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# Comprehensive analysis of molecular mechanism of Serine deficiency by computational approach

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## Abstract

L -serine (L-Ser), a dispensable amino acid, is synthesized via de novo synthesis from the glycolytic intermediate 3-phosphoglycerate with 3-phosphoglycerate dehydrogenase (Phgdh) catalyzing the first reaction step. L-Ser serves as a necessary precursor for the synthesis of proteins, sphingolipids, folate metabolites, and amino acids such as D-serine and glycine. Previous in vivo study demonstrated that severe L-Ser deficiency in mice with systemic targeted disruption of Phgdh, resulted in intrauterine growth retardation, multiple organ malformation, and embryonic lethality. L-Ser biosynthesis defects in humans resulting from PHGDH mutations were identified to be a cause of L-Ser deficiency disorders and Neu–Laxova syndrome, the symptoms of which include severe fetal growth retardation, microcephaly, still birth and/or perinatal lethality. These findings have demonstrated that de novo L-Ser synthesis is essential for embryonic development and survival in mice and humans. Moreover, resent study demonstrate that the decrease of L-Ser availability appears to correlate with symptoms of metabolic diseases and psychiatric diseases. These studies raise the possibility that elucidation of the pathological mechanisms underlying L-Ser deficiency could provide an opportunity to develop new therapies to alleviate symptoms of various diseases associated with reduced L-Ser availability. In this study, I aim to elucidate the molecular mechanism of cytotoxicity induced by Ser deficiency under pathological condition. To understand the physiological significance of Ser in the brain, I extracted characteristic gene expression pattern using microarray data and detected the active/inactive pathways caused by Ser deficiency.

## Biography

Momoko Hamano has completed her PhD in 2019 from Kyushu University, Japan. She is the researcher of Kyushu University and Kyushu Institute of Technology, Japan. She can elucidate the molecular mechanism of response of amino acid deficiency or some disease by both experimental approach and computational approach. She is good at handling RNA-seq and microarray data to clarify the molecular mechanism. Recently, she is interested in single-cell RNA-seq analysis combing bioinformatics, system biology and computational biology.

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