

Physiological and Genomic Properties of an Endophytic Quorum Quenching Agent, *Variovorax paradoxus* S110

Jong-In Han¹, Seung-won Lee², and Jina Kim¹

¹Department of Civil and Environmental Engineering, KAIST, 335 Gwahangno, Yuseong-gu, Daejeon 305-701

²Bioinformatics Research Center, KRIBB, 111 Gwahangno, Yuseong-gu, Daejeon, 305-333

Some of the most intense interactions between microorganisms and plants occur in the rhizosphere on the plant root or in its close vicinity. More recently, evidence has emerged that bacteria can form a more intimate association with host plants and colonize interior plant tissues. These unique endophytic bacteria may have an ecological advantage over rhizophytes because internal tissues of plants offer more uniform and protective niches for microbes compared with the competitive, high-stress environment of the soil.

Many microbes have enhanced their ability to compete, survive or colonize a particular host by adopting a co-operative group behavior known as quorum-sensing (QS). QS is a signalling system by which a local population of bacteria synchronize activities. For example, by employing QS when invading hosts, bacterial pathogens can avoid the premature expression of virulence factors which could otherwise alert the host and elicit proactive defensive responses. QS offers an effective time-control mechanism that allows the pathogen to amass, without being sensed by the host, until a large enough population is achieved to overwhelm the host. A variety of microbes produce enzymes that degrade the signal molecules used in QS. These quorum quenching (QQ) enzymes, when expressed in plants, have blocked QS and thus disrupted community behaviors of bacterial plant pathogens. Similarly, treatment of plants with bacteria expressing these enzymes significantly reduced pathogenesis.

We have recently isolated a QQ bacteria, *Variovorax paradoxus* S110 from the interior of the potato plants and obtained the complete genome sequence in collaboration with the Joint Genome Institute (JGI). This bacterial species, in addition to the QQ capability, has a variety of interesting characteristics that are ecologically important and potentially useful for the field applications. *Variovorax* species is catabolically very diverse and engage in mutually beneficial interactions with other bacterial species in many biodegradations. For example, a soil methanotroph, only when co-cultured together with a *V. paradoxus* strain, exhibits the high affinity for methane (a potent greenhouse gas), and this trait is not usually observed in laboratory cultures. Similarly a close relative of *Variovorax* found to be the central, nonphotosynthetic partner within the phototrophic consortium "*Chlorochromatium aggregatum*." Moreover, *Variovorax* can intimately interact with other biota (e.g., plants) in various ecosystems. *Variovorax* also appears well poised in its metabolic potential to compete for gasses and organics typically produced and released into the environment in oligotrophic amounts

during the metabolism of other biota. Moreover, *Variovorax*, residing in the rhizospheric and/or endophytic regions, can promote plant growth via the reduction of ethylene level and repression of quorum-sensing controlled pathogenesis, and the increase of resistance to heavy metals, which greatly benefits phytoremediation.

Thus, *V. paradoxus* is an excellent choice for continued studies on novel biodegradation, as well as microbe-microbe and microbe-plant interactions. Sequence information allows us to reveal the ecological roles of *Variovorax* in biota involved in diverse biodegradation and contribute to our understanding of the evolution and ecology of catabolic pathways for compounds including explosives, energetic materials, and pesticides.

References

- [1] Leadbetter, J. R. and E.P. Greenberg, 182:6921-6926, 2000.
- [2] Kanzler, B. E., K. R. Pfannes, K. Vogl, and J. Overmann, *Appl. Environ. Microbiol.* 71:7434-7441, 2005.
- [3] Zhang, L. H., and Y. H. Dong, *Mol. Microbiol.* 53:1563-1571, 2004.
- [4] Dunfield, P. F., W. Liesack, T. Henckel, R. Knowles, and R. Conrad, *Appl. Environ. Microbiol.* 65:1009-1014. 1999.
- [5] *Variovorax paradoxus* S110 genome sequence information is available at http://genome.ornl.gov/microbial/vpar_s110