

WHAT IS CLAIMED IS:

1. A method of assessing the risk of a patient for developing phenytoin-induced adverse drug reactions (ADRs), comprising the steps of:
 - detecting the presence of SNPs (Single Nucleotide Polymorphism) in or nearby CYP2C genes on chromosome 10 from a sample of the patient; and
 - associating the presence of SNPs in or nearby CYP2C genes on chromosome 10 with an increased risk for phenytoin-induced adverse drug reactions, which includes Stevens-Johnson syndrome (SJS), toxic epidermal necrolysis (TEN), drug reaction with eosinophilia and systemic symptoms (DRESS), or maculo-papular eruptions (MPE).
2. The method of assessing the risk of a patient for developing phenytoin-induced ADRs of claim 1, wherein the detecting the presence of SNPs in or nearby CYP2C genes includes the step of detecting SNPs on CYP2C variants including CYP2C9, CYP2C8, CYP2C18 and CYP2C19.
3. The method of assessing the risk of a patient for developing phenytoin-induced ADRs of claim 2, wherein the step of associating the presence SNPs in or nearby CYP2C on chromosome 10 with an increased risk for phenytoin-induced ADRs comprising the step of combining one or more SNPs to predict the risk for phenytoin-induced ADRs.
4. The method of assessing the risk of a patient for developing phenytoin-induced adverse drug reactions (ADRs) of claim 1, wherein the step of detecting the presence of genetic variants in or nearby CYP2C genes on chromosome 10 includes the step of using an oligonucleotide that specifically hybridizes with the nucleic acid coding for the variant.
5. The method of assessing the risk of a patient for developing phenytoin-induced adverse drug reactions (ADRs) of claim 1, wherein the step of detecting the presence of genetic variants in or nearby CYP2C genes on chromosome 10 includes the step of using DNA

prepared from the peripheral blood of the patient.

6. A method of assessing the risk of a patient for developing phenytoin-induced adverse drug reactions (ADRs), comprising the steps of:

detecting the presence of HLA alleles, including HLA-A, HLA-B and HLA-DRB1; and

associating the presence of the HLA alleles with an increased risk for phenytoin-induced adverse drug reactions, which includes Stevens-Johnson syndrome (SJS), toxic epidermal necrolysis (TEN), drug reaction with eosinophilia and systemic symptoms (DRESS), or maculo-papular eruptions (MPE).

7. The method of assessing the risk of a patient for developing phenytoin-induced adverse drug reactions (ADRs) of claim 6, wherein the step of detecting the presence of HLA alleles including the step of using PCR-SSO to identify HLA-A, HLA-B and HLA-DRB1 genotypes.

8. The method of assessing the risk of a patient for developing phenytoin-induced adverse drug reactions (ADRs) of claim 6, wherein the step of detecting the presence of HLA alleles includes the step of using an oligonucleotide that specifically hybridizes to the allele.

9. The method of assessing the risk of a patient for developing phenytoin-induced adverse drug reactions (ADRs) of claim 6, wherein the step of detecting the presence of HLA alleles includes the step of using DNA prepared from the peripheral blood of the patient.

10. A method of assessing the risk of a patient for developing phenytoin-induced adverse drug reactions (ADRs), comprising the steps of:

detecting phenytoin concentration in the patient's plasma; and

associating the phenytoin concentration with an increased risk for phenytoin-induced adverse drug reactions, which includes Stevens-Johnson syndrome (SJS), toxic epidermal

necrolysis (TEN), drug reaction with eosinophilia and systemic symptoms (DRESS), or maculo-papular eruptions (MPE).

11. A method of assessing the risk of a patient for developing phenytoin-induced adverse drug reactions (ADRs) of claim 10, wherein the step of detecting phenytoin concentration in the patient's plasma includes the steps of using HPLC to analyze the phenytoin concentration and estimating the phenytoin concentration by non-linear pharmacokinetics formula:

$$t = \frac{K_m \times \ln\left(\frac{C_1}{C_2}\right) + (C_1 - C_2)}{V_{\max}} \times V_d$$

12. The method of assessing the risk of a patient for developing phenytoin-induced ADRs of claim 1, further comprising the step of detecting the change amino acids.

13. The method of assessing the risk of a patient for developing phenytoin-induced ADRs of claim 2, wherein the step of detecting SNPs on CYP2C variants (including CYP2C9, CYP2C8, CYP2C18 and CYP2C19) comprises the step of detecting the presence of CYP2C9*3 variants.

WHAT IS CLAIMED IS:

1. A method of assessing the risk of a patient for developing phenytoin-induced hypersensitivity reactions, comprising the steps of:

detecting the presence of SNPs (Single Nucleotide Polymorphism) in or nearby CYP2C genes on chromosome 10 from a sample of the patient; and

associating the presence of SNPs in or nearby CYP2C genes on chromosome 10 with an increased risk for phenytoin-induced hypersensitivity reactions, which includes Stevens-Johnson syndrome (SJS), toxic epidermal necrolysis (TEN), drug reaction with eosinophilia and systemic symptoms (DRESS), or maculo-papular eruptions (MPE).

2. The method of assessing the risk of a patient for developing phenytoin-induced hypersensitivity reactions of claim 1, wherein the detecting the presence of SNPs in or nearby CYP2C genes includes the step of detecting SNPs on CYP2C variants including CYP2C9, CYP2C8, CYP2C18 and CYP2C19.

3. The method of assessing the risk of a patient for developing phenytoin-induced hypersensitivity reactions of claim 2, wherein the step of associating the presence SNPs in or nearby CYP2C on chromosome 10 with an increased risk for phenytoin-induced hypersensitivity reactions comprising the step of combining one or more SNPs to predict the risk for phenytoin-induced hypersensitivity reactions.

4. The method of assessing the risk of a patient for developing phenytoin-induced hypersensitivity reactions) of claim 1, wherein the step of detecting the presence of genetic variants in or nearby CYP2C genes on chromosome 10 includes the step of using an oligonucleotide that specifically hybridizes with the nucleic acid coding for the variant.

5. The method of assessing the risk of a patient for developing phenytoin-induced hypersensitivity reactions of claim 1, wherein the step of detecting the presence of genetic variants in or nearby CYP2C genes on chromosome 10 includes the step of using DNA prepared from the peripheral blood of the patient.

6. The method of assessing the risk of a patient for developing phenytoin-induced hypersensitivity reactions of claim 1, further comprising the step of detecting the change amino acids.

7. The method of assessing the risk of a patient for developing phenytoin-induced hypersensitivity reactions of claim 2, wherein the step of detecting SNPs on CYP2C variants comprises the step of detecting the presence of CYP2C9*3 variants.