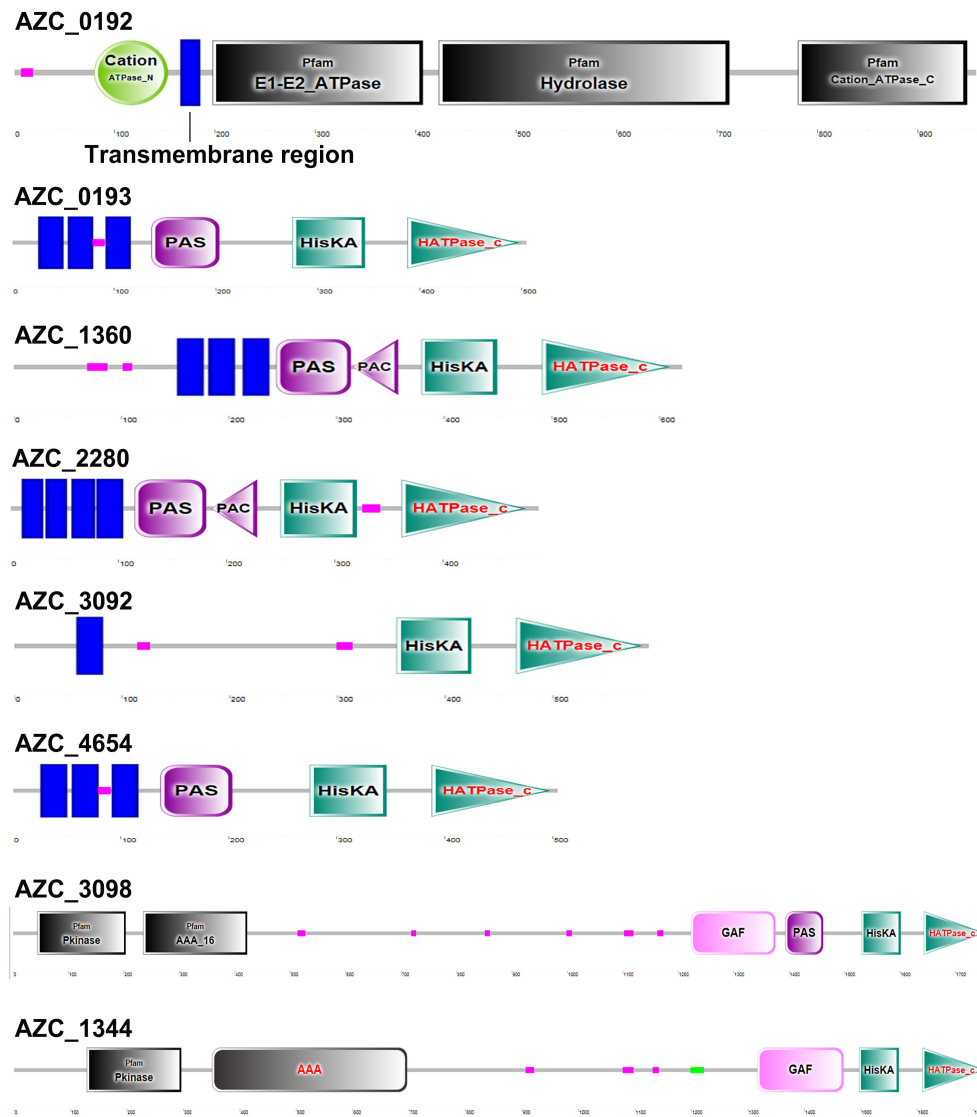


Fig. S2 Domain structures of proteins that predicted in Fig. S1. The protein domains were predicted by using the SMART program. There are eight predicted interaction proteins (AZC_0278, 2411, 2412, 3126, 3970, 3971, 3914, and 0489). Six of eight proteins with HATPase_c and HisKA domains. Abbreviations: PAS, Per-Arnt-Sim domain; PAC, Motif C-terminal to PAS motifs; GAF, Domain present in phytochromes and cGMP-specific phosphodiesterases; HATPase_c, Histidine kinase-like ATPases; HisKA, His Kinase A (phospho acceptor) domain.

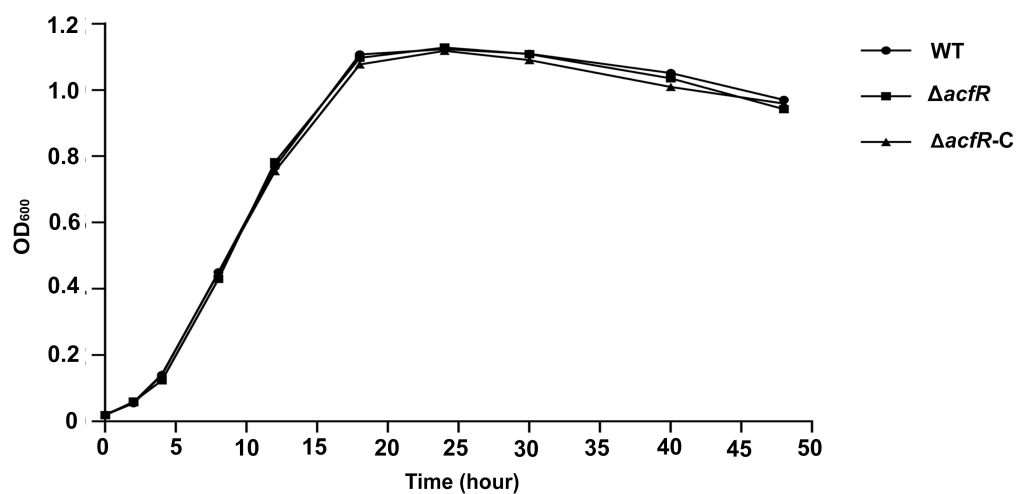


Fig. S3 Growth rates of the wild-type, mutant, and complemented strain are similar.

Growth curves of the WT, $\Delta acfR$, and $\Delta acfR-C$ in L3 liquid medium with 10 mM sodium lactate as sole carbon source and 10 mM NH_4Cl as nitrogen source.