(pro)renin receptor: A stable molecule

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Abstract

Background: Basically, (pro)renin acts via a specifi c receptor, (pro)renin receptor (PRR) binding between renin and prorenin, its inactive proenzyme form. The study on the molecular level of PRR can give useful knowledge to help understand many renal disorders. **Method:** Here, the author focuses on the stability of the PRR molecule. The mutation prone positions within the PRR molecule was assessed using standard reference technique. **Result:** The study showed there is no identifi ed mutation prone position within the PRR molecule. **Conclusion:** This imply the high stability of PRR. This means that PRR rarely undergoes mutation. The reported mutation in PRR should be a very rare episode and the study on the specifi c cause is warranted.

Key words: (pro)renin receptor, mutation

INTRODUCTION

Renin system is a well-known biochemical system that plays an important role in the renal system of human beings. At present, the focus is shifting from renin to (pro)renin. Actually, (pro)renin acts via a specific receptor, (pro)renin receptor (PRR) binding between renin and prorenin, its inactive proenzyme form.^[1,2] The receptor-bound prorenin leads to generation of an enzymatic activity that activates the mitogen-activated protein (MAP) kinase ERK1/2 and p38 pathways and, subsequently, upregulation of profibrotic and cyclo-oxygenase-2 genes, independent of angiotensin II generation.^[2] Inhibition of PRR can lead to inhibition of renin and be useful for treatment of many renal disorders.^[3] The study of PRR on a molecular level can yield useful knowledge to help understand many renal disorders.^[3] In addition, new evidences show the important role of PRR in hypertension and cardiovascular disease.^[4,5] A linkage between polymorphism of PRR and hypertension has also been shown.^[5]

Access this article online	
Quick Response Code:	Website: www.jnsbm.org
	DOI: 10.4103/0976-9668.92321

Here, the author focuses on the stability of the PRR molecule. Detection of the mutation prone position within the PRR molecule is done by a standard referencing bioinformatics approach.

MATERIALS AND METHODS

The mutation prone positions within the PRR molecule was assessed using standard reference technique; the technique was first proposed by Wiwanitkit.^[6] Briefly, a search for the sequence of PRR in standard molecule database was performed. Subsequently, a bioinformatics tool, GlobPlot, was used for finding the mutation prone position within the derived PRR sequence. The protocol in this work is standard protocol acceptable and used in many previously published papers.^[6-12]

RESULTS

The study showed that there is no identified mutation prone position within the PRR molecule.

DISCUSSION

PRR was discovered about 20 years ago.^[13] Cousin *et al.*^[14] reported that there were evidences for a correlation between polymorphism in the PRR gene and increased ambulatory blood pressure. Nevertheless, a mutation in the

PRR gene that is responsible for mental retardation and epilepsy is also mentioned.^[14-16] The study on the genetic stability of PRR is useful for improving our knowledge on molecular pathogenesis of kidney and other diseases (eg, hypertension, cardiovascular disease, cancer, etc^[4]).

Based on this study, it can be noted that there is no predicted mutation prone position within the PRR. This implies the high stability of PRR. Therefore, PRR rarely undergoes mutation. Indeed, this can be a good explanation for the question: "Why there are only a few reports on mutation of PRR?" The reported mutation in PRR should be a rare episode and a study on the specific cause is warranted. Finally, it should be noted that although this is a standard informatics study, this is only a predictive study using a predictive tool. The result predicted as a mutated position by the tool might not completely lead to the final expression. Hence, even if any point is identified, it may not result in expression of sense mutation.

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How to cite this article: Wiwanitkit V. (pro)renin receptor: A stable molecule. J Nat Sc Biol Med 2011;2:209-10.

Source of Support: Nil. Conflict of Interest: None declared.