



## Review

## Interindividual variations in the efficacy and toxicity of vaccines

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## ABSTRACT

A number of currently available vaccines have shown significant differences in the magnitude of immune responses and toxicity in individuals undergoing vaccination. A number of factors may be involved in the variations in immune responses, which include age, gender, race, amount and quality of the antigen, the dose administered and to some extent the route of administration, and genetics of immune system. Hence, it becomes imperative that researchers have tools such as genomics and proteomics at their disposal to predict which set of population is more likely to be non-responsive or develop toxicity to vaccines. In this article, we briefly review the influence of pharmacogenomics biomarkers on the efficacy and toxicity of some of the most frequently reported vaccines that showed a high rate of variability in response and toxicity towards hepatitis B, measles, mumps, rubella, influenza, and AIDS/HIV.

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## 1. Introduction

Similar to interindividual differences in drug response (Bhathena and Spear, 2008), a number of currently available vaccines have shown significant differences in the magnitude of immune responses in individuals undergoing vaccination. It has been postulated that, a number of factors may be involved in these variations in immune responses. These factors include age, gender, race, amount and quality of the antigen, the dose administered and to some extent the route of administration, and genetics of immune system. Most of these factors can be grouped into variations caused by biology and genomics of the

host and the pathogen. In addition, the environmental factors such as smoking, alcohol consumption and diet can potentially alter biology and genomic factors (Poland et al., 2008a). In a recent study (Poland et al., 2007), the term “vaccinomics” was defined as the areas of immunogenetics and immunogenomics which provide a far better understanding of how an array of factors and/or molecules play critical roles in the regulation of innate and adaptive immune responses. The examples of such molecules include human leukocyte antigen (*HLA*), toll like receptor (TLR) and their signaling components, cytokine receptors and genes as well as transporter associated with antigen processing (TAP), which play a role in contributing to the variations in the immune response due to genetic polymorphisms (Poland et al., 2007).

The role of genomics in determining the extent of immune response is still in its infancy with only a handful of diseases investigated in this regard. Some of the most extensively researched

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