CLAIMS

Now, therefore, the following is claimed:

1. A method for using immunorepertoire diversity to assess a normal or abnormal status of an individual patient's immunorepertoire, the method comprising the steps of:

(a) determining the pCDR3 sequences, the commonly-shared CDR3 sequences identified from a reference group of individuals, comprising comparing each sample from the reference group and identifying those CDR3 sequences that are most-frequently shared within said reference group;

(b) using primers directed to pCDR3 sequences to detect the presence in the patient's immunorepertoire of individual CDR3s within that shared group of pCDR3 sequences; and

(c) calculating the normality index, comprising dividing the number of pCDR3 sequences from the reference group by the number of pCDR3 sequences present in the patient's immunorepertoire; and

(d) assessing the status of the patient's immunorepertoire, wherein the normality index is compared with a predetermined minimum percentage of shared pCDR3 sequences, such that the immunorepertoire of the patient is considered normal when the normality index meets or exceeds the minimum percentage of shared pCDR3 sequences and the immunorepertoire of the patient is considered abnormal when the normality index is below the minimum percentage of shared pCDR3 sequences.

2. The method of claim 1 wherein the CDR3 sequences are from a population of cells selected from the group consisting of all T cells [panT], CD8+ T cells [cytotoxic T (Ta)], CD4+ T cells and their subsets [TH1, TH2, TH17, regulatory T (Treg), follicular T (TFH)], developmental subsets of T cells, such as naive T (Tn), activated T (Ta), memory T (Tm), all B cells (panB), naive B (Br), activated B (Ba), memory B (Bm), plasma and plasmablast B cells.

3. The method of claim 1, wherein the minimum percentage of pCDR3 is a percentage number selected from about 25 percent to about 75 percent.

4. The method of claim 1, wherein the minimum percentage of pCDR3 is about 25 percent.

5. The method of claim 1, where the pCDR3 is composed of about the 1000 most-frequently-shared CDR3.

6. The method of claim 1, where the pCDR3 is composed of more than 1000 of the most-frequently-shared CDR3.

7. The method of claim 1, where the pCDR3 is composed of fewer than 1000 of the most-frequently-shared CDR3.

8. The method of claim 1, wherein the pCDR3 is composed of CDR3 shared by at least 25 percent of a pool of individuals.

9. The method of claim 1, wherein the pCDR3 is composed of CDR3 shared by at least 50 percent of a pool of individuals.

10. The method of claim 9, wherein the pool contains at least 100 individuals.

11. The method of claim 9, wherein the pool contains about 1000 individuals.

12. A method for using immunorepertoire diversity to assess a normal or abnormal status of an individual patient's immunorepertoire, the method comprising:

(a) amplifying polynucleotides from a population of white blood cells from a human or animal subject in a reaction mix comprising target-specific nested primers to produce a set of first amplicons, at least a portion of the target-specific nested primers comprising additional nucleotides which, during amplification, serve as a template for incorporating into the first amplicons a binding site for at least one common primer;

(b) transferring a portion of the first reaction mix containing the first amplicons to a second reaction mix comprising at least one common primer;

(c) amplifying, using the at least one common primer, the first amplicons to produce a set of second amplicons;

(d) sequencing the second amplicons to identify CDR3 sequences in the subpopulation of white blood cells;

(e) determining the pCDR3 sequences, the commonly-shared CDR3 sequences identified from a reference group of individuals, comprising comparing each

sample from the reference group and identifying those CDR3 sequences that are most-frequently shared within said reference group;

(f) using the identified CDR3 sequences to calculate the normality index, comprising dividing the number of pCDR3 sequences from the reference group by the number of pCDR3 sequences present in the patient's identified CDR3 sequences; and

(g) assessing the status of the patient's immunorepertoire, wherein the normality index is compared with a predetermined minimum percentage of shared pCDR3 sequences, such that the immunorepertoire of the patient is considered normal when the normality index meets or exceeds the minimum percentage of shared pCDR3 sequences and the immunorepertoire of the patient is considered abnormal when the normality index is below the minimum percentage of shared pCDR3 sequences.

13. The method of claim 12, wherein the population of cells is selected from the group consisting of all T cells [panT], CD8+ T cells [cytotoxic T (Ta)], CD4+ T cells and their subsets [TH1, TH2, TH17, regulatory T (Treg), follicular T (TFH)], developmental subsets of T cells, such as naive T (Tn), activated T (Ta), memory T (Tm), all B cells (panB), naive B (Br), activated B (Ba), memory B (Bm), plasma and plasmablast B cells.

14. The method of claim 12, wherein the population of white blood cells is about 100,000 randomly-selected cells.

15. The method of claim 12, wherein the method is repeated about 10 to 100 times, each time with a random selection of cells, to determine the average percentage of pCDR3 expressed by the patient.

16. The method of claim 12, wherein the minimum percentage of pCDR3 is a percentage number from about 25 to about 75.

17. The method of claim 12, wherein the minimum percentage of pCDR3 is about 25 percent.

18. The method of claim 12, wherein the pCDR3 is composed of at least the 1000 most-frequently-shared CDR3.

19. The method of claim 12, wherein the pCDR3 includes SEQ ID NO:1 through SEQ ID NO: 4014.

20. The method of claim 12, wherein the pCDR3 is composed of CDR3 shared by at least 50 percent of a pool of individuals.

21. The method of claim 20, wherein the pool contains at least 100 individuals.

22. The method of claim 20, wherein the pool contains about 1000 individuals.

23. The method of claim 20, wherein the pool is composed of healthy control individuals.

24. The method of claim 20, wherein the pool is composed of individuals with one or more specific disease states.

25. The method of claim 20, wherein the pool of individuals is approximately age-matched to the patient.

26. The method of claim 20, wherein the pool of individuals is gender-matched to the patient.