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(71) Applicants: **ADAPTIVE BIOTECHNOLOGIES CORPORATION** [US/US]; 1551 Eastlake Avenue East, Suite 200, Seattle, Washington 98102 (US). **FRED HUTCHINSON CANCER RESEARCH CENTER** [US/US]; Division of Basic Sciences, Mail Stop A3-100, P.O. Box 190, Seattle, Washington 98109 (US).

(72) Inventors: **ROBINS, Harlan S.**; c/o Adaptive Biotechnologies Corporation, 1551 Eastlake Avenue East, Suite 200, Seattle, Washington 98102 (US). **EMERSON, Ryan O.**; c/o Adaptive Biotechnologies Corporation, 1551 Eastlake Avenue East, Suite 200, Seattle, Washington 98102 (US). **DEWITT, William Sumner, III**; c/o Adaptive Biotechnologies Corporation, 1551 Eastlake Avenue East, Suite 200, Seattle, Washington 98102 (US).

(74) Agents: **FULLER, Alyson C.** et al.; Cooley LLP, 1299 Pennsylvania Avenue, NW, Suite 700, Washington, District of Columbia 20004 (US).

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(57) Abstract: Methods of monitoring and measuring dynamic adaptive immune cell responses are provided. High-throughput sequencing of T cell receptor and immunoglobulin loci is used to characterize the breadth of an effector cell response to a stimulus, such as a vaccine or infection. Unique responding effector cell clones and abundance thereof can be determined. Additionally, methods for determining the contribution of responding effector cells to the immunological memory compartment are provided.



WO 2016/086029 A1

CHARACTERIZATION OF ADAPTIVE IMMUNE RESPONSE TO VACCINATION OR INFECTION USING IMMUNE REPERTOIRE SEQUENCING

CROSS REFERENCE TO RELATED APPLICATIONS

This application claims the benefit of U.S. Provisional Application No. 62/084,470, filed November 25, 2014, which is hereby incorporated in its entirety by reference.

STATEMENT REGARDING FEDERALLY SPONSORED RESEARCH OR DEVELOPMENT

[0001] This invention was made with government support under Grant No. R56 AI0181860 awarded by the National Institutes of Health. The government has certain rights in the invention.

BACKGROUND OF THE INVENTION

Field of the Invention

[0002] The disclosure relates to methods of characterizing an adaptive immune response to an infection or a vaccination by analyzing the repertoire of rearranged CDR3 regions of T cell receptor genes or immunoglobulin genes.

Description of the Related Art

[0003] Researchers have attempted to study the adaptive immune response to an infection caused by foreign pathogens, such as parasites, bacteria or viruses, which can inform the dynamics of the response to the infection or the effectiveness of a treatment.

[0004] For instance, the detailed characterization of the dynamics and breadth of the human immune response to a vaccination can greatly contribute to a basic understanding of the immune system and guide the design of effective new vaccines. Both neutralizing antibodies produced by B cells and effector T cells, especially CD8⁺ T cells (cytotoxic T lymphocytes, or CTLs), have been shown to be critical for the effective resolution of acute viral infections.

[0005] Moreover, during the acute response to a viral infection, viral antigen-specific effector B cell and T cell clones become activated and expand as they recognize and eliminate infected host cells (Kaeck and Wherry, 2007, Immunity 27:393-405; Wherry et al. 2007 Immunity 27:670-684). The antigen specificity of a B cell clone and a T cell clone is determined by the B cell receptor (BCR) and T cell receptor (TCR), respectively, which are encoded by random, RAG-mediated V(D)J recombination. Thus, each T cell clone may be identified by its unique TCR β CDR3 region, formed from the joining of the V, D and J gene

segments, with CDR3 being the primary determinant of antigen specificity (Engel and Hedrick, 1988, *Cell* 54:473-484; Jorgensen et al. 1992, *Nature* 355:224-230). Similarly, each B cell clone may be identified by its unique immunoglobulin heavy chain (IgH) CDR3 region, formed from the joining of the V, D and J gene segments.

[0006] The identification and tracking of virus-specific T cell clones has resulted in the extensive characterization of the phenotype and function of virus-specific T cells (McHeyzer-Williams and Davis, 1995, *Science* 268:106-111; Miller et al. 2008, *Immunity* 28:710-722; Newell et al. 2012, *Immunity* 36:142-152; Precopio et al. 2007, *The Journal of Experimental Medicine* 204:1405-1416). Importantly, responses to chronic and acute viruses seem to be characterized by different patterns of activation and waning of effector cells, as well as different memory cell phenotypes, which might be related to the different patterns of exposures to viral antigens in the two types of infections (Ahmed and Akondy, 2011, *Immunology and cell biology* 89:340-345).

[0007] The identification of virus-specific T cells during the course of an infection has allowed the measurement of the number of unique clones responding to a particular viral epitope (Akondy et al. 2009, *Journal of immunology* 183:7919-7930; Co et al. 2002, *Virology* 293:151-163; Turner et al. 2003, *Immunity* 18:549-559). These studies suggest that the magnitude of the T cell clonal response to different viral antigens is not uniform. For example, in the case of the yellow fever vaccine (YFV), peptide NS4b induces a more robust T cell response than peptide NS5 (Akondy et al. 2009, *Journal of immunology* 183:7919-7930; Blom et al. 2013, *Journal of immunology* 190:2150-2158). Moreover, there is extensive variability in the number of unique clones activated by a particular viral epitope (Manuel et al. 2006, *Journal of virology* 80:12032-12040; Miconnet et al. 2011, *Journal of immunology* 186:7039-7049), which depends on both the quantity of peptide presented (Henrickson et al. 2013, *Immunity* 39:496-507) and on the microenvironment of the lymph node where the T cell encounters antigen (Newell et al. 2012, *Immunity* 36:142-152). Finally, major histocompatibility complexes (MHC) polymorphisms lead to variable epitope presentation in different individuals (Achour et al. 2002, *Immunity* 17:757-768; Eckle et al. 2013, *Current Opinion in Immunology* 25:653-659), complicating the characterization of dominant and non-dominant clonal CTL responses.

[0008] The formation of virus-specific memory cells is also believed to be dependent on the magnitude of the clonal response to antigen (Hou et al. 1994, *Nature* 369:652-654; Vezys et al. 2009, *Nature* 457:196-199). After an acute infection is resolved, the virus-specific effector cell pool contracts (Badovinac et al. 2002, *Nature immunology* 3:619-626),

and a much smaller number of long-lived memory cells that are capable of responding to subsequent infections are maintained (Sung et al. 2012, *Cell* 150:1249-1263). It is thought that effector cell clones present in high abundance are recruited to the memory repertoire with higher frequency than less abundant clones (Turner et al. 2003, *Immunity* 18:549-559; Flynn et al. 1998, *Immunity* 8:683-691; Sourdive et al. 1998, *The Journal of experimental medicine* 188:71-82), but it is not clear whether this simply reflects the limitations of currently available techniques. Therefore highly sensitive techniques are necessary to establish the contribution of less abundant clones to the memory pool (Blom et al. 2013, *Journal of Immunology* 190:2150-2158). Furthermore, to date, it has not been possible to relate the magnitude and diversity of the effector cell response to the subsequent abundance of individual clones in the memory cell repertoire.

[0009] Since exposure to YFV is geographically limited, and YFV is a very effective vaccine that elicits an optimal, long-term protective immune response upon administration of a single dose, this model has been used extensively to explore the human immune response to a controlled, self-resolving acute viral infection (reviewed in Ahmed R, Akondy RS. 2011. Insights into human CD8(+) T-cell memory using the yellow fever and smallpox vaccines. *Immunol Cell Biol* 89: 340–345, and Pulendran B. 2009. Learning immunology from the yellow fever vaccine: innate immunity to systems vaccinology. *Nat Rev Immunol* 9:741–747). These seminal studies have shown that (i) the ability of YF-17D to infect dendritic cells and signal through multiple Toll-like receptors may be related to the effectiveness of this vaccine (Querec T, et al. 2006. Yellow fever vaccine YF-17D activates multiple dendritic cell subsets via TLR2, 7, 8, and 9 to stimulate polyvalent immunity. *J Exp Med* 203:413– 424.); (ii) neutralizing antibodies (nAbs) are the best surrogate marker for protection against YFV and remain detectable for many years (Jonker EF, et al. 2013. Advances and controversies in yellow fever vaccination. *Ther Adv Vaccines* 1:144–152; Reinhardt B, et al. 1998. Development of viremia and humoral and cellular parameters of immune activation after vaccination with yellow fever virus strain 17D: a model of human flavivirus infection. *J Med Virol* 56:159–167.); and (iii) CD8+ T cells expand massively before nAbs can be detected (and are thus likely involved in the control of viremia) and persist in the memory compartment for decades (Miller JD, et al. 2008. Human effector and memory CD8+ T cell responses to smallpox and yellow fever vaccines. *Immunity* 28:710–722; Santos AP, et al. 2005. Lymphocyte subset analyses in healthy adults vaccinated with yellow fever 17DD virus. *Mem Inst Oswaldo Cruz* 100:331–337.).

[0010] The current understanding of the CD4⁺ response to YFV, however, is limited. Although helper T cells are clearly required for the production of YFV-specific Abs (including nAbs), different studies have reported variable levels of induction of CD4⁺ T cells upon vaccination with YFV (Santos et al. 2005; Kohler S, et al. 2012. The early cellular signatures of protective immunity induced by live viral vaccination. *Eur J Immunol* 42:2363–2373.). Some analyses have revealed that cytokine producing YFV-specific CD4⁺ T cells can be detected as early as day 2 post-vaccination and that they return to baseline by day 28, suggesting that the kinetics of CD4⁺ T cells precede those of CD8⁺ T cells (Blom K, et al. 2013. Temporal dynamics of the primary human T cell response to yellow fever virus 17D as it matures from an effector- to a memory-type response. *J Immunol* 190: 2150–2158; Kohler et al. 2012). Recently, James et al. used class II HLA-DR restricted, YFV-specific tetramers to characterize the CD4⁺ response to YFV in more depth, showing that all 10 proteins in the YFV genome contain antigenic epitopes recognized by CD4⁺ T cells (James EA, LaFond RE, Gates TJ, Mai DT, Malhotra U, Kwok WW. 2013. Yellow fever vaccination elicits broad functional CD4⁺ T cell responses that recognize structural and nonstructural proteins. *J Virol* 87: 12794–12804.). This study also revealed a wide range of frequencies of CD4⁺ T cells specific for a limited number of YFV epitopes in peripheral blood (from 0 to 100 cells per million CD4⁺ T cells) and established that YFV-specific T cells, which display a predominant Th1-like memory phenotype, occur at ~10- to 100-fold higher frequencies in vaccinated versus unvaccinated individuals, depending on the time point considered. *Id.* In contrast, there have been several detailed analyses of the kinetics and phenotype of CD8⁺ T cells induced by vaccination with YFV. For example, Miller et al. showed that activated effector CD8⁺ T cells (TAE) peak 2 weeks after administration of the YFV and defined the YFV-specific subpopulation of CD8⁺ CTL cells as CD38⁺ HLA-DR⁺ Ki-67⁺ Bcl-2^{lo}. In addition, this study established a strong correlation between the levels of CD38⁺ HLA-DR⁺ CD8⁺ T cells and the expression of gamma interferon (IFN- γ) by total CD8⁺ T cells in response to YF virus-infected cells, and it demonstrated that stimulation of CD8⁺ T cells from YFV-vaccinated volunteers with a comprehensive pool of peptides that span the YF virus polyprotein also induced IFN- γ . Since unrelated memory CD8⁺ T cells (such as those specific for chronic viruses like Epstein-Barr virus (EBV) and cytomegalovirus (CMV) and therefore presumed to preexist at the time of vaccination with YFV) were not found among the expanded CD8⁺ T cell population, these observations suggest that, at least in the case of YFV, the bystander effect is minimal, and they also imply that the vast majority of TAE clones observed after administration of YF-17D are YF virus specific. Finally, those authors

showed that Ag specific cells could be identified more than 30 days post-vaccination, indicating that the YFV-specific effector CD8⁺ T cells had waned and also that a certain proportion of them had entered the memory compartment (Miller et al. 2008). Subsequent work from the same group employed an array of overlapping peptides that spanned the entire YF virus polyprotein to demonstrate that vaccination with YFV induces a broad CD8⁺ T response that targets several epitopes in each of the 10 viral proteins (Akondy RS, et al. 2009). The yellow fever virus vaccine induces a broad and polyfunctional human memory CD8⁺ T cell response. *J Immunol* 183:7919–7930.). The use of tetramers carrying an immunodominant epitope from the nonstructural NS4b protein helped define the phenotypes of YFV-specific CD8⁺ T cells through the expansion, contraction, and memory phases of the immune response, further confirming that CD38⁺ HLA-DR⁺ CD8⁺ T cells dramatically expand after YFV-17D administration and produce cytotoxic effector molecules. *Id.* Similar results were observed by Co et al., who identified YFV-specific proliferation and cytolytic responses on day 14 postvaccination and isolated CD8⁺ T cell lines that were specific for epitopes from structural and nonstructural YF virus proteins, some of which persisted for up to 19 months postvaccination (Co MD, Terajima M, Cruz J, Ennis FA, Rothman AL. 2002. Human cytotoxic T lymphocyte responses to live attenuated 17D yellow fever vaccine: identification of HLA-B35-restricted CTL epitopes on nonstructural proteins NS1, NS2b, NS3, and the structural protein E. *Virology* 293:151–163. Again, follow-up data from a tetramer-based approach showed that YFV-specific CD8⁺ T cells could be identified as early as 7 to 9 days post-vaccination, before IFN- γ production was detectable, that memory cells corresponded mostly to a differentiated effector phenotype (CD45RA⁺ CCR7⁻ CD62L⁻), and that these peptide-specific responses lasted for at least 54 months (Co MD, et al. 2009. Dynamics of the CD8 T-cell response following yellow fever virus 17D immunization. *Immunology* 128:e718–e727.). A more recent study using a limited set of YF virus HLA-tetramer epitopes suggested that the CD8⁺ response to YFV is broad and complex and that responses to different epitopes vary in magnitude and duration (Blom K, et al. 2013. Temporal dynamics of the primary human T cell response to yellow fever virus 17D as it matures from an effector- to a memory-type response. *J Immunol* 190: 2150–2158). Those authors also found that YFV-specific effector CD8⁺ T cells were CD45RA^{hi} CCR7⁻ PD1⁻ CD27^{hi} and that only some of these cells transition to the T cell memory compartment, at which point they became CD45RA⁺ CCR7⁻ PD1⁻ CD27^{lo} (Blom et al. 2013, *Journal of Immunology* 190:2150-2158).

[0011] Thus, it is essential to characterize the dynamics of the B cell and T cell repertoires in response to an infection to determine the breadth of the immune response, to characterize the formation of immunological memory, and to understand how the human immune system responds to infection or vaccination. The present disclosure addresses these needs and more.

BRIEF SUMMARY OF THE INVENTION

[0012] One aspect of the invention provides a method of measuring T cell response to a vaccine in a subject, comprising: performing high-throughput sequencing of nucleic acid molecules comprising rearranged CDR3 regions of TCR loci obtained from a first biological sample of the subject at a first time point prior to vaccination; performing high-throughput sequencing of nucleic acid molecules comprising rearranged CDR3 regions of TCR loci obtained from a second biological sample of the subject at a second time point post vaccination; and identifying T cell clones having CDR3 regions of significantly higher proportional abundance in the second biological sample in comparison to the first biological sample, thereby identifying vaccine-induced responsive clones.

[0013] In one embodiment, the TCR loci are selected from the group consisting of the TCR α locus, TCR β locus, TCR γ locus, and TCR δ locus. In one embodiment, the biological samples comprise peripheral blood mononuclear cells (PBMCs). In certain embodiments, the biological samples comprise memory T cells. In one embodiment, the second biological sample is obtained at least 10 days post vaccination.

[0014] In another embodiment, the method further comprises performing multiplex PCR amplification of genomic templates comprising rearranged CDR3 regions to produce nucleic acid molecules for sequencing. In one embodiment, identifying comprises calculating a false discovery rate, and wherein the calculating comprises performing a computation on a computer.

[0015] In one embodiment, the activated T cell clones are vaccine antigen-specific T cells. In another embodiment, the activated T cell clones are CD8⁺ effector T cells.

[0016] In one embodiment, the vaccine is a vaccine for an infectious agent or a cancer vaccine. In a related embodiment, the infectious agent is a virus selected from the group consisting of yellow fever virus, influenza virus, smallpox virus, herpes simplex virus, cytomegalovirus, Epstein-barr virus and human papilloma virus.

[0017] In another embodiment, the method further comprises sorting the activated T cell clones in the second biological sample by flow cytometry. In one embodiment, the

method further comprises sorting the first biological sample for memory T cells using flow cytometry.

[0018] In a related aspect, the method of measuring T cell response to a vaccine in a subject further comprises: performing high-throughput sequencing of nucleic acid molecules comprising rearranged CDR3 regions of TCR loci obtained from a third biological sample of the subject at a third time point post vaccination; and identifying newly recruited memory T cell clones corresponding to the vaccine-induced responsive clones that are not present in the first biological sample and that have been recruited to a memory T cell population post vaccination.

[0019] In one embodiment, the identifying newly recruited memory T cell clones comprises sorting memory T cells by flow cytometry. In another embodiment, identifying newly recruited memory T cell clones comprises comparing a first set of memory T cell clones in the first biological sample to a second set of memory T cell clones in the third biological sample to identify one or more newly recruited memory T cell clones that have been recruited to the memory T cell population post vaccination. In a related embodiment, the method further comprises comparing the identified one or more newly recruited memory T cell clones with one or more vaccine-induced responsive clones from the second biological sample to find matches between the newly recruited memory T cell clones and the one or more vaccine-induced responsive clones. In one embodiment, the matched memory T cell clones are a significant proportion of total memory T cell population and are identified as biomarkers for vaccine-specific response. In one embodiment, the memory T cell clones are $CD8^+CD45RO^+CD62L^{lo}$ effector memory T cells. In another embodiment, the memory T cell clones are $CD8^+CD45RO^+CD62L^{hi}$ central memory T cells. In one embodiment, the third time point is at least 30 days post vaccination.

[0020] In certain embodiments, the method does not require an enrichment step by sorting for effector cells with flow cytometry. In one embodiment, a degree of recruitment of vaccine-induced responsive clones to immunological memory is identified as a biomarker for vaccine efficacy.

[0021] Another aspect of the invention provides a method of measuring T cell response to a vaccine in a subject, comprising: performing high-throughput sequencing of nucleic acid molecules comprising rearranged CDR3 regions of TCR loci obtained from a first biological sample of the subject at a first time point post vaccination; sorting activated T cells from a subset of the first biological sample using flow cytometry to generate a set of activated T cells; performing high-throughput sequencing of nucleic acid molecules

comprising rearranged CDR3 regions of TCR loci obtained from the set of activated T cells; and identifying activated T cell clones in the set having CDR3 regions of significantly higher proportional abundance in the activated T cell population in comparison to the first biological sample, thereby identifying vaccine-induced responsive clones.

[0022] In one embodiment, the TCR loci are selected from the group consisting of the TCR α locus, TCR β locus, TCR γ locus, and TCR δ locus. In another embodiment, the biological samples comprise peripheral blood mononuclear cells (PBMCs). In one embodiment, the biological samples comprise memory T cells. In another embodiment, the first biological sample is obtained at least 10 days post vaccination. In one embodiment, the method further comprises performing multiplex PCR amplification of genomic templates comprising rearranged CDR3 regions to produce nucleic acid molecules for sequencing. In another embodiment, identifying comprises calculating a false discovery rate, and wherein the calculating comprises performing a computation on a computer.

[0023] In one embodiment, the activated T cell clones are vaccine antigen-specific T cells. In another embodiment, the activated T cell clones are CD8⁺ effector T cells. In one embodiment, the vaccine is a vaccine for an infectious agent or a cancer vaccine.

[0024] In a related aspect, the method of measuring T cell response to a vaccine in a subject further comprises: performing high-throughput sequencing of nucleic acid molecules comprising rearranged CDR3 regions of TCR loci obtained from a second biological sample of the subject at a second time point post vaccination; and identifying newly recruited memory T cell clones corresponding to the vaccine-induced responsive clones that have been recruited to a memory T cell population post vaccination.

[0025] In one embodiment, identifying newly recruited memory T cell clones comprises sorting memory T cells by flow cytometry. In another embodiment, identifying newly recruited memory T cell clones comprises comparing a first set of memory T cell clones in the first biological sample to a second set of memory T cell clones in the second biological sample to identify one or more newly recruited memory T cell clones that have been recruited to the memory T cell population post vaccination. In one embodiment, the method further comprises comparing the identified one or more newly recruited memory T cell clones with one or more vaccine-induced responsive clones from the set of activated T cells to find matches between the newly recruited memory T cell clones and the one or more vaccine-induced responsive clones. In a related embodiment, the matched memory T cell clones are a significant number of the vaccine-induced responsive clones and are identified as

biomarkers for vaccine-specific response. In another embodiment, the matched memory T cell clones are a significant proportion of total memory T cell population and are identified as biomarkers for vaccine-specific response.

[0026] In one embodiment, the memory T cell clones are $CD8^+CD45RO^+CD62L^{lo}$ effector memory T cells. In another embodiment, the memory T cell clones are $CD8^+CD45RO^+CD62L^{hi}$ central memory T cells. In one embodiment, the second time point is at least 30 days post vaccination.

[0027] One aspect of the invention provides a method for determining the effectiveness of a vaccine comprising: performing high-throughput sequencing of nucleic acid molecules comprising rearranged CDR3 regions of TCR loci obtained from a first biological sample of the subject at a first time point prior to vaccination; performing high-throughput sequencing of nucleic acid molecules comprising rearranged CDR3 regions of TCR loci obtained from a second biological sample of the subject at a second time point post vaccination; identifying T cell clones having CDR3 regions of significantly higher proportional abundance in the second biological sample in comparison to the first biological sample, thereby identifying vaccine-induced responsive clones; performing high-throughput sequencing of nucleic acid molecules comprising rearranged CDR3 regions of TCR loci obtained from a third biological sample of the subject at a third time point post vaccination; identifying newly recruited memory T cell clones corresponding to the vaccine-induced responsive clones that have been recruited to a memory T cell population post vaccination; and comparing a degree of recruitment of vaccine-induced responsive clones to immunological memory to a reference degree of recruitment, wherein the vaccine is effective when the degree of recruitment is greater than or equal to the reference degree of recruitment.

[0028] In one embodiment, identifying newly recruited memory T cell clones comprises comparing the identified one or more newly recruited memory T cell clones with one or more vaccine-induced responsive clones from the second biological sample to find matches between the newly recruited memory T cell clones and the one or more vaccine-specific responsive clones. In another embodiment, the degree of recruitment is a percentage of vaccine-induced responsive clones that match newly recruited memory T cell clones. In one embodiment, the reference degree of recruitment is a degree of recruitment following a candidate vaccine. In another embodiment, the reference degree of recruitment is a degree of recruitment following a reference vaccine. In one embodiment, the reference degree of recruitment is a degree of recruitment following an infection.

[0029] Another aspect of the invention provides a method of measuring a T cell response to an infection in a subject, comprising: performing high-throughput sequencing of nucleic acid molecules comprising rearranged CDR3 regions of TCR loci obtained from a first biological sample of the subject at a first time point prior to infection; performing high-throughput sequencing of nucleic acid molecules comprising rearranged CDR3 regions of TCR loci obtained from a second biological sample of the subject at a second time point after infection; and identifying T cell clones having CDR3 regions of significantly higher proportional abundance in the second biological sample in comparison to the first biological sample, thereby identifying infection-induced responsive clones.

[0030] In one embodiment, the method of measuring a T cell response to an infection further comprises: performing high-throughput sequencing of nucleic acid molecules comprising rearranged CDR3 regions of TCR loci obtained from a third biological sample of the subject at a third time point post infection; and identifying newly recruited memory T cell clones corresponding to the infection-induced responsive clones that are not present in the first biological sample and that have been recruited to a memory T cell population post infection.

[0031] In one embodiment, identifying newly recruited memory T cell clones comprises comparing a first set of memory T cell clones in the first biological sample to a second set of memory T cell clones in the second biological sample to identify one or more newly recruited memory T cell clones that have been recruited to the memory T cell population post infection. In another embodiment, the infection is selected from the group consisting of viral infection, bacterial infection, and parasitic infection. In a related embodiment, the viral infection is an acute viral infection.

[0032] One aspect of the invention provides a method of measuring a T cell response to an infection in a subject, comprising: performing high-throughput sequencing of nucleic acid molecules comprising rearranged CDR3 regions of TCR loci obtained from a first biological sample of the subject at a first time point post infection; sorting activated T cells from a subset of the first biological sample using flow cytometry to generate a set of activated T cells; performing high-throughput sequencing of nucleic acid molecules comprising rearranged CDR3 regions of TCR loci obtained from the set of activated T cells; and identifying activated T cell clones in the set having CDR3 regions of significantly higher proportional abundance in the activated T cell population in comparison to the first biological sample, thereby identifying infection-induced responsive clones.

[0033] In one embodiment, the method of measuring a T cell response to an infection further comprises: performing high-throughput sequencing of nucleic acid molecules comprising rearranged CDR3 regions of TCR loci obtained from a second biological sample of the subject at a second time point post infection; and identifying newly recruited memory T cell clones corresponding to the infection-induced responsive clones that are not present in the first biological sample and that have been recruited to a memory T cell population post infection. In one embodiment, identifying newly recruited memory T cell clones comprises comparing a first set of memory T cell clones in the first biological sample to a second set of memory T cell clones in the second biological sample to identify one or more newly recruited memory T cell clones that have been recruited to the memory T cell population post infection. In another embodiment, the infection is selected from the group consisting of viral infection, bacterial infection, and parasitic infection. In a related embodiment, the viral infection is an acute viral infection.

[0034] Another aspect of the invention provides a method for measuring B cell response to a vaccine in a subject, comprising: performing high-throughput sequencing of nucleic acid molecules comprising rearranged CDR3 regions of immunoglobulin (Ig) loci obtained from a first biological sample of the subject at a first time point prior to vaccination; performing high-throughput sequencing of nucleic acid molecules comprising rearranged CDR3 regions of Ig loci obtained from a second biological sample of the subject at a second time point post vaccination; clustering groups of CDR3 sequences of common descent comprising clones having undergone somatic hypermutation, wherein said clustering employs a clustering algorithm using a string distance metric; and identifying B cell clones having CDR3 sequence clusters of significantly higher proportional abundance in the second biological sample in comparison to the first biological sample, thereby identifying vaccine-induced responsive clones.

[0035] In one embodiment, the Ig loci are selected from the group consisting of the Ig heavy chain (IGH) locus, Ig kappa light chain (IGK) locus, and Ig lambda light chain (IGL) locus. In another embodiment, the biological samples comprise PBMCs. In one embodiment, the biological samples comprise memory B cells. In another embodiment, the second biological sample is obtained at least 1 day post vaccination.

[0036] In one embodiment, the high-throughput sequencing comprises multiplex PCR amplification of the nucleic acid molecules comprising rearranged CDR3 regions. In another embodiment, identifying comprises calculating a false discovery rate, and wherein the calculating comprises performing a computation on a computer.

[0037] In one embodiment, the activated B cell clones are vaccine antigen-specific B cells. In another embodiment, the vaccine is a vaccine for an infectious agent or a cancer vaccine.

[0038] In a related aspect, the method of measuring B cell response to a vaccine further comprises: performing high-throughput sequencing of nucleic acid molecules comprising rearranged CDR3 regions of Ig loci obtained from a third biological sample of the subject at a third time point post vaccination; and identifying newly recruited memory B cell clones corresponding to the vaccine-induced responsive clones that are not present in the first biological sample and have been recruited to a memory B cell population post vaccination.

[0039] In one embodiment, identifying comprises sorting memory B cells by flow cytometry. In another embodiment, identifying comprises comparing a first set of memory B cell clones in the first biological sample to a second set of memory B cell clones in the third biological sample to identify one or more newly recruited memory B cell clones that have been recruited to the memory B cell population post vaccination.

[0040] One embodiment further comprises comparing the identified one or more newly recruited memory B cell clones with one or more vaccine-induced responsive clones from the second biological sample to find matches between the newly recruited memory B cell clones and the one or more vaccine-induced responsive clones. In another embodiment, the matched memory B cell clones are identified as biomarkers for vaccine-specific response.

[0041] In one embodiment, the memory B cell clones are CD19⁺CD20⁺CD38⁻CD40⁺ memory B cells. In another embodiment, the memory B cell clones are non-switched memory B cells. In one embodiment, the memory B cell clones are switched memory B cells. In a related embodiment, the switched memory B cells are IgG⁺.

[0042] One aspect of the invention provides a method of measuring B cell response to a vaccine in a subject, comprising: performing high-throughput sequencing of nucleic acid molecules comprising rearranged CDR3 regions of Ig loci obtained from a first biological sample of the subject at a first time point post vaccination; sorting activated B cells from a subset of the first biological sample using flow cytometry to generate a set of activated B cells; performing high-throughput sequencing of nucleic acid molecules comprising rearranged CDR3 regions of Ig loci obtained from the set of activated B cells; clustering groups of CDR3 sequences of common descent comprising clones having undergone somatic hypermutation, wherein said clustering employs a clustering algorithm using a string distance metric; and identifying activated B cell clones in the set having CDR3 sequence clusters of

significantly higher proportional abundance in the activated B cell population in comparison to the first biological sample, thereby identifying vaccine-induced responsive clones.

[0043] In one embodiment, the Ig loci are selected from the group consisting of the IGH locus, IGK locus, and IGL locus. In another embodiment, the biological samples comprise peripheral blood mononuclear cells (PBMCs). In one embodiment, the biological samples comprise memory B cells. In another embodiment, the first biological sample is obtained at least 1 day post vaccination.

[0044] In one embodiment, the method of measuring B cell response to a vaccine further comprises performing multiplex PCR amplification of genomic templates comprising rearranged CDR3 regions to produce nucleic acid molecules for sequencing. In another embodiment, identifying comprises calculating a false discovery rate, and wherein the calculating comprises performing a computation on a computer.

[0045] In one embodiment, the activated B cell clones are vaccine antigen-specific B cells. In another embodiment, the vaccine is a vaccine for an infectious agent or a cancer vaccine.

[0046] In a related aspect, the method of measuring B cell response to a vaccine further comprises: performing high-throughput sequencing of nucleic acid molecules comprising rearranged CDR3 regions of Ig loci obtained from a second biological sample of the subject at a second time point post vaccination; and identifying newly recruited memory B cell clones corresponding to the vaccine-induced responsive clones that have been recruited to a memory B cell population post vaccination.

[0047] In one embodiment, the identifying newly recruited memory B cell clones comprises sorting memory B cells by flow cytometry. In another embodiment, identifying newly recruited memory B cell clones comprises comparing a first set of memory B cell clones in the first biological sample to a second set of memory B cell clones in the second biological sample to identify one or more newly recruited memory B cell clones that have been recruited to the memory B cell population post vaccination. In another embodiment, the method further comprises comparing the identified one or more newly recruited memory B cell clones with one or more vaccine-induced responsive clones from the set of activated B cells to find matches between the newly recruited memory B cell clones and the one or more vaccine-induced responsive clones. In a related embodiment, the matched memory B cell clones are a significant number of the vaccine-induced responsive clones and are identified as biomarkers for vaccine-specific response. In another embodiment, the matched memory B cell clones are a significant proportion of total memory B cell population and are identified as

biomarkers for vaccine-specific response. In one embodiment, the second time point is at least 30 days post vaccination.

[0048] Another aspect of the invention provides a method for determining the effectiveness of a vaccine comprising: performing high-throughput sequencing of nucleic acid molecules comprising rearranged CDR3 regions of immunoglobulin (Ig) loci obtained from a first biological sample of the subject at a first time point prior to vaccination; performing high-throughput sequencing of nucleic acid molecules comprising rearranged CDR3 regions of Ig loci obtained from a second biological sample of the subject at a second time point post vaccination; clustering groups of CDR3 sequences of common descent comprising clones having undergone somatic hypermutation, wherein said clustering employs a clustering algorithm using a string distance metric; and identifying B cell clones having CDR3 sequence clusters of significantly higher proportional abundance in the second biological sample in comparison to the first biological sample, thereby identifying vaccine-induced responsive clones; performing high-throughput sequencing of nucleic acid molecules comprising rearranged CDR3 regions of Ig loci obtained from a third biological sample of the subject at a third time point post vaccination; identifying newly recruited memory B cell clones corresponding to the vaccine-induced responsive clones that are not present in the first biological sample and have been recruited to a memory B cell population post vaccination; and comparing a degree of recruitment of vaccine-induced responsive clones to immunological memory to a reference degree of recruitment, wherein the vaccine is effective when the degree of recruitment is greater than or equal to the reference degree of recruitment.

[0049] In one embodiment, identifying comprises comparing the identified one or more newly recruited memory B cell clones with one or more vaccine-induced responsive clones from the second biological sample to find matches between the newly recruited memory B cell clones and the one or more vaccine-specific responsive clones. In another embodiment, the degree of recruitment is a percentage of vaccine-induced responsive clones that match newly recruited memory B cell clones. In one embodiment, the reference degree of recruitment is a degree of recruitment following a candidate vaccine. In another embodiment, the reference degree of recruitment is a degree of recruitment following a reference vaccine. In one embodiment, the reference degree of recruitment is a degree of recruitment following an infection.

[0050] One aspect of the invention provides a method of measuring a B cell response to an infection in a subject, comprising: performing high-throughput sequencing of nucleic acid molecules comprising rearranged CDR3 regions of immunoglobulin (Ig) loci obtained

from a first biological sample of the subject at a first time point prior to infection; performing high-throughput sequencing of nucleic acid molecules comprising rearranged CDR3 regions of Ig loci obtained from a second biological sample of the subject at a second time point post infection; clustering groups of CDR3 sequences of common descent comprising clones having undergone somatic hypermutation, wherein said clustering employs a clustering algorithm using a string distance metric; and identifying B cell clones having CDR3 sequence clusters of significantly higher proportional abundance in the second biological sample in comparison to the first biological sample, thereby identifying vaccine-induced responsive clones.

[0051] In one embodiment, the method further comprises: performing high-throughput sequencing of nucleic acid molecules comprising rearranged CDR3 regions of Ig loci obtained from a third biological sample of the subject at a third time point post infection; and identifying newly recruited memory B cell clones corresponding to the infection-induced responsive clones that are not present in the first biological sample and have been recruited to a memory B cell population post infection. In one embodiment, identifying newly recruited memory B cell clones comprises comparing a first set of memory B cell clones in the first biological sample to a second set of memory B cell clones in the second biological sample to identify one or more newly recruited memory T cell clones that have been recruited to the memory B cell population post infection. In another embodiment, the infection is selected from the group consisting of viral infection, bacterial infection, and parasitic infection. In a related embodiment, the viral infection is an acute viral infection.

[0052] Another aspect of the invention provides a method of measuring B cell response to an acute viral infection in a subject, comprising: performing high-throughput sequencing of nucleic acid molecules comprising rearranged CDR3 regions of Ig loci obtained from a first biological sample of the subject at a first time point post infection; sorting activated B cells from a subset of the first biological sample using flow cytometry to generate a set of activated B cells; performing high-throughput sequencing of nucleic acid molecules comprising rearranged CDR3 regions of Ig loci obtained from the set of activated B cells; clustering groups of CDR3 sequences of common descent comprising clones having undergone somatic hypermutation, wherein said clustering employs a clustering algorithm using a string distance metric; and identifying activated B cell clones having CDR3 sequence clusters of significantly higher proportional abundance in the activated B cell population in comparison to the first biological sample, thereby identifying infection-induced responsive clones.

[0053] In one embodiment, the method further comprises: performing high-throughput sequencing of nucleic acid molecules comprising rearranged CDR3 regions of Ig loci obtained from a second biological sample of the subject at a second time point post infection; and identifying newly recruited memory B cell clones corresponding to the infection-induced responsive clones that have been recruited to a memory B cell population post infection. In another embodiment, identifying newly recruited memory B cell clones comprises comparing a first set of memory B cell clones in the first biological sample to a second set of memory B cell clones in the third biological sample to identify one or more newly recruited memory B cell clones that have been recruited to the memory B cell population post infection. In one embodiment, the infection is selected from the group consisting of viral infection, bacterial infection, and parasitic infection. In a related embodiment, the viral infection is an acute viral infection.

BRIEF DESCRIPTION OF THE DRAWINGS

[0054] Figure (FIG.) 1A and FIG. 1B show data used for selection of FDR thresholds. FIG. 1A shows the number of clones classified as YFV induced for various FDR significance thresholds for all subjects. By examining the number of significant tests at various Q value thresholds (FDR thresholds), an appropriate threshold can be selected. Here, a threshold of 0.01 was selected. FIG. 1B shows the number of clones classified as putatively reactive clones for various FDR significance thresholds for all subjects. A threshold of 0.05 was selected. Each subject is represented by a different tone of gray, as indicated in the legend.

[0055] FIGs. 2A and 2B show the identification of YFV-induced clones. FIG. 2A shows a graph of the abundance of unique clones identified by statistical enrichment on the activated effector CD38⁺ HLA-DR⁺ CD8⁺ T cell compartment on day 14 post-vaccination (TAE-14) versus those present in the corresponding total PBMC sample from the same time point for subject 1. FIG. 2B shows the same for subjects 2 to 9. Clones were classified into four categories based both on their presence in the TAE-14 and the TM-0 compartments. Red clones are present in the TAE-14 compartment, whereas gray clones are not; while clones absent in the TM-0 compartment have a black edge and those present in the TM-0 compartment do not. Darker colors indicate that multiple data points have been superimposed in that particular position. Regions bound by dashed lines indicate clones present in only one sample. YFV-induced clones were significantly enriched in the CD38⁺ HLA-DR⁺ CD8⁺ T cell-sorted population compared to the corresponding total PBMC sample.

[0056] FIGs. 3A and 3B show recruitment of YFV-induced clones to immunological memory compartments. FIG. 3A shows the efficiency of recruitment of YFV-induced clones to the effector (T_{EM}^+ T_{CM}^-) and central (T_{EM}^- T_{CM}^+) memory compartments, or both (T_{EM}^+ T_{CM}^+) as a percentage of all clones classified as YFV induced. FIG. 3A shows that, respectively, 3.1% and 2.5% of YFV-induced clones absent in T_{M0} were identified exclusively in the T_{EM} or the T_{CM} compartments, while 6.7% were identified in both.

[0057] FIG. 4A shows the proportion of YFV-induced clones newly recruited to the effector (T_{EM-90}) and central (T_{CM-90}) memory compartments on day 90 post-vaccination, computed both by clone and template counts. The YFV-induced clones that were newly recruited to the T_{EM} or the T_{CM} compartments represent 0.43% and 0.45% of their respective memory compartments, as measured by unique clone counts, or 0.41% and 0.28% as measured by template abundance of the corresponding memory compartment aggregated over all samples. FIG. 4B shows the number of templates per YFV-induced clone identified in the T_{EM-90} and T_{CM-90} memory compartments. More templates per clone were observed in the T_{EM-90} compartment, indicating that these clones were more highly expanded. The aggregated data for all subjects are shown; subject-wise source data can be found in Table 4 in the Appendix.

[0058] FIG. 5A shows the abundance of unique clones identified by statistical enrichment in the day 14 post-vaccination total PBMC sample compared to the pre-vaccination day 0 total PBMC sample from subject 1. Putatively reactive clones are enclosed by a circle in FIG. 5A. FIG. 5B shows the same for subjects 2 to 9. Significant enrichment (or expansion) was defined based on a q value threshold, with 1% and 5% expected false-positive rates for YFV-induced and putatively reactive clones, respectively, as described above. Clones were classified into four categories based both on their presence in the TAE-14 and the TM-0 compartments, as indicated in the legend. Darker colors indicate that multiple data points are superimposed in that particular position. Regions bound by dashed lines indicate clones present in only one sample.

DETAILED DESCRIPTION

[0059] The present disclosure relates to in-depth analysis of the dynamics of T cell and B cell repertoires before, during, and after an infection. A vaccination model is used to understand the adaptive immune response to a viral infection. The in-depth analysis provides methods for characterizing the adaptive immune response to an infection or vaccination by identification and enumeration of unique T cell and B cell clones specifically induced by the

vaccination or infection through a combined experimental and bioinformatics approach. The methods described herein can be used to identify responsive T cell and B cell clones and to further identify which responding clones were recruited to immunological memory. The methods described herein provide certain advantages, including, e.g., the capability to identify responding clones utilizing high throughput sequencing without first enriching the cell population (e.g., sorting using flow cytometry). Additionally, particular methods described herein provide for the identification of responding clones using only a single time point after vaccination or infection.

[0060] Recruitment of T cell or B cell clones to immunological memory can be defined as a number of infection-induced T cell or B cell clones that are identified as memory cells at a time point after infection (or vaccination) and were not found in memory at an earlier time point.

[0061] These methods apply to analyzing the adaptive immune response for various types of infections, for example, infection caused by a foreign pathogen, such as a virus, bacteria, or parasite. The infection can be an acute viral infection. An acute viral infection is characterized by rapid onset of disease, a relatively brief period of symptoms, and resolution within days. It is usually accompanied by early production of infectious virions and elimination of infection by the host immune system. In some embodiments, the infection is a chronic viral infection.

Definitions

[0062] Terms used in the claims and specification are defined as set forth below unless otherwise specified.

[0063] As used herein, adaptive immune receptor (AIR) refers to an immune cell receptor, e.g., a T cell receptor (TCR) or an Immunoglobulin (Ig) receptor found in mammalian cells. In certain embodiments, the adaptive immune receptor is encoded by a TCRB, TCRG, TCRA, TCRD, IGH, IGK, and IGL gene or gene segment.

[0064] The term "primer," as used herein, refers to an oligonucleotide sequence capable of acting as a point of initiation of DNA synthesis under suitable conditions. A primer is complementary to (or hybridizes to) a target template (e.g., DNA, cDNA or mRNA template). Such conditions include those in which synthesis of a primer extension product complementary to a nucleic acid strand is induced in the presence of four different nucleoside triphosphates and an agent for extension (e.g., a DNA polymerase or reverse transcriptase) in an appropriate buffer and at a suitable temperature.

[0065] In some embodiments, as used herein, the term "gene" refers to the segment of DNA involved in producing a polypeptide chain, such as all or a portion of a TCR or Ig polypeptide (e.g., a CDR3-containing polypeptide); it includes regions preceding and following the coding region "leader and trailer" as well as intervening sequences (introns) between individual coding segments (exons), regulatory elements (e.g., promoters, enhancers, repressor binding sites and the like), or recombination signal sequences (RSSs), as described herein.

[0066] The nucleic acids of the present embodiments, also referred to herein as polynucleotides, and including oligonucleotides, can be in the form of RNA or in the form of DNA, including cDNA, genomic DNA, and synthetic DNA. The DNA can be double-stranded or single-stranded, and if single stranded can be the coding strand or non-coding (anti-sense) strand. A coding sequence which encodes a TCR or an Ig or a region thereof (e.g., a V region, a D segment, a J region, a C region, etc.) for use according to the present embodiments can be identical to the coding sequence known in the art for any given TCR or immunoglobulin gene regions or polypeptide domains (e.g., V-region domains, CDR3 domains, etc.), or can be a different coding sequence, which as a result of the redundancy or degeneracy of the genetic code, encodes the same TCR or immunoglobulin region or polypeptide.

[0067] The term "sufficient amount" means an amount sufficient to produce a desired effect, e.g., an amount sufficient to modulate protein aggregation in a cell.

[0068] The term "therapeutically effective amount" is an amount that is effective to ameliorate a symptom of a disease. A therapeutically effective amount can be a "prophylactically effective amount" as prophylaxis can be considered therapy.

[0069] Unless specific definitions are provided, the nomenclature utilized in connection with, and the laboratory procedures and techniques of, molecular biology, analytical chemistry, synthetic organic chemistry, and medicinal and pharmaceutical chemistry described herein are those well-known and commonly used in the art. Standard techniques can be used for recombinant technology, molecular biological, microbiological, chemical syntheses, chemical analyses, pharmaceutical preparation, formulation, and delivery, and treatment of patients.

[0070] Unless the context requires otherwise, throughout the present specification and claims, the word "comprise" and variations thereof, such as, "comprises" and "comprising" are to be construed in an open, inclusive sense, that is, as "including, but not limited to." By "consisting of" is meant including, and typically limited to, whatever follows the phrase

"consisting of." By "consisting essentially of" is meant including any elements listed after the phrase, and limited to other elements that do not interfere with or contribute to the activity or action specified in the disclosure for the listed elements. Thus, the phrase "consisting essentially of" indicates that the listed elements are required or mandatory, but that no other elements are required and can or cannot be present depending upon whether or not they affect the activity or action of the listed elements.

[0071] It must be noted that, as used in the specification and the appended claims, the singular forms "a," "an" and "the" include plural referents unless the context clearly dictates otherwise.

[0072] Reference throughout this specification to "one embodiment" or "an embodiment" or "an aspect" means that a particular feature, structure or characteristic described in connection with the embodiment is included in at least one embodiment of the present invention. Thus, the appearances of the phrases "in one embodiment" or "in an embodiment" in various places throughout this specification are not necessarily all referring to the same embodiment. Furthermore, the particular features, structures, or characteristics can be combined in any suitable manner in one or more embodiments.

Cells

[0073] The sample can include T cells and/or B cells. T cells (T lymphocytes) include, for example, cells that express T cell receptors. T cells include Helper T cells (effector T cells or Th cells), cytotoxic T cells (CTLs), memory T cells, and regulatory T cells. The sample can include a single cell in some applications or more generally at least 1,000, at least 10,000, at least 100,000, at least 250,000, at least 500,000, at least 750,000, at least 1,000,000 T cells, or at least 10,000,000 T cells.

[0074] B cells include, for example, plasma B cells, memory B cells, B1 cells, B2 cells, marginal-zone B cells, and follicular B cells. B cells can express immunoglobulins (antibodies, B cell receptor). The sample can include a single cell in some applications or more generally at least 1,000, at least 10,000, at least 100,000, at least 250,000, at least 500,000, at least 750,000, at least 1,000,000 B-cells, or at least 10,000,000 B cells.

[0075] The sample can include nucleic acid molecules such as DNA (e.g., genomic DNA or mitochondrial DNA) or RNA (e.g., messenger RNA or microRNA) or cDNA (complementary DNA). In some embodiments, the nucleic acid is cell-free DNA. In other embodiments, the sample is a formalin fixed paraffin embedded tissue.

[0076] B cells and T cells can be obtained from a variety of tissue samples including marrow, thymus, lymph glands, peripheral tissues, solid tumors, and blood. Peripheral blood is most easily accessed. Peripheral blood samples are obtained by phlebotomy from subjects. Peripheral blood mononuclear cells (PBMCs) are isolated by techniques known to those of skill in the art, e.g., by Ficoll-Hypaque® density gradient separation. In one embodiment, whole PBMCs are used for analysis.

[0077] In one embodiment, the B cells and/or T cells are sorted from the sample into separate populations prior to sequencing. For example, T cells may be separated from non-T cells, and B cells may be separated from non-B cells. PBMCs are referred to herein for illustrative purposes as the sample from which particular cell populations are sorted, however the cells may be sorted in a similar fashion from other types of biological samples. In one embodiment, memory T cells are sorted from PBMCs. In a particular embodiment, central memory T cells are sorted from PBMCs. In another embodiment, effector memory T cells are sorted from PBMCs. In one embodiment, activated effector T cells are sorted from PBMCs. In a particular embodiment, memory T cells and activated effector T cells are sorted from the same PBMC sample. In one embodiment, CD4⁺ T cells are sorted from PBMCs. In another embodiment, CD8⁺ T cells are sorted from PBMCs. In another embodiment, memory B cells are sorted from PBMCs. In one embodiment, activated, antibody-producing B cells are sorted from PBMCs. In one embodiment, switched memory B cells (e.g., IgM⁻ IgD⁻) are sorted from PBMCs. In another embodiment, non-switched memory B cells (e.g., IgM⁺ or IgD⁺) are sorted from PBMCs. In a particular embodiment, memory B cells and activated B cells are sorted from the same PBMC sample. In one embodiment, PBMCs remaining after sorting out one or more populations, or cell types, are a distinct cell population.

[0078] Various cell populations may be sorted, or separated, from other cell types using any of a variety of techniques known in art including, e.g., flow cytometry sorting and magnetic bead separation. These techniques often distinguish between different cell types and states of activation based upon markers, such as cell surface markers. In one embodiment, memory B cells are CD19⁺CD20⁺CD38⁻CD40⁺ cells. In one embodiment, activated effector T cells are identified as CD38⁺HLA-DR⁺. In one embodiment, memory T cells are identified as CD45RA⁻CD45RO⁺. In one embodiment, effector memory T cells are identified as CD45RA⁻CD45RO⁺CD62L^{lo}. In one embodiment, central memory T cells are identified as CD45RA⁻CD45RO⁺CD62L^{hi}.

[0079] In one embodiment, T cells may be flow sorted into multiple compartments for each time point: e.g., CD8⁺CD45RO^{+/-} and CD4⁺CD45RO^{+/-} using fluorescently labeled anti-human antibodies, e.g., CD4 FITC (clone M-T466, Miltenyi Biotec), CD8 PE (clone RPA-T8, BD Biosciences), CD45RO ECD (clone UCHL-1, Beckman Coulter), and CD45RO APC (clone UCHL-1, BD Biosciences). Staining of total PBMCs may be done with the appropriate combination of antibodies, followed by washing cells before analysis. Lymphocyte subsets can be isolated by FACS sorting, e.g., by a BD FACSAria™ cell-sorting system (BD Biosciences) and by analyzing results with FlowJo software (Treestar Inc.), and also by conceptually similar methods involving specific antibodies immobilized to surfaces or beads.

Nucleic Acid Extraction

[0080] Total genomic DNA is extracted from cells using any of a variety of methods known in the art, such as, e.g., by using the QIAamp® DNA blood Mini Kit (QIAGEN®). The approximate mass of a single haploid genome is 3 pg. Preferably, at least 100,000 to 200,000 cells are used for analysis of diversity, i.e., about 0.6 to 1.2 µg DNA from diploid T cells. Using PBMCs as a source, the number of T cells can be estimated to be about 30% of total cells. The number of B cells can also be estimated to be about 30% of total cells in a PBMC preparation.

[0081] In other embodiments, the nucleic acid is RNA. The RNA molecules can be transcribed to cDNA using known reverse-transcription kits, such as the SMARTer™ Ultra Low RNA kit for Illumina sequencing (Clontech, Mountain View, CA) essentially according to the supplier's instructions.

Immune Repertoire Sequencing (Multiplex PCR and High Throughput Sequencing)

[0082] The invention includes using compositions and methods for quantitative detection of sequences of substantially all possible TCR and IG gene rearrangements that can be present in a sample containing lymphoid cell DNA. Amplified nucleic acid molecules comprising rearranged TCR or IG regions obtained from a biological sample are sequenced using high-throughput sequencing. In one embodiment, a multiplex PCR system is used to amplify rearranged TCR or IG loci from genomic DNA as described in U.S. Pub. No. 2010/0330571, filed on June 4, 2010, U.S. Pub. No. 2012/0058902, filed on Aug. 24, 2011, International App. No. PCT/US2013/062925, filed on Oct. 1, 2013, which is each incorporated by reference in its entirety.

[0083] In one embodiment, the nucleic acid molecule to be sequenced comprises a TCR α , TCR β , TCR γ or TCR δ CDR3 region. In a particularly preferred embodiment, the nucleic acid to be sequenced comprises a TCR β CDR3 region. In one embodiment, the nucleic acid to be sequenced comprises an IgH, Ig κ or Ig λ CDR3 region. In a particularly preferred embodiment, the nucleic acid to be sequenced comprises an IgH CDR3 region.

[0084] In general, a multiplex PCR system may use 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, or 25, preferably 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, or 39, most preferably 40, 41, 42, 43, 44, or 45 forward primers. In some embodiments, the forward primer is specific to a sequence corresponding to one or more V region segments. "Specific to" can mean complementary to and/or hybridizes to a target sequence. In other embodiments, there are 3, 4, 5, 6, or 7, preferably 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20 or more reverse primers. In some embodiments, the reverse primer is specific to a sequence corresponding to one or more J region segments. Most preferably, there is a single J segment primer that is complementary to each J segment. In another embodiment, there are no consensus J primers.

[0085] In certain embodiments, the primers are designed not to cross an intron/exon boundary. The forward primers must preferably anneal to the V segments in a region of relatively strong sequence conservation between V segments so as to maximize the conservation of sequence among these primers. Accordingly, this minimizes the potential for differential annealing properties of each primer, and so that the amplified region between V and J primers contains sufficient TCR V sequence information to identify the specific V gene segment used.

[0086] Preferably, the J segment primers hybridize with a conserved element of the J segment, and have similar annealing strength. Most preferably, all J segment primers anneal to the same conserved framework region motif.

[0087] The forward and reverse primers can have an adaptor sequence on the 5'-end. In some embodiments, the forward and reverse primers comprise a universal sequencing oligonucleotide on the 5'-ends.

[0088] Thermal cycling conditions may follow methods of those skilled in the art. For example, using a PCR Express thermal cycler (Hybaid, Ashford, UK), the following cycling conditions may be used: 1 cycle at 95° C for 15 minutes, 25 to 40 cycles at 94° C for 30 seconds, 59° C for 30 seconds and 72° C for 1 minute, followed by one cycle at 72° C for 10 minutes.

[0089] In some embodiments, the method provides amplification of substantially all of the rearranged adaptive immune receptor (AIR) sequences in a lymphoid cell and is capable of quantifying the diversity of the TCR or IG repertoire of at least 10^6 , 10^5 , 10^4 , or 10^3 unique rearranged AIR sequences in a sample.

[0090] Multiplex quantitative PCR is described further in Robins *et al.*, 2009 *Blood* 114, 4099; Robins *et al.*, 2010 *Sci. Translat. Med.* 2:47ra64; Robins *et al.*, 2011 *J. Immunol. Meth.* doi:10.1016/j.jim.2011.09. 001; Sherwood *et al.* 2011 *Sci. Translat. Med.* 3:90ra61; U.S.S.N. 13/217,126, U.S.S.N. 12/794,507, WO/2010/151416, WO/2011/106738 (PCT/US2011/026373), WO2012/027503 (PCT/US2011/049012), U.S.S.N. 61/550,311, and U.S.S.N. 61/569,118, which are incorporated by reference in their entireties. Exemplary V segment and J segment primers are described in U.S.S.N. 13/217,126, U.S.S.N. 12/794,507, WO/2010/151416, WO/2011/106738 (PCT/US2011/026373), WO2012/027503 (PCT/US2011/049012), U.S.S.N. 61/550,311, and U.S.S.N. 61/569,118, which are incorporated by reference in their entireties.

Single Molecule Labeling

[0091] In one embodiment, single molecule barcoding is employed to uniquely label DNA target molecules prior to amplification. The barcode is associated with the DNA target sequence throughout the amplification process. Single molecule barcoding may be used in conjunction with high throughput sequencing. Compositions and methods for uniquely tagging rearranged gene segments encoding a TCR and/or an immunoglobulin are described in International App. Pub. Nos. WO 2013/188831 and WO 2014/145992, each of which is incorporated by reference in its entirety.

[0092] For mRNA templates, reverse transcription methods can be used to generate cDNA molecules. In one embodiment, reverse transcription can be performed using the SMARTer™ Ultra Low RNA kit for Illumina sequencing (Clontech, Mountain View, CA) essentially according to the supplier's instructions. In one embodiment, mRNA molecules can be amplified in multiple wells.

[0093] In some embodiments, the cDNA templates can be amplified using non-multiplexed RACE primers and C segment primers. In other embodiments, a plurality of V segment primers and C segment primers are used to amplify mRNA templates.

[0094] In some embodiments, the cDNA molecules undergo an additional PCR amplification with tailing primers to incorporate a barcode sequence and a universal primer sequence. In certain embodiments, the tailing primers include a random oligonucleotide

sequence (e.g., 6 or 8 bp random oligonucleotide sequence). The resulting cDNA molecules can include at least one barcode sequence, a random oligonucleotide sequence, and universal primer sequences for use with a sequencer. The cDNA templates can then be pooled and sequenced as described herein.

[0095] As noted above, further description for methods of single molecule labeling and amplification of mRNA templates can be found in WO 2013/188831 and WO 2014/145992.

Amplification Bias Control

[0096] Multiplex PCR assays can result in a bias in the total numbers of amplicons produced from a sample, given that certain primer sets are more efficient in amplification than others. To overcome the problem of such biased utilization of subpopulations of amplification primers, methods can be used that provide a template composition for standardizing the amplification efficiencies of the members of an oligonucleotide primer set, where the primer set is capable of amplifying rearranged DNA encoding a plurality of adaptive immune receptors (TCR or Ig) in a biological sample that comprises DNA from lymphoid cells.

[0097] In some embodiments, a template composition is used to standardize the various amplification efficiencies of the primer sets. The template composition can comprise a plurality of diverse template oligonucleotides of general formula (I):

[0098] 5'-U1-B1-V-B2-R-J-B3-U2-3' (I)

[0099] The template oligonucleotides can vary in nucleotide sequence considerably from one another as a function of significant sequence variability among the large number of possible TCR or BCR variable (V) and joining (J) region polynucleotides. Sequences of individual template oligonucleotide species can also vary from one another as a function of sequence differences in U1, U2, B (B1, B2 and B3) and R oligonucleotides that are included in a particular template within the diverse plurality of templates.

[00100] In certain embodiments, V is a polynucleotide comprising at least 20, 30, 60, 90, 120, 150, 180, or 210, and not more than 1000, 900, 800, 700, 600 or 500 contiguous nucleotides of an adaptive immune receptor variable (V) region encoding gene sequence, or the complement thereof, and in each of the plurality of template oligonucleotide sequences V comprises a unique oligonucleotide sequence.

[00101] In some embodiments, J is a polynucleotide comprising at least 15-30, 31-60, 61-90, 91-120, or 120-150, and not more than 600, 500, 400, 300 or 200 contiguous

nucleotides of an adaptive immune receptor joining (J) region encoding gene sequence, or the complement thereof, and in each of the plurality of template oligonucleotide sequences J comprises a unique oligonucleotide sequence.

[00102] U1 and U2 can be each either nothing or each comprise an oligonucleotide having, independently, a sequence that is selected from (i) a universal adaptor oligonucleotide sequence, and (ii) a sequencing platform-specific oligonucleotide sequence that is linked to and positioned 5' to the universal adaptor oligonucleotide sequence.

[00103] B1, B2 and B3 can be each either nothing or each comprise an oligonucleotide B that comprises a first and a second oligonucleotide barcode sequence, wherein in each of the plurality of template oligonucleotide sequences B comprises a unique oligonucleotide sequence in which (i) the first barcode sequence uniquely identifies the unique V oligonucleotide sequence of the template oligonucleotide and (ii) the second barcode sequence uniquely identifies the unique J oligonucleotide sequence of the template oligonucleotide.

[00104] R can be either nothing or comprises a restriction enzyme recognition site that comprises an oligonucleotide sequence that is absent from V, J, U1, U2, B1, B2 and B3.

[00105] In certain embodiments, the template composition includes a random oligonucleotide sequence. The random oligonucleotide sequence may be inserted in various sections between or within the components in the general formula I (5'-U1-B1-V-B2-R-B3-J-B4-U2-3') and be of various lengths in size (e.g., 8 base pairs in length).

[00106] Methods are used with the template compositions for determining non-uniform nucleic acid amplification potential among members of a set of oligonucleotide amplification primers that are capable of amplifying productively rearranged DNA encoding one or a plurality of adaptive immune receptors in a biological sample that comprises DNA from lymphoid cells of a subject.

[00107] Based on the determined non-uniform nucleic acid amplification potentials of each of the primers, the multiplex primer sets can be adjusted to reduce amplification bias. These bias-controlled primers can then be used on biological templates.

[00108] Further description about bias control methods are provided in U.S. Provisional Application No. 61/726,489, filed November 14, 2012, U.S. Provisional Application No. 61/644,294, filed on May 8, 2012, and International Patent App. Publ. No. WO 2013/169957, which are incorporated by reference in their entireties.

High Throughput Sequencing

[00109] Sequencing can be performed using any of a variety of available high throughput single molecule sequencing machines and systems. Illustrative sequence systems include sequence-by-synthesis systems, such as the Illumina Genome Analyzer and associated instruments (Illumina HiSeq) (Illumina, Inc., San Diego, CA), Helicos Genetic Analysis System (Helicos BioSciences Corp., Cambridge, MA), Pacific Biosciences PacBio RS (Pacific Biosciences, Menlo Park, CA), or other systems having similar capabilities. Sequencing is achieved using a set of sequencing platform-specific oligonucleotides that hybridize to a defined region within the amplified DNA molecules. The sequencing platform-specific oligonucleotides are designed to sequence up amplicons, such that the V- and J- encoding gene segments can be uniquely identified by the sequences that are generated. See, *e.g.*, U.S.A.N. 13/217,126; U.S.A.N. 12/794,507; PCT/US2011/026373; or PCT/US2011/049012, which is each incorporated by reference in its entirety.

[00110] In some embodiments, the raw sequence data is preprocessed to remove errors in the primary sequence of each read and to compress the data. A nearest neighbor algorithm can be used to collapse the data into unique sequences by merging closely related sequences, to remove both PCR and sequencing errors. See, *e.g.*, U.S.A.N. 13/217,126; U.S.A.N. 12/794,507; PCT/US2011/026373; or PCT/US2011/049012, which is each incorporated by reference in its entirety.

Processing Sequence Data

[00111] Sequenced reads are filtered for those including CDR3 sequences. Sequencer data processing involves a series of steps to remove errors in the primary sequence of each read, and to compress the data. In one embodiment, a complexity filter is used to remove approximately 20% of the sequences that are misreads from the sequencer. Then, sequences are required to have a minimum of a six base match to both one of the J-regions and one of the V-regions. Applying the filter to the control lane containing phage sequence, on average only one sequence in 7-8 million passes these steps. Finally, a nearest neighbor algorithm may be used to collapse the data into unique sequences by merging closely related sequences, in order to remove both PCR error and sequencing error.

[00112] Further description for methods of processing sequence reads can be found in US App. Publ. No. 2012/0058902, US App. Publ. No. 2010/0330571, and International Patent App. Publ. No. WO/2010/151416, which are each incorporated by reference in its entirety.

PCR Template Abundance Estimation

[00113] In order to estimate the average read coverage per input template in the multiplex PCR and sequencing approach, a set of unique synthetic TCR or Ig analog templates, comprising each possible combination of V β and J β gene segments is employed (Carlson et al. 2013, Nature Communications 4:2680). These molecules are included in each PCR reaction at a low concentration selected so that most unique synthetic templates are not observed in the sequencing output. Using the known concentration of each synthetic template in the pool, the relationship between the number of observed unique synthetic molecules and the total number of synthetic molecules added to reaction was simulated (which closely matches a one-to-one relationship at the selected concentration). This information is then used to calculate, for each PCR reaction, the mean number of sequencing reads obtained per molecule of PCR template, and finally estimate the number of B cells or T cells in the input material bearing each unique Ig or TCR rearrangement, respectively.

Identification of Expanded and Enriched Effector Cell Clones

[00114] A B cell clone or a T cell clone may be defined as the population of cells bearing a unique IgH or TCR β rearrangement, respectively.

[00115] In certain embodiments, a statistic is computed for each clone based on the frequency or size of the clone in a sample population. The statistic can be computed for a clone at different time points. In some embodiments, the clone is determined to be expanded or contracted at a second time point compared to a first time point based on the value of the statistic. In some embodiments, the frequency or size of the clone must be statistically significantly different between the two or more time points to be considered expanded or contracted. In certain embodiments, a proportion or percentage of the total T or B cell population or total number of genomes in the sample can be calculated for each clone.

[00116] In one embodiment, to computationally identify those clones whose frequencies differ between samples from a subject at different time points, or between cell populations (e.g., between total PBMCs and a specific sorted T cell population for the same time point), the algorithm described below can be used. The input data consists of the abundance for each clone in each of the two samples.

[00117] It is assumed that the repertoire contains S distinct clones, and their proportional abundances at time points 1 and 2 are given by the multinomial vectors $\pi^{(1)} = \{ \pi^{(1)}_1, \pi^{(1)}_2, \dots, \pi^{(1)}_S \}$ and $\pi^{(2)} = \{ \pi^{(2)}_1, \pi^{(2)}_2, \dots, \pi^{(2)}_S \}$, with $\sum_{i=1}^S \pi_i^{(j)} = 1$. Supposing that n

clones have changed in abundance between the two time points, these clones were identified with the n -element index vector Δ .

[00118] Next, it can be assumed that the aggregated proportional change of all truly changed clone abundances is small (i.e., $\sum_{i \in \Delta} (\pi_i^{(2)} - \pi_i^{(1)}) \ll 1$). In this regime, each observed clone can be independently tested for significance using a 2x2 contingency table. The Fisher exact test is employed to compute a p-value for each clone across the two samples. Specifically, suppose clone i is observed with abundance $k_i^{(1)}$ at time point 1 and $k_i^{(2)}$ at time point 2. A p-value for the 2x2 contingency table containing these abundances in one row was computed, and the remaining abundances (for clones other than i) on the other. By summing over hypergeometric probabilities, the Fisher exact test gives the p-value for the null hypothesis that the proportion of clone i in the repertoire is the same at both time points, that

$$\pi_i^{(1)} = \pi_i^{(2)}.$$

[00119] s is defined as representing the number of distinct clones actually observed across the two samples, where in general $s \leq S$. Without loss of generality, indices 1 through s of the repertoire clones correspond to the observed clones. After performing the above analysis on each of the s observed clones, a vector of p-values, $p = \{p_1, p_2, \dots, p_s\}$, is used.

[00120] To choose a rejection region (thereby identifying a set of significantly changed clones between the two samples under consideration), the positive false discovery rate (pFDR) method of Storey, which defines (Storey, 2002, J. R. Statist. Soc. B 64:479-498) the pFDR as the expected proportion of true null hypotheses among all rejected hypothesis, can be used:

$$\begin{aligned} \text{pFDR}(\gamma) &= \Pr \left(\pi_i^{(1)} = \pi_i^{(2)} \mid p_i \leq \gamma \right) \\ &= \frac{\pi_0 \Pr \left(p_i \leq \gamma \mid \pi_i^{(1)} = \pi_i^{(2)} \right)}{\Pr(p_i \leq \gamma)} \\ &= \frac{\pi_0 \gamma}{\Pr(p_i \leq \gamma)} \end{aligned}$$

[00121] The second equality follows from Bayes' theorem with π_0 being the prior probability that a hypothesis is null. The last equality follows from the definition of a p-value, if the p-values themselves are regarded as independent and identically distributed random variables.

[00122] For each p-value (p_i) the associated q-value (q_i) may be estimated, which is the minimum pFDR that can occur when rejecting p-values less than or equal to p_i . By

examining the number of significant tests at various q-value thresholds, an appropriate threshold can be selected (e.g., see FIGs. 1A and 1B). Control of pFDR is preferred to control of the family-wise error rate (FWER), the probability of one or more false alternative hypotheses. The latter, which is typically controlled by the Bonferroni method, is overly conservative, failing to reject many false null hypotheses in order to attain any nontrivial FWER. The pFDR, on the other hand, rejects these hypotheses at the cost of a specifiable, small proportion of rejected true null hypotheses. The resulting set of significance tests allow the identification of B cell and T cell clones whose frequencies vary (i.e., dynamic B cell and T cell clones).

Monitoring T cell and B cell Response to Vaccination

[00123] Using high-throughput sequencing, lymphocyte clones responding to a vaccine may be detected. The vaccine may be a commonly used reference vaccine, or the vaccine may be a candidate vaccine. In one embodiment, the vaccine is for an infectious agent. Examples of target infectious agents for vaccine include, but are not limited to, influenza, HIV, HPV, malaria, smallpox, CMV, rabies, hepatitis A or B, and HSV. In one embodiment, the vaccine is a cancer vaccine. Examples of target cancers for a cancer vaccine include, but are not limited to, cervical cancer, pancreatic cancer, breast cancer, bladder cancer, and prostate cancer. In another embodiment, the vaccine can be live attenuated vaccines, inactivated vaccines, toxoid vaccines, subunit/conjugate vaccines, or biosynthetic vaccines. The vaccine may comprise DNA, RNA, virion capsule, etc. In one aspect, T cell clones induced by vaccination are detected.

Identifying Vaccine-Induced Responsive Clones

[00124] Methods provided herein may be used to identify B cell and T cell clones that are responsive to a vaccine. Vaccine responsive clones expand rapidly upon interacting with antigen, and clones present in a biological sample at a significantly high cell number, frequency, proportion, or abundance, can be identified.

Responsive T cell Clones

[00125] In one embodiment, nucleic acid molecules comprising rearranged CDR3 regions of TCR loci obtained from 1) a first biological sample of a subject at a first time point prior to vaccination are sequenced and 2) a second biological sample of a subject at a second time point post vaccination are sequenced. Individual T cell clones can be detected by the presence of the uniquely rearranged CDR3 region. T cell clones that are responsive to

vaccination are expanded, in a statistically significant fashion, in cell number in the second biological sample in comparison to the first biological sample. Relative abundance of the CDR3 region correlates to the number of T cells from the sample for the specific clone. In this way, by identifying T cell clones of significantly high abundance, or higher proportional abundance, in the second sample in comparison to the first sample, vaccine-induced responsive T cell clones are detected.

[00126] In one embodiment, the second biological sample is obtained at a time point at or around the peak of the immune response to the vaccine. For example, in one embodiment, the second time point is about 10-14 days post vaccination. In one embodiment, the second biological sample is obtained at least 10 days post vaccination. In one embodiment, the subject has received one dose of the vaccine. In another embodiment, the subject has received more than one dose of the vaccine (e.g., one or more boosters).

[00127] In one embodiment, the vaccine-induced responsive T cell clones are vaccine antigen-specific T cells. Antigen specificity can be determined using any of a variety of methods known in the art including, but not limited to, cell proliferation assays (e.g., ^3H -thymidine incorporation), cytotoxicity assays (e.g., ^{51}Cr release), MHC-peptide tetramer staining assays, enzyme-linked immunospot (ELISPOT) assays, and intracellular cytokine assays.

[00128] In one embodiment, activated effector T cells are sorted from the second biological sample prior to sequencing to identify significantly expanded T cell clones. In one embodiment, activated T cells are $\text{CD38}^+\text{HLA-DR}^+$ cells. In one embodiment, activated T cells are not sorted from the second biological sample, and vaccine-induced responsive T cell clones are identified from whole PBMCs.

[00129] In another embodiment, vaccine-induced responsive clones are identified by sequencing rearranged CDR3 regions from a single time point obtained post vaccination without comparison to a sample obtained prior to vaccination. Preferably, the activated effector T cells are sorted from the biological sample prior to sequencing, and the clones from the sort are compared to clones identified in a non-sorted sample from the same time point, with clones expanded (in a statistically significant manner) in the sort compared to the non-sorted sample considered vaccine-induced responsive clones.

[00130] For example, in one embodiment, a first biological sample and a second biological sample of a subject are obtained at a first time point post vaccination. The activated effector T cells are sorted from the second biological sample to obtain an activated T cell population. Nucleic acid molecules comprising rearranged CDR3 regions of TCR loci

from the first sample and the sorted activated T cell population are sequenced. Vaccine-induced responsive clones are identified by identifying CDR3 regions of significantly high abundance in the activated T cell population in comparison to the first biological sample, wherein the CDR3 regions of high abundance correspond to expanded T cell clones in the activated T cell population.

Responsive B cell Clones

[00131] In one embodiment, nucleic acid molecules comprising rearranged CDR3 regions of Ig loci obtained from 1) a first biological sample of a subject at a first time point prior to vaccination and 2) a second biological sample of a subject at a second time point post vaccination are sequenced. Once the CDR3 regions are sequenced, a clustering algorithm may be applied to cluster groups of CDR3 sequences of common descent comprising clones having undergone somatic hypermutation. B cell clones that are responsive to vaccination are significantly expanded in cell number in the second biological sample in comparison to the first biological sample, and clusters of clonally related B cells are detected by the rearranged CDR3 sequence clusters. Relative abundance of the CDR3 cluster correlates to the number of B cells from the sample for the specific clone. In this way, by identifying B cell clones of significantly high abundance in the second sample in comparison to the first sample, vaccine-induced responsive B cell clones are detected.

[00132] In one embodiment, the second biological sample is obtained at a time point at or around the peak of the immune response to the vaccine. For example, in one embodiment, the second time point is about 1-2 days post vaccination. In another embodiment, the second time point is about 10-14 days post vaccination. In one embodiment, the second biological sample is obtained at least 1 day post vaccination. In one embodiment, the subject has received one dose of the vaccine. In another embodiment, the subject has received more than one dose of the vaccine (e.g., one or more boosters).

[00133] In one embodiment, the vaccine-induced responsive B cell clones are vaccine antigen-specific B cells. Antigen specificity can be determined using any of a variety of methods known in the art including, but not limited to, capture assays (e.g., antigen-coated solid matrix), fluorescent-labeled antigen staining assays (e.g., microscopy and flow cytometry), and ELISPOT assays.

[00134] In one embodiment, activated, effector B cells are sorted from the second biological sample prior to sequencing to identify significantly expanded B cell clones. In one embodiment, activated B cells are CD25⁺CD69⁺CD80⁺CD86⁺ cells. In one embodiment,

activated B cells are not sorted from the second biological sample, and vaccine-induced responsive B cell clones are identified from whole PBMCs.

[00135] In another embodiment, vaccine-induced responsive clones are identified by sequencing rearranged CDR3 regions from a single time point obtained post vaccination without comparison to a sample obtained prior to vaccination. Preferably, the activated B cells are sorted from the biological sample prior to sequencing, and the highly abundant clones are compared to clones identified in a non-sorted sample from the same time point.

[00136] For example, in one embodiment, a first biological sample and a second biological sample of a subject are obtained at a first time point post vaccination. The activated, effector B cells are sorted from the second biological sample to obtain an activated B cell population. Nucleic acid molecules comprising rearranged CDR3 regions of Ig loci from the first sample and the sorted activated B cell population are sequenced. Clonally related CDR3 regions are clustered. Vaccine-induced responsive clones are identified by identifying CDR3 clusters of significantly high abundance in the activated B cell population in comparison to the first biological sample, wherein the CDR3 clusters of high abundance correspond to expanded B cell clones in the activated B cell population.

Identifying Newly Recruited Memory Clones

[00137] The methods described herein may further be utilized to identify vaccine-induced responsive B cell and/or T cell clones that are recruited to the memory compartment. In particular, the number of vaccine-induced responsive effector cell clones recruited to memory may be determined, and the percentage of vaccine-induced responsive effector cell clones that are recruited to memory may also be determined. Furthermore, correlations between the expansion of a particular effector cell clone in response to vaccination and recruitment to the memory compartment can be examined. In order to detect newly recruited memory cells, the biological sample is obtained at a time sufficient for the B cells or T cells to transition from activated cells to memory cells. In one embodiment, the biological sample is obtained at least about 30 days following vaccination. In a particular embodiment, the biological sample is obtained about 90 days following vaccination. In another embodiment, the biological sample is obtained about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12 or more months following vaccination. In one embodiment, the biological sample is obtained about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more years following vaccination.

Memory T cell Clones

[00138] In one embodiment, nucleic acid molecules comprising rearranged CDR3 regions of TCR loci obtained from a third biological sample of a subject at a third time point post vaccination are sequenced in order to identify memory T cells that correspond to the vaccine-induced responsive T cell clones identified in the second sample. In one embodiment, the memory T cells clones of the third sample are compared to memory T cell clones of the first sample in order to identify newly recruited memory T cell clones corresponding to the vaccine-induced responsive T cell clones. Upon identifying newly recruited vaccine-induced memory T cell clones, it can be determined what proportion of the total memory T cell compartment is the newly recruited memory T cell clones. In this way, a degree of recruitment of vaccine-induced responsive clones to immunological memory can be identified. In one embodiment, a degree of recruitment may comprise the proportion of unique clones present in the set of vaccine-induced response clones which have been recruited to memory. In another embodiment, a degree of recruitment may comprise the proportion of T cells in the memory compartment that were recruited from among the vaccine-induced responsive clones. In one embodiment, a degree of recruitment of vaccine-induced responsive clones to the memory compartment is a biomarker for vaccine efficacy.

Memory B cell Clones

[00139] In one embodiment, nucleic acid molecules comprising rearranged CDR3 regions of Ig loci obtained from a third biological sample of a subject at a third time point post vaccination are sequenced in order to identify memory B cells that correspond to the vaccine-induced responsive B cell clones identified in the second sample. In one embodiment, the memory B cells clones of the third sample are compared to memory B cell clones of the first sample in order to identify newly recruited memory B cell clones corresponding to the vaccine-induced responsive B cell clones. Upon identifying newly recruited vaccine-induced memory B cell clones, it can be determined what proportion of the total memory B cell compartment is the newly recruited memory B cell clones. In this way, a degree of recruitment of vaccine-induced responsive clones to immunological memory can be identified. In one embodiment, a degree of recruitment may comprise the proportion of unique clones present in the set of vaccine-induced response clones which have been recruited to memory. In another embodiment, a degree of recruitment may comprise the proportion of B cells in the memory compartment that were recruited from among the vaccine-induced responsive clones. In one embodiment, a degree of recruitment of vaccine-induced responsive clones to the memory compartment is a biomarker for vaccine efficacy.

Monitoring T cell and B cell Response to Infection

[00140] In another aspect, the adaptive immune response to infection can be monitored to identify T cell and/or B cell clones activated in response to infection. The infection can be caused by a virus, bacteria, parasite, or other pathogen. The infection can be acute (e.g., acute viral infection) or chronic. As used herein, the term “acute infection” refers to an infection characterized by rapid onset and resolution within, e.g., 14 days. In contrast, the term “chronic infection” refers to an infection that does not rapidly resolve. For example, a chronic infection may persist for years. The number of responsive clones and their relative abundance can be determined. Additionally, the recruitment of responsive clones to immunological memory can also be measured. The methods described herein may be used in, e.g., animal models and human patients.

[00141] Examples of viruses that cause acute viral infections include, but are not limited to, influenza, yellow fever virus (YFV), and smallpox. Examples of viruses that cause chronic viral infections include, but are not limited to, Epstein-Barr virus (EBV), hepatitis A virus (HAV), hepatitis B virus (HBV), hepatitis C virus (HCV), herpes simplex virus-1 (HSV-1), herpes simplex virus-2 (HSV-2), human immunodeficiency virus (HIV), human papilloma virus (HPV), and varicella zoster virus (VZV).

Identifying Infection-Induced Responsive Clones

[00142] Methods provided herein may be utilized to identify B cell and T cell clones that are responsive to an infection. Infection responsive clones expand rapidly upon interacting with antigen from the pathogen (e.g., viral antigen), and clones present in a biological sample at a significantly high cell number, or abundance, can be identified.

Responsive T cell Clones

[00143] In one embodiment, nucleic acid molecules comprising rearranged CDR3 regions of TCR loci obtained from 1) a first biological sample of a subject at a first time point prior to infection are sequenced and 2) a second biological sample of a subject at a second time point post infection. T cell clones that are responsive to infection are significantly expanded in cell number in the second biological sample in comparison to the first biological sample, and individual T cell clones are detected by the presence of the uniquely rearranged CDR3 region. Relative abundance of the CDR3 region correlates to the number of T cells from the sample for the specific clone. In this way, by identifying T cell clones of significantly high abundance in the second sample in comparison to the first sample, infection-induced responsive T cell clones are detected.

[00144] In one embodiment, the second biological sample is obtained at a time point at or around the peak of the immune response to the infection. For example, in one embodiment, the second time point is about 1-2 days post inoculation with the virus. In another example, the second time point is 10-14 days post inoculation with a pathogen (e.g., virus or bacteria). In one embodiment, the second biological sample is obtained at least 1 day after inoculation. In another embodiment, the second biological sample is obtained at least 10 days post inoculation with a pathogen. In one embodiment, the second biological sample is obtained at a time point when the subject is experiencing symptomatic infection (e.g., fever, rash, vomiting, or diarrhea).

[00145] In one embodiment, the infection-induced responsive T cell clones are pathogen (e.g., viral) antigen-specific T cells. Antigen specificity can be determined using any of a variety of methods known in the art including, but not limited to, cell proliferation assays (e.g., ^3H -thymidine incorporation), cytotoxicity assays (e.g., ^{51}Cr release), MHC-peptide tetramer staining assays, ELISPOT assays, and intracellular cytokine assays.

[00146] In one embodiment, activated, effector T cells are sorted from the second biological sample prior to sequencing to identify significantly expanded T cell clones. In one embodiment, activated T cells are $\text{CD}38^+\text{HLA-DR}^+$ cells. In one embodiment, activated T cells are not sorted from the second biological sample, and infection-induced responsive T cell clones are identified from whole PBMCs.

[00147] In another embodiment, infection-induced responsive clones are identified by sequencing rearranged CDR3 regions from a single time point obtained post infection without comparison to a sample obtained prior to infection. Preferably, the activated, effector T cells are sorted from the biological sample prior to sequencing, and the highly abundant clones are compared to clones identified in a non-sorted sample from the same time point.

[00148] For example, in one embodiment, a first biological sample and a second biological sample of a subject are obtained at a first time point post infection. The activated, effector T cells are sorted from the second biological sample to obtain an activated T cell population. Nucleic acid molecules comprising rearranged CDR3 regions of TCR loci from the first sample and the sorted activated T cell population are sequenced. Infection-induced responsive clones are identified by identifying CDR3 regions of significantly high abundance in the activated T cell population in comparison to the first biological sample, wherein the CDR3 regions of high abundance correspond to expanded T cell clones in the activated T cell population.

Responsive B cell Clones

[00149] In one embodiment, nucleic acid molecules comprising rearranged CDR3 regions of TCR loci obtained from 1) a first biological sample of a subject at a first time point prior to infection are sequenced and 2) a second biological sample of a subject at a second time point post infection. Once the CDR3 regions are sequenced, a clustering algorithm may be applied to cluster groups of CDR3 sequences of common descent comprising clones having undergone somatic hypermutation. B cell clones that are responsive to infection are significantly expanded in cell number in the second biological sample in comparison to the first biological sample, and clusters of clonally related B cells are detected by the rearranged CDR3 sequence clusters. Relative abundance of the CDR3 cluster correlates to the number of B cells from the sample for the specific clone. Relative abundance of the CDR3 clusters correlates to the number of B cells from the sample for the specific clone. In this way, by identifying B cell clones of significantly high abundance in the second sample in comparison to the first sample, infection-induced responsive B cell clones are detected.

[00150] In one embodiment, the second biological sample is obtained at a time point at or around the peak of the immune response to the infection. For example, in one embodiment, the second time point is about 1-2 days post inoculation with a pathogen (e.g., virus or bacteria). In another example, in one embodiment, the second time point is about 10 days post inoculation with a pathogen. In another embodiment, the second biological sample is obtained at least one day post inoculation with a pathogen. In another embodiment, the second biological sample is obtained 10 days post inoculation with a virus. In one embodiment, the second biological sample is obtained at a time point when the subject is experiencing symptomatic infection (e.g., fever, rash, vomiting, or diarrhea).

[00151] In one embodiment, the infection-induced responsive B cell clones are pathogen (e.g., viral) antigen-specific B cells. Antigen specificity can be determined using any of a variety of methods known in the art including, but not limited to, capture assays (e.g., antigen-coated solid matrix), fluorescent-labeled antigen staining assays (e.g., microscopy and flow cytometry), and ELISPOT assays.

[00152] In one embodiment, activated, effector B cells are sorted from the second biological sample prior to sequencing to identify significantly expanded B cell clones. In one embodiment, activated B cells are CD25⁺CD69⁺CD80⁺CD86⁺ cells. In one embodiment, activated B cells are not sorted from the second biological sample, and infection-induced responsive B cell clones are identified from whole PBMCs.

[00153] In another embodiment, infection-induced responsive clones are identified by sequencing rearranged CDR3 clusters from a single time point obtained post infection

without comparison to a sample obtained prior to infection. Preferably, the activated, effector B cells are sorted from the biological sample prior to sequencing, and the highly abundant clones are compared to clones identified in a non-sorted sample from the same time point.

[00154] For example, in one embodiment, a first biological sample and a second biological sample of a subject are obtained at a first time point post infection. The activated, effector B cells are sorted from the second biological sample to obtain an activated B cell population. Nucleic acid molecules comprising rearranged CDR3 regions of Ig loci from the first sample and the sorted activated B cell population are sequenced. Infection-induced responsive clones are identified by identifying CDR3 clusters of significantly high abundance in the activated B cell population in comparison to the first biological sample, wherein the CDR3 clusters of high abundance correspond to expanded B cell clones in the activated B cell population.

Identifying Newly Recruited Memory Clones

[00155] The methods described herein may further be utilized to identify infection-induced responsive T cell clones that are recruited to the memory compartment. In particular, the number of infection-induced responsive effector cell clones recruited to memory may be determined, and the percentage of infection-induced responsive effector cell clones that are recruited to memory may also be determined. Furthermore, correlations between the expansion of a particular effector cell clone in response to infection and recruitment to the memory compartment can be examined. In order to detect newly recruited memory cells, the biological sample is obtained at a time sufficient for the B cells or T cells to transition from activated, effector cells to memory cells. In one embodiment, the biological sample is obtained at least about 30 days following infection. In a particular embodiment, the biological sample is obtained about 90 days following infection. In another embodiment, the biological sample is obtained about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12 or more months following infection. In one embodiment, the biological sample is obtained about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more years following infection.

Memory T cell Clones

[00156] In one embodiment, nucleic acid molecules comprising rearranged CDR3 regions of TCR loci obtained from a third biological sample of a subject at a third time point post infection are sequenced in order to identify memory T cells that correspond to the infection-induced responsive T cell clones identified in the second sample. In one embodiment, the memory T cells clones of the third sample are compared to memory T cell

clones of the first sample in order to identify newly recruited memory T cell clones corresponding to the infection-induced responsive T cell clones. Upon identifying newly recruited infection-induced memory T cell clones, it can be determined what proportion of the total memory T cell compartment is the newly recruited memory T cell clones. In this way, a degree of recruitment of infection-induced responsive clones to immunological memory can be identified.

Memory B cell Clones

[00157] In one embodiment, nucleic acid molecules comprising rearranged CDR3 regions of Ig loci obtained from a third biological sample of a subject at a third time point post infection are sequenced in order to identify memory B cells that correspond to the infection-induced responsive B cell clones identified in the second sample. In one embodiment, the memory B cells clones of the third sample are compared to memory B cell clones of the first sample in order to identify newly recruited memory B cell clones corresponding to the infection-induced responsive B cell clones. Upon identifying newly recruited infection-induced memory B cell clones, it can be determined what proportion of the total memory B cell compartment is the newly recruited memory B cell clones. In this way, a degree of recruitment of infection-induced responsive clones to immunological memory can be identified.

Determining Vaccine Effectiveness

[00158] In another aspect, the methods described herein are utilized to determine the effectiveness of a vaccine. In particular, a vaccine may be compared to a reference vaccine, e.g., a standard vaccine or a candidate vaccine.

[00159] In one embodiment, a method for determining the effectiveness of a vaccine comprises performing high-throughput sequencing of nucleic acid molecules comprising rearranged CDR3 regions of TCR and/or Ig loci obtained from a first biological sample of a subject at a first time point prior to vaccination, a second biological sample of the subject at a second time point post vaccination, and a third biological sample of the subject at a third time point post vaccination. Vaccine-induced responsive clones are identified as activated lymphocytes correlating to CDR3 regions that are of significantly high abundance in the second biological sample in comparison to the first biological sample. Newly recruited memory cell clones corresponding to the vaccine-induced responsive clones are then

identified in the third sample. A degree of recruitment of vaccine-induced responsive clones to immunological memory is compared to a reference degree of recruitment, wherein the vaccine is effective when the degree of recruitment is greater than or equal to the reference degree of recruitment.

[00160] A degree of recruitment can be measured in relation to breadth and depth. Breadth is defined as how many vaccine responsive clones are recruited into memory and depth is the strength of the clones that are recruited into memory. Depth can be assessed by either clonal abundance or by a separate test of broad neutralization.

[00161] When analyzing B cells, a clustering algorithm may be applied to cluster groups of CDR3 sequences of common descent comprising clones having undergone somatic hypermutation. B cell clones that are responsive to vaccination are significantly expanded in cell number in the second biological sample in comparison to the first biological sample, and clusters of clonally related B cells are detected by the rearranged CDR3 sequence clusters. Relative abundance of the CDR3 cluster correlates to the number of B cells from the sample for the specific clone.

[00162] In one embodiment, newly recruited memory cell clones are identified by comparing the one or more newly recruited memory cell clones from the third sample with one or more vaccine-induced responsive clones from the second sample to find matches between the newly recruited memory cell clones and the one or more vaccine-induced responsive clones.

[00163] The reference degree of recruitment may be based, e.g., on a degree of recruitment measured following a candidate vaccine, a reference vaccine, or an infection. In one embodiment, the degree of recruitment is a percentage of vaccine-induced responsive clones that match newly recruited memory cell clones. In one embodiment, the degree of recruitment is a percentage of vaccine-induced responsive clones that match newly recruited memory cell clones. In one embodiment, the degree of recruitment is a percentage of the total number of unique vaccine-induced responsive clones identified from the second sample. In one embodiment, the degree of recruitment is a percentage of the total population of vaccine-induced responsive clones identified from the second sample.

[00164] In this way, the number of unique vaccine-induced responsive clones, the total number of vaccine-induced responsive clones, and/or the degree of recruitment can be used as a benchmark to screen potential new vaccine candidates. In addition, the dynamics of T cell and B cell responses to a vaccine can be compared to the T cell and B cell responses to the corresponding infectious agent.

EXAMPLES**EXAMPLE 1****Identifying Vaccine-Induced Activated T cells**

[00165] The investigation of pathogen-induced effector T cells is essential to accurately characterize the dynamics and breadth of the human immune response. The Yellow Fever vaccine (YFV) has been broadly used as a model to understand how a controlled, self-resolving acute viral infection induces an effective, long-term protective immune response. In order to analyze the dynamics of the T cell repertoire before, during, and after vaccination, human volunteers with the live attenuated yellow fever vaccine YF-17D, which constitutes an established model of a controlled acute viral infection. High-throughput sequencing was used to characterize the breadth of the anti-viral effector cell response.

[00166] In this study, vaccination with the yellow fever vaccine YF-Vax®, which is based on the YF-17D204 attenuated strain, was used as a model of infection, in particular acute viral infection.

[00167] In addition, the methods of the invention used to characterize the viral infection are equally applicable for other types of infection, for example, by parasites or bacteria. The methods described here are also applicable to assessing the breadth and depth of an immunoglobulin response to an infection or a vaccination.

[00168] The attenuated virus contained in YF-17D only harbors 20 amino acid changes as compared to the wild type strain; most of these are found in the E protein and are thought to result in changes in viral tissue tropism (Lee and Lobigs, 2008, Journal of Virology 82:6024-6033). In addition, this attenuated virus is replication-competent, so that administration of the YFV results in a mild viral infection that is predicted to elicit an immune response that is almost identical in quality to that induced by wild type infection (SanofiPasteur. YF-VAX® prospectus, Document LE6445-LE6446).

Materials and Methods**Vaccination and Sample Collection**

[00169] Nine volunteers between the ages of 18 and 45 received the yellow fever single dose vaccine YF-VAX® (based on the YF-17D204 strain of the yellow fever virus, (SanofiPasteur. YF-VAX® prospectus, Document LE6445-LE6446)), and to have 200 mL of blood drawn at three different time points: immediately before vaccination (day 0), two weeks post-vaccination (day 14), and 3 months post-vaccination (day 90). Written informed

consent to use the blood samples in this study was obtained from each donor. The administration of the YF vaccine and all blood draws and were performed at the UWVRC.

Cell Sorting

[00170] Whole blood samples (200 ml) were collected and PBMCs were isolated by Histopaque (Sigma-Aldrich, St. Louis, MO) density gradient centrifugation. CD8⁺ T cells were isolated from total PBMCs by magnetic separation using CD8 MicroBeads and the autoMACs Pro Separator (both from Miltenyl Biotec, Auburn, CA), followed by staining with anti-CD3-Alexa Fluor 700, anti-CD8-APC-H7, anti-CD38-PE, HLA-DR-FITC, anti-CD14-Pacific Blue, anti-CD19-V450, anti-CD45RO-PE Cy7, anti-CD45RA-APC, anti-CD62L-PerCP Cy5.5, and DAPI (all obtained from BD BioSciences, San Jose, CA). Cells were also stained with propidium iodide (PI) to detect cell viability. T cell subpopulations were sorted using the BD FACS Aria II and FACSDiva v6.1.3 software (BD Biosciences). First, cells were gated on PI⁻CD14⁻CD19⁻ to remove dead cells, monocytes and B cells. Cells were then gated on CD3⁺CD8⁺ to exclude non-T cell lymphocytes, and finally four different CD8⁺ T cell subsets were isolated: CD3⁺CD8⁺CD14⁻CD19⁻CD45RA⁻CD45RO⁺ memory T cells (T_M, day 0 only); CD3⁺CD8⁺CD14⁻CD19⁻CD38⁺HLA-DR⁺ antigen-experienced, activated effector T cells (T_{AE}, day 14 only), CD3⁺CD8⁺CD14⁻CD19⁻CD45RA⁻CD45RO⁺CD62L^{lo} effector memory T cells (T_{EM}, day 90 only), and CD3⁺CD8⁺CD14⁻CD19⁻CD45RA⁻CD45RO⁺CD62L^{hi} central memory T cells (T_{CM}, day 90 only). To avoid contamination, CD38⁺HLA-DR⁺ cells were excluded from the effector memory and central memory T cell populations. Day 90 samples from three of the volunteers were discarded due to contamination.

DNA Extraction and Immune Repertoire Sequencing

[00171] Genomic DNA was purified from total PBMC and each sorted T cell population sample using the QIAmp DNA Blood Mini Kit (Qiagen). For each sample, DNA was extracted from ~1 million T cells, and the TCRβ CDR3 regions were amplified and sequenced using the methods described herein, (ImmunoSEQ™, Adaptive Biotechnologies, Seattle, WA previously described (Robins et al. 2009, Blood 114:4099-4107)). In brief, bias-controlled V and J gene primers were used to amplify rearranged V(D)J segments for high throughput sequencing at about 20x coverage, as described above. After correcting sequencing errors via a clustering algorithm, CDR3 segments were annotated according to the International ImMunoGeneTics collaboration (Lefranc et al. 2004, In Silico Biol 4:17-29;

Yousfi et al. 2004, Bioinformatics (Oxford, England) 20 Suppl 1:i379-385), to identify the V, D, and J genes that contributed to each rearrangement. Sequences were classified as non-productive if it was determined that non-templated insertions or deletions produced frame-shifts or premature stop codons.

PCR Template Abundance Estimation

[00172] In order to estimate the average read coverage per input template in the multiplex PCR and sequencing approach, a set of approximately 850 unique synthetic TCR analog templates, comprising each possible combination of V β and J β gene segments, was employed (Carlson et al. 2013, Nature Communications 4:2680). These molecules were included in each PCR reaction at a low concentration selected so that most unique synthetic templates were not observed in the sequencing output. Using the known concentration of each synthetic template in the pool, the relationship between the number of observed unique synthetic molecules and the total number of synthetic molecules added to reaction was simulated (which closely matches a one-to-one relationship at the selected concentration). This information was then used to calculate, for each PCR reaction, the mean number of sequencing reads obtained per molecule of PCR template, and finally estimate the number of T cells in the input material bearing each unique TCR rearrangement.

Identification of Expanded and Enriched Effector T Cell Clones

[00173] A T cell clone was defined as the population of T cells bearing a unique TCR β rearrangement. To computationally identify those T cell clones whose frequencies differ between samples from a given volunteer taken at different time points, or between cell populations (e.g. between total PBMCs and a specific sorted T cell population for the same time point), the algorithm described below was used. The input data consists of the abundance for each TCR β clone in the sample.

[00174] It was assumed that the repertoire contains S distinct clones, and their proportional abundances at time points 1 and 2 are given by the multinomial vectors $\pi^{(1)} = \{ \pi^{(1)}_1, \pi^{(1)}_2, \dots, \pi^{(1)}_S \}$ and $\pi^{(2)} = \{ \pi^{(2)}_1, \pi^{(2)}_2, \dots, \pi^{(2)}_S \}$, with $\sum_{i=1}^S \pi_i^{(j)} = 1$. Supposing that n clones have changed in abundance between the two time points, these clones were identified with the n -element index vector Δ .

[00175] Next, it was assumed that the aggregated proportional change of all truly changed clone abundances is small (i.e., $\sum_{i \in \Delta} (\pi_i^{(2)} - \pi_i^{(1)}) \ll 1$). In this regime, each observed clone can be independently tested for significance using a 2x2 contingency table. The Fisher exact test was employed to compute a p-value for each clone across the two

samples. Specifically, suppose clone i is observed with abundance $k_i^{(1)}$ at time point 1 and $k_i^{(2)}$ at time point 2. A p-value for the 2x2 contingency table containing these abundances in one row was computed, and the remaining abundances (for clones other than i) on the other. By summing over hypergeometric probabilities, the Fisher exact test gives the p-value for the null hypothesis that the proportion of clone i in the repertoire is the same at both time points, that

$$\pi_i^{(1)} = \pi_i^{(2)}.$$

[00176] s was defined as representing the number of distinct clones observed across the two samples, where in general $s \leq S$. Without loss of generality, indices 1 through s of the repertoire clones correspond to the observed clones. After performing the above analysis on each of the s observed clones, a vector of p-values, $p = \{p_1, p_2, \dots, p_s\}$, was used.

[00177] To choose a rejection region (thereby identifying a set of significantly changed clones between the two samples under consideration), we use the positive false discovery rate (pFDR) method of Storey, which defines (Storey, 2002, J. R. Statist. Soc. B 64:479-498), the pFDR as the expected proportion of true null hypotheses among all rejected hypothesis:

$$\begin{aligned} \text{pFDR}(\gamma) &= \Pr \left(\pi_i^{(1)} = \pi_i^{(2)} \mid p_i \leq \gamma \right) \\ &= \frac{\pi_0 \Pr \left(p_i \leq \gamma \mid \pi_i^{(1)} = \pi_i^{(2)} \right)}{\Pr(p_i \leq \gamma)} \\ &= \frac{\pi_0 \gamma}{\Pr(p_i \leq \gamma)} \end{aligned}$$

[00178] The second equality follows from Bayes' theorem with π_0 being the prior probability that a hypothesis is null. The last equality follows from the definition of a p-value, if the p-values themselves are regarded as independently and identically distributed random variables.

[00179] For each p-value (p_i) the associated q-value (q_i) may be estimated, which is the minimum pFDR that can occur when rejecting p-values less than or equal to p_i . By examining the number of significant tests at various q-value thresholds, an appropriate threshold can be selected (e.g., see FIGs. A and 4B1). Control of pFDR is preferred to control of the family-wise error rate (FWER) – the probability of one or more false alternative hypotheses. The latter, which is typically controlled by the Bonferroni method, is overly conservative, failing to reject many false null hypotheses in order to attain any nontrivial FWER. The pFDR, on the other hand, rejects these hypotheses at the cost of a specifiable, small proportion of rejected true null hypotheses.

[00180] The resulting set of significance tests allow the identification of T cell clones whose frequencies vary (i.e., dynamic T cell clones). For example, applying this algorithm to the comparison of total PBMCs isolated on day 14 post-vaccination to activated CD8⁺ T cells purified from the same sample identifies a set of enriched, activated CD8⁺ T cells that are expected to be YFV-specific. In contrast, the comparison of total PBMCs obtained from the same volunteer on day 0 (pre-vaccination) and on day 14 post-vaccination identifies a set of putative YFV-reactive clones.

Results

[00181] It is well established that effector CD8⁺ T cells expand in response to an acute viral infection (Pulendran and Ahmed, 2011, *Nature Immunology* 12:509-517). Expanded clones can either bind specifically to a pathogen-derived epitope presented by a type I HLA molecule, or they can be induced to expand non-specifically by cytokines released by other cells, in a process known as bystander effect (Murali-Krishna et al. 1998, *Immunity* 8:177-187). In the case of the YFV model, which has been extensively used to characterize the human antiviral immune response since it results in a self-limited, acute viral infection (Ahmed and Akondy, 2011, *Immunology and Cell Biology* 89:340-345; Pulendran, 2009, *Nature Reviews Immunology* 9:741-747), activated effector CD8⁺ T cells peak two weeks post-vaccination, and express a particular set of phenotypic markers, including CD38, HLA-DR, Ki-67 and Bcl-2 (Miller et al. 2008, *Immunity* 28:710-722). The massive expansion of activated effector CD8⁺ T cells in response to vaccination with YFV is specific since existing memory CD8⁺ T cells specific for other viruses such as CMV or EBV do not contribute to the activated, proliferating pool of CD8⁺ T cells (Miller et al. 2008, *Immunity* 28:710-722).

[00182] To further explore the dynamics of the T cell repertoire in response to an acute viral infection, a single dose of the live attenuated YFV (YF-VAX®, based on the YF-17D204 strain of the YF virus (SanofiPasteur. YF-VAX® prospectus, Document LE6445-LE6446)) was administered to nine healthy volunteers, none of whom reported being previously exposed to the YF virus or having received YFV. 200 mL of peripheral blood were drawn from each participant on day 0 (immediately prior to vaccination), and on days 14 and 90 post-vaccination (Table 1, Appendix). To identify CD8⁺ T cells present in the memory compartment prior to immunization, a fraction of the total PBMCs obtained from all volunteers on day 0 was sorted into CD8⁺ memory T cells (TM0, defined as CD3⁺CD8⁺CD14⁻CD19⁻CD45RA⁻CD45RO⁺ cells). In addition, to characterize the activated effector CD8⁺ T cells induced by vaccination with YFV, a fraction of the total PBMCs

obtained on day 14 post-vaccination was sorted by selecting $CD3^{+}CD8^{+}CD14^{-}CD19^{-}CD38^{+}HLA-DR^{+}$ activated effector $CD8^{+}$ T cells (TX 14) (Miller et al. 2008, Immunity 28:710-722). Finally, to determine which of these clones enter the memory compartment, a fraction of the total PBMCs obtained on day 90 was sorted into effector memory (T_{EM-90}) and central memory (T_{CM-90}) $CD8^{+}$ T cells (respectively $CD8^{+}CD45RO^{+}CD62L^{lo}$ and $CD8^{+}CD45RO^{+}CD62L^{hi}$) (Sallusto et al. 1999, Nature 401:708-712). Table 1 (Appendix) shows the cell populations studied (including the surface markers used for sorting when applicable), and the days post-immunization that the samples were collected. Three of the samples on day 90 had to be discarded due to contamination.

[00183] Genomic DNA was extracted from about 1 million T cells for either total PBMCs or sorted T cell populations (Table 1), and the CDR3 regions of rearranged TCR β loci were PCR amplified and high-throughput sequenced as previously described (Robins et al. 2009, Blood 114:4099-4107). The resulting TCR β sequences are nearly unique for each clone, so that the data can be used to assess the dynamics of the cellular adaptive immune response both over time and between T cell subpopulations. Additionally, the number of original templates corresponding to each PCR-amplified clonal sequence was determined by assessing the amplification of a set of synthetic templates, thus providing an estimate of the cellular abundance for each clone in each sample.

Identification of Vaccine-Induced Clones

[00184] To assess the dynamics of the YFV-induced effector T cell repertoire, it was determined whether each unique clone (as defined by sequencing the CDR3 region of the TCR β chain) was enriched in the day 14 post-vaccination, YFV-induced effector T cell compartment (as defined by the expression of CD38 and HLA-DR (Miller et al. 2008, Immunity 28:710-722)), in comparison to the total PBMC sample obtained from the same individual at the same time point.

[00185] To do this, a novel statistical method described above was developed to identify clones with significant proportional abundance differences between two samples.

[00186] FIGs. 1A and 1B show data used for selection of FDR thresholds. FIG. 1A shows the number of clones classified as YFV induced for various FDR significance thresholds for all subjects. By examining the number of significant tests at various Q value thresholds (FDR thresholds), an appropriate threshold can be selected. Here, a threshold of 0.01 was selected. FIG. 1B shows the number of clones classified as putatively reactive

clones for various FDR significance thresholds for all subjects. A threshold of 0.05 was selected. Each subject is represented by a different tone of gray, as indicated in the legend.

[00187] This approach controlled for the false positive rate and accounted for experimental errors that result in the presence of false positives in the YFV-induced effector CD8⁺ T cell population (e.g., cells that do not have the indicated surface markers). This avoided overstating the number of YFV-induced clones, which would result from a simple enumeration of clones present in the sorted population. Instead, a clone was considered to be YFV-induced if (a) it was significantly enriched in the effector CD8⁺ T cell population with respect to the corresponding total PBMC sample, and (b) it carried a productive TCR β rearrangement. Since the volunteers who participated in this study had not been previously exposed to either the YF virus or the YFV, it was also taken into consideration whether each unique CD8⁺ T cell clone identified was present in the day 0 pre-vaccination memory cell population (T_{M0}). Based on these criteria, T cell clones were classified into four categories, as follows: YFV-induced clones (i.e. enriched in the day 14 CD38⁺ HLA-DR⁺ sort vs. the day 14 PBMC sample from that individual, but absent in the corresponding T_{M0} sample); cross-reacting or by-stander clones (i.e. enriched in the day 14 CD38⁺ HLA-DR⁺ sort vs. the corresponding PBMCs but present in T_{M0}), and those not enriched in the CD38⁺ HLA-DR⁺ sort, which could be absent in the T_{M0} sample (i.e. corresponding either to YFV-induced cells that did not express surface markers previously defined for activated effector CD8⁺ T cells (Miller et al. 2008, Immunity 28:710-722), or to false negatives, i.e. cells that failed to be sorted into the activated effector compartment by flow cytometry) or present in T_{M0} (i.e., clones similar to those in the previous category but pre-existing in the memory compartment at the time of vaccination with YFV).

[00188] FIGs. 2A and 2B show the identification of YFV-induced clones. FIG. 2A shows a graph of the abundance of unique clones identified by statistical enrichment on the activated effector CD38⁺ HLA-DR⁺ CD8⁺ T cell compartment on day 14 post-vaccination (TAE-14) versus those present in the corresponding total PBMC sample from the same time point for subject 1. FIG. 2B shows the same for subjects 2 to 9. Clones were classified into four categories based both on their presence in the TAE-14 and the T_{M0} compartments. Red clones are present in the TAE-14 compartment, whereas gray clones are not; while clones absent in the T_{M0} compartment have a black edge and those present in the T_{M0} compartment do not. Darker colors indicate that multiple data points have been superimposed in that particular position. Regions bound by dashed lines indicate clones present in only one

sample. YFV-induced clones were significantly enriched in the CD38⁺ HLA-DR⁺ CD8⁺ T cell-sorted population compared to the corresponding total PBMC sample.

[00189] For the nine subjects in the study, an average of 2,000 clones were detected that were enriched in the activated, effector CD8⁺ T cell subpopulation as compared to the corresponding PBMC sample from the same individual (2135 $\pm$ 770) (Table 2, Appendix). This number, therefore, constitutes a direct estimate of the number of activated effector CD8⁺ T cell clones that expand upon binding to HLA:YFV-derived epitope complexes. In addition, the vast majority of these clones (on average 91.5%, Table 2, Appendix) were absent in the T_{M0} population, and were thus very likely YFV-specific.

EXAMPLE 2

Characterization of the Recruitment of Individual Clones to Immunological Memory

[00190] In order to determine which of the YFV-induced clones identified in the previous example entered the long-term central and effector memory compartments, samples obtained from six of the volunteers ninety days post-vaccination were analyzed (Table 1, Appendix). Preliminary studies have demonstrated that YFV-induced activated effector CD8⁺ T cells return to baseline levels 30 days post-immunization, and suggest that YFV antigen-specific cells that are detected beyond this time point correspond to memory cells (Miller et al. 2008, Immunity 28:710-722). Therefore, YFV-induced clones identified as enriched on the d14 activated, effector T cell post-immunization compartment, but absent from the T_{M0} compartment in the corresponding day 90 post-immunization samples (i.e., the putative YFV-specific clones) were tracked to determine which clones were contained in the effector memory compartment (T_{EM}, defined as CD3⁺, CD8⁺ CD14⁻, CD19⁻, CD45RA⁻, CD45RO⁺ CD62L^{lo}), the central memory compartment (T_{CM}, defined as CD3⁺, CD8⁺ CD14⁻, CD19⁻, CD45RA⁻, CD45RO⁺ CD62L^{hi}), or both.

[00191] FIGs. 3A and 3B show recruitment of YFV-induced clones to immunological memory compartments. FIG. 3A shows the efficiency of recruitment of YFV-induced clones to the effector (TEM⁺ TCM⁻) and central (TEM⁻ TCM⁺) memory compartments, or both (TEM⁺ TCM⁺) as a percentage of all clones classified as YFV induced. FIG. 3A shows that, respectively, 3.1% and 2.5% of YFV-induced clones absent in T_{M0} were identified exclusively in the T_{EM} or the T_{CM} compartments, while 6.7% were identified in both.

[00192] FIG. 3B shows the efficiency of recruitment to the effector and central memory compartments (or both) for YFV-induced clones absent from the day 0 pre-

vaccination total PBMC samples, classified into categories based on their abundance in the day 14 post-vaccination total PBMC samples. Clones with a higher degree of expansion are more efficiently recruited to the memory compartment. The aggregated data for all subjects are shown; subject-wise source data can be found in Table 3 (Appendix). Table 3 shows the number of YFV-induced clones absent on the T_{M-0} compartment, classified based on their recruitment to the T_{CM-90} and T_{EM-90} compartments as well as the level of expansion, measured by their abundance on the day 14 post-vaccination total PBMC samples.

[00193] Composition of the effector and central memory compartments on day 90 post-vaccination. FIG. 4A shows the proportion of YFV-induced clones newly recruited to the effector (T_{EM-90}) and central (T_{CM-90}) memory compartments on day 90 post-vaccination, computed both by clone and template counts. The YFV-induced clones that were newly recruited to the T_{EM} or the T_{CM} compartments represent 0.43% and 0.45% of their respective memory compartments, as measured by unique clone counts, or 0.41% and 0.28% as measured by template abundance of the corresponding memory compartment aggregated over all samples. FIG. 4B shows the number of templates per YFV-induced clone identified in the T_{EM-90} and T_{CM-90} memory compartments. More templates per clone were observed in the T_{EM-90} compartment, indicating that these clones were more highly expanded. The aggregated data for all subjects are shown; subject-wise source data can be found in Table 4 in the Appendix. While the number of templates per unique $CD8^+$ T cell clone in the T_{EM} compartment averaged 8.3, those in the T_{CM} compartment averaged 2.8, indicating that YFV-induced clones recruited to the effector memory are more significantly expanded than those recruited to the central memory compartment (FIG. 4B). Finally, whether any indicator of specificity (such as CDR3 length or V-J gene usage) correlated with the probability that a given $CD8^+$ T cell clone would be recruited to memory compartment was analyzed. Although no simple indicator showed association, it was found that both the degree of expansion and the specificity determined by effector sorting positively associated with recruitment to memory (Tables 3-5, Appendix).

EXAMPLE 3

Concordance between the Expansion in Total PBMCs and Enrichment in the Activated Effector $CD8^+$ T cell Compartment

[00194] In addition to the data presented above, the approach disclosed herein also allowed for the identification of activated, effector $CD8^+$ T cells that expanded massively in response to YFV through the direct comparison of the unsorted total PBMC repertoires

isolated on days 0 and 14 post-immunization. The statistical method described in detail above can be applied to the identification of T cell clones that have significantly expanded in the d14 PBMC sample as compared to the day 0 pre-immunization sample from the same individual (FIG. 1B and 5).

[00195] Identification of YFV putatively reactive clones. FIG. 5A shows the abundance of unique clones identified by statistical enrichment in the day 14 post-vaccination total PBMC sample compared to the pre-vaccination day 0 total PBMC sample from subject 1. Putatively reactive clones are enclosed by a circle in FIG. 5A. FIG. 5B shows the same for subjects 2 to 9. Significant enrichment (or expansion) was defined based on a q value threshold, with 1% and 5% expected false-positive rates for YFV-induced and putatively reactive clones, respectively, as described above. Clones were classified into four categories based both on their presence in the TAE-14 and the TM-0 compartments, as indicated in the legend. Darker colors indicate that multiple data points are superimposed in that particular position. Regions bound by dashed lines indicate clones present in only one sample.

[00196] Among all the cells present in the day 14 post-immunization sample, a set of clones that were highly expanded, but that were not captured by the antiviral-specific effector sort were identified (i.e., $CD38^+$ $HLA-DR^+$ $CD8^+$ T cells). These clones could correspond to non- $CD8^+$ T cells that express the TCR β receptor (e.g., $CD4^+$ T cells, NK T cells or $\gamma\delta$ T cells), YF-induced $CD8^+$ T cells that possess different surface markers than those previously reported by Miller *et al.* (2008, Immunity 28:710-722), or non-specific clonal expansions.

EXAMPLE 4

Identifying Vaccine-Induced Activated T cells without Enrichment

[00197] High-throughput sequencing was used to determine the contribution of all unique virus-specific clones to the long-lived memory T cell repertoire. In order to assess how well the expanded $CD8^+$ T cell clones detected in the PBMC population using only immune repertoire sequencing (i.e., not sorted by flow-cytometry) concord with the previously identified activated effector $CD38^+$ $HLA-DR^+$ $CD8^+$ T cell clones (i.e., those identified statistically after flow-cytometry sorting), it was determined how many expanded $CD8^+$ T cells carrying productive rearrangements identified in the total PBMC sample analysis were classified as YFV-induced through the statistical analysis of flow-cytometry sorted $CD38^+$ $HLA-DR^+$ $CD8^+$ T cell clones described above.

[00198] Table 6 (Appendix) shows the concordance between clones identified as putatively reactive in the total PBMC sample and YFV-induced clones identified by presence in the activated, effector CD8⁺ T cell compartment. Table 6 shows the counts and percentage of clones identified in the total PBMC sample that were also identified in the effector compartment as YFV-induced for each subject, and as a cumulative total.

[00199] A significant proportion of these putatively-reactive clones, between 25% and 95.2%, depending on the subject, are present in the CD38⁺ HLA-DR⁺ CD8⁺ T cell sort, suggesting they are induced by the YFV. In aggregate, 62% of the putatively-reactive clones identified as expanded in the d14 post-immunization total PBMC population (as compared to the equivalent population pre-immunization) can be classified as YFV-induced. The analysis demonstrates the potential of identifying vaccine-specific responding clones by identifying clones expanded in the total PBMC population exclusively using immune repertoire sequencing data.

[00200] As described herein, the dynamics of the effector and memory CD8⁺ T cell repertoires across three time points (pre-vaccination, 14 days post-vaccination, and 90 days post-vaccination) for volunteers who received the YF-17D vaccine were examined. Total PBMCs were isolated, and flow cytometry was used to sort a fraction of the samples into CD8⁺CD38⁺HLA-DR⁺ T cells on day 14 at the peak of their abundance, and into memory CD8⁺ T cells on days 0 and 90. High-throughput sequencing of the rearranged TCR β locus allowed identification of CD8⁺ T cell clones in each sample, as well as estimated abundances for each clone. The synthesis of these sorting protocols with high-throughput sequencing enabled measurement of T cell response to infection at unprecedented resolution.

[00201] Importantly, it was shown that these YFV-induced CD8⁺ T cell clones can also be identified from peripheral blood, thus eliminating the need to select particular cellular populations through flow-cytometry.

[00202] Thus, it was determined that an average of approximately 2,000 different CD8⁺ T cell clonal lineages were activated by vaccination with YFV during the acute phase of the immune response, and that about 12% of them were detected in the long-term memory compartment (including both central and effector memory CD8⁺ T cells).

[00203] Using the methods described above, it can be determined if a similar number of CD8⁺ T cell clonal lineages are induced by other viral vaccines, or by naturally-occurring acute viral infections.

[00204] It was also observed that clones that were most expanded on the total PBMC sample from day 14 post-vaccination were more likely to enter the memory compartment 10

weeks later, in agreement with previous data (12). Although it was difficult to identify other defining characteristics that differentiate CD8⁺ T cell clones that expand in response to YFV vaccination and are present in the memory compartment on day 90 post-vaccination from those that wane during that period, additional studies can be performed to characterize these two populations further, including their epitope specificity, since this would constitute valuable information that could guide the design of vaccines against other pathogens. Interestingly, almost all of the clones that are markedly expanded in the total PBMC sample from day 14 post-vaccination (as compared to the corresponding day 0 pre-vaccination total PBMC sample from the same individual) were classified as YFV-induced CD8⁺ T cells by the combination of flow cytometry and statistical analysis. In fact, very few clonally-expanded T cells in the periphery were observed that were not identified as YFV-induced clones, in agreement with previous reports showing that while CD8⁺ T cells greatly expand in response to vaccination with YFV, the CD4⁺ expansion is much less dramatic (6, 30, 32, 33). It is important to consider that the sampling depth used in this study limits the detection of bystander CD8⁺ cells, or CD4⁺ T cells that are only modestly expanded. Thus, the current level of detection is likely not sufficient to distinguish CD4⁺ T cell expansion above the intrinsic system noise.

[00205] A particular pattern of V(D)J gene usage among the expanded CD8⁺ T clone repertoire was not observed. This result partially agrees with a preliminary study of V gene usage performed by Co *et al.* (34), which used a limited set of anti-human V β antibodies. These authors did not observe a dominant V β family that predominated among the tetramer-specific CD8⁺ T cells in two individuals vaccinated with YFV, but reported that although gene usage changed over time from the acute to the memory phase no particular V genes persisted between the acute and memory phases of the anti-viral response (34).

[00206] Finally, it is noteworthy that many of the CD8⁺ T cell clones identified as expanded through the comparison of the day 14 post-vaccination and the day 0 pre-vaccination total PBMC samples were classified as likely YFV-specific in our initial characterization of clones enriched in the activated effector CD8⁺ T cells vs. the total PBMC sample on day 14 post-vaccination. Thus, this approach is capable of identifying a fraction of the highly expanded CD8⁺ T cells by immune repertoire sequencing of total PBMCs prior to infection or vaccination and during the acute response (i.e. 10-14 days post-vaccination), and could be used to ascertain the establishment of long-term memory by sorting memory T cells a few months after infection (or later) and tracking the CD8⁺ T cells previously identified as

being viral-induced. Additional experiments can be performed to address the epitope-specificity of the YFV-induced CD8⁺ clones, using, for example, tetramer technology to purify clones that bind to previously identified immunodominant YFV epitopes.

[00207] Similar methods are applicable to the evaluation of the B cell response to vaccines and viral infections. In conclusion, immune repertoire sequencing methods, as described above, can be used to characterize the strength and breadth of the B and T cell response induced by vaccines and viral infections, and has the potential to be utilized to evaluate novel vaccines in terms of their potential ability to induce effective long-term protective immune responses.

APPENDIX**TABLE 1**

Cell population	Surface markers used for sorting	No. of subjects analyzed on:		
		Day 0	Day 14	Day 90 ^b
Total PBMCs	NA	9	9	
YFV-induced effector CD8 ⁺ T cells	CD3 ⁺ CD8 ⁺ CD14 ⁻ CD19 ⁻ CD38 ⁺ HLA-DR ⁺		9	
CD8 ⁺ memory T cells (T _{M-0})	CD3 ⁺ CD8 ⁺ CD14 ⁻ CD19 ⁻ CD45RA ⁻ CD45RO ⁺	9		
CD8 ⁺ effector memory T cells (T _{EM-90})	CD3 ⁺ CD8 ⁺ CD14 ⁻ CD19 ⁻ CD45RA ⁻ CD45RO ⁺ CD62L ^{lo}			6
CD8 ⁺ central memory T cells (T _{CM-90})	CD3 ⁺ CD8 ⁺ CD14 ⁻ CD19 ⁻ CD45RA ⁻ CD45RO ⁺ CD62L ^{hi}			6

^a Included are the cell populations studied, the surface markers used for sorting by flow cytometry, the days the samples were collected (day 0 prevaccination and days 14 and 90 postvaccination), and the number of subjects analyzed in each group. NA, not applicable.

^b Day 90 samples from 3 subjects had to be discarded due to contamination.

TABLE 2

Number of YFV-induced clones separated by presence or absence in the memory compartment before immunization (M_0)

TABLE 2 Number of YFV-induced clones^a

Presence or absence in T_{M-0}	No. of YFV-induced clones in subject no.:				
	1	2	3	4	5
+	139	241	36	139	426
-	2,303	2,126	3,804	2,010	1,618
Total (% absent)	2,442 (94.3)	2,367 (89.8)	3,840 (99.1)	2,149 (93.5)	2,044 (79.2)

6	7	8	9	Avg	Total (%)
163	57	181	256	182	1,638 (8.5)
1,764	1,538	1,653	757	1,953	17,573 (91.5)
1,927 (91.5)	1,595 (96.4)	1,834 (90.1)	1,013 (74.7)	2,135 (91.5)	21,346 (82.3)

^a For each subject, the table shows the number of YFV-induced clones present (+) or absent (-) in the memory compartment on day 0 before vaccination (T_{M-0}), as well as the total number of YFV-induced clones identified and the percentage of those that were absent from T_{M-0} . The last two columns correspond to the aggregated data (average, total, and percentage) from all 9 subjects.

TABLE 3

Number of YFV-induced clones absent on the T_{M-0} compartment, classified based on their recruitment to the T_{CM-90} and T_{EM-90} compartments as well as the level of expansion, measured by their abundance on the day 14 post-vaccination total PBMC samples.

		Abundance						
		1	2-3	4-7	8-15	16-31	32-63	≥64
Subject 2	CM*EM ⁺	14	346	385	231	67	17	6
	CM*EM ⁺	0	4	8	5	6	4	2
	CM*EM ⁺	0	10	13	10	7	2	0
	CM*EM ⁺	0	16	18	20	15	4	1
Subject 4	CM*EM ⁺	7	328	304	190	53	11	2
	CM*EM ⁺	0	6	8	6	10	8	8
	CM*EM ⁺	0	4	16	14	5	3	0
	CM*EM ⁺	0	16	24	18	3	2	1
Subject 5	CM*EM ⁺	9	172	186	114	46	10	0
	CM*EM ⁺	0	8	6	8	6	2	3
	CM*EM ⁺	2	5	11	15	9	0	1
	CM*EM ⁺	1	21	28	21	16	5	2
Subject 7	CM*EM ⁺	1	131	168	274	277	99	76
	CM*EM ⁺	0	0	0	3	8	1	14
	CM*EM ⁺	0	0	2	4	9	6	8
	CM*EM ⁺	0	3	10	18	51	31	27
Subject 8	CM*EM ⁺	11	227	219	133	61	17	7
	CM*EM ⁺	0	1	2	4	5	0	1
	CM*EM ⁺	0	3	3	6	2	3	4
	CM*EM ⁺	0	9	8	13	8	6	5
Subject 9	CM*EM ⁺	1	74	98	88	42	28	11
	CM*EM ⁺	0	1	2	4	2	8	11
	CM*EM ⁺	0	1	3	6	5	5	8
	CM*EM ⁺	0	4	9	9	14	9	10

TABLE 4

Composition of the day 90 memory compartment. Shown are the number of new, YFV-induced clones contributing to the TEM-90 and TCM-90 memory compartments as compared to the non-YFV-induced clones, counted both by number of clones and by number of templates.

		clone counts		template counts	
		new YFV-induced	not YFV-induced	new YFV-induced	not YFV-induced
Subject 2	EM	96	34,584	668	173,024
	CM	144	39,683	245	119,443
Subject 4	EM	124	20,309	431	159,933
	CM	151	37,911	321	148,867
Subject 5	EM	139	30,260	327	132,558
	CM	225	51,247	769	136,699
Subject 7	EM	66	27,295	117	171,953
	CM	184	33,914	375	102,844
Subject 8	EM	51	11,485	135	104,340
	CM	95	18,658	563	131,258
Subject 9	EM	68	14,163	2818	119,083
	CM	92	27,776	251	93,823

TABLE 5

Number of YFV-induced clones newly recruited to the TCM-90 and TEM-90 memory compartments

	Subject						Total	%
	2	4	5	7	8	9		
CM⁺EM⁺	37	59	63	33	19	29	240	2.5%
CM⁺EM⁻	59	65	76	33	32	39	304	3.1%
CM⁻EM⁺	107	92	162	151	76	63	651	6.7%
CM⁻EM⁻	1,923	1,794	1,317	1,321	1,526	626	8507	87.7%
Total	2,126	2,010	1,618	1,321	1,653	757	9702	

For each subject, the table shows the number of YFV-induced clones newly recruited to the TCM-90 and TEM-90 memory compartments (CM+EM+), the TCM-90 only (CM+EM-), the TEM-90 only (CM-EM+) or neither (CM-EM-), as well as the total number of clones. The last two columns correspond to the aggregated data (total and percentage) from the 6 subjects for whom the memory populations were studied.

TABLE 6

Concordance between identified as “putatively reactive” in the total PBMC sample and YFV-induced clones identified by their presence in the activated effector CD8+ T cell compartment.

Presence or absence in T _{AE-14} compartment	No. of “putatively reactive” clones in subject no.:					
	1	2	3	4	5	6
+	127	59	118	56	3	44
-	106	20	6	3	9	56
Total (% present in T _{AE-14})	233 (54.5)	59 (66.1)	124 (95.2)	39 (92.3)	12 (25.0)	100 (44.0)

Presence or absence in T _{AE-14} compartment	7	8	9	Avg	Total (%)
+	288	74	119	94.2	848 (62.2)
-	190	38	87	57.2	515 (37.8)
Total (% present in T _{AE-14})	478 (60.3)	112 (66.1)	206 (57.8)	151.4 (62.4)	1,363 (62.2)

For each subject, Table 6 shows the number of “putatively reactive” clones identified in the total PBMC sample that were present (+) or absent (-) in the corresponding T_{AE-14}. The last two columns correspond to the aggregated data (average, total, percentage) from all 9 subjects.

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What is claimed:

1. A method of measuring T cell response to a vaccine in a subject, comprising:
performing high-throughput sequencing of nucleic acid molecules comprising rearranged CDR3 regions of TCR loci obtained from a first biological sample of the subject at a first time point prior to vaccination;
performing high-throughput sequencing of nucleic acid molecules comprising rearranged CDR3 regions of TCR loci obtained from a second biological sample of the subject at a second time point post vaccination; and
identifying T cell clones having CDR3 regions of significantly higher proportional abundance in the second biological sample in comparison to the first biological sample, thereby identifying vaccine-induced responsive clones.
2. The method of claim 1, wherein the TCR loci are selected from the group consisting of the TCR α locus, TCR β locus, TCR γ locus, and TCR δ locus.
3. The method of claim 1, wherein the biological samples comprise peripheral blood mononuclear cells (PBMCs).
4. The method of claim 1, wherein the biological samples comprise memory T cells.
5. The method of claim 1, wherein the second biological sample is obtained at least 10 days post vaccination.
6. The method of claim 1, further comprising performing multiplex PCR amplification of genomic templates comprising rearranged CDR3 regions to produce nucleic acid molecules for sequencing.
7. The method of claim 1, wherein identifying comprises calculating a false discovery rate, and wherein the calculating comprises performing a computation on a computer.

8. The method of claim 1, wherein the activated T cell clones are vaccine antigen-specific T cells.
9. The method of claim 1, wherein the activated T cell clones are CD8⁺ effector T cells.
10. The method of claim 1, wherein the vaccine is a vaccine for an infectious agent or a cancer vaccine.
11. The method of claim 10, wherein the infectious agent is a virus selected from the group consisting of yellow fever virus, influenza virus, smallpox virus, herpes simplex virus, cytomegalovirus, Epstein-Barr virus and human papilloma virus.
12. The method of claim 1, further comprising sorting the activated T cell clones in the second biological sample by flow cytometry.
13. The method of claim 1, further comprising sorting the first biological sample for memory T cells using flow cytometry.
14. The method of claim 1, further comprising:
 - performing high-throughput sequencing of nucleic acid molecules comprising rearranged CDR3 regions of TCR loci obtained from a third biological sample of the subject at a third time point post vaccination; and
 - identifying newly recruited memory T cell clones corresponding to the vaccine-induced responsive clones that are not present in the first biological sample and that have been recruited to a memory T cell population post vaccination.
15. The method of claim 14, wherein the identifying newly recruited memory T cell clones comprises sorting memory T cells by flow cytometry.
16. The method of claim 14, wherein identifying newly recruited memory T cell clones comprises comparing a first set of memory T cell clones in the first biological sample to a second set of memory T cell clones in the third biological sample to identify one or more newly

recruited memory T cell clones that have been recruited to the memory T cell population post vaccination.

17. The method of claim 16, further comprising comparing the identified one or more newly recruited memory T cell clones with one or more vaccine-induced responsive clones from the second biological sample to find matches between the newly recruited memory T cell clones and the one or more vaccine-induced responsive clones.

18. The method of claim 17, wherein the matched memory T cell clones are a significant proportion of total memory T cell population and are identified as biomarkers for vaccine-specific response.

19. The method of claim 14, wherein the memory T cell clones are $CD8^{+}CD45RO^{+}CD62L^{lo}$ effector memory T cells.

20. The method of claim 14, wherein the memory T cell clones are $CD8^{+}CD45RO^{+}CD62L^{hi}$ central memory T cells.

21. The method of claim 14, wherein the third time point is at least 30 days post vaccination.

22. The method of claim 1, wherein the method does not require an enrichment step by sorting for effector cells with flow cytometry.

23. The method of claim 14, wherein a degree of recruitment of vaccine-induced responsive clones to immunological memory is identified as a biomarker for vaccine efficacy.

24. A method of measuring T cell response to a vaccine in a subject, comprising:
performing high-throughput sequencing of nucleic acid molecules comprising rearranged CDR3 regions of TCR loci obtained from a first biological sample of the subject at a first time point post vaccination;
sorting activated T cells from a subset of the first biological sample using flow cytometry to generate a set of activated T cells;

performing high-throughput sequencing of nucleic acid molecules comprising rearranged CDR3 regions of TCR loci obtained from the set of activated T cells; and

identifying activated T cell clones in the set having CDR3 regions of significantly higher proportional abundance in the activated T cell population in comparison to the first biological sample, thereby identifying vaccine-induced responsive clones.

25. The method of claim 24, wherein the TCR loci are selected from the group consisting of the TCR α locus, TCR β locus, TCR γ locus, and TCR δ locus.

26. The method of claim 24, wherein the biological samples comprise peripheral blood mononuclear cells (PBMCs).

27. The method of claim 24, wherein the biological samples comprise memory T cells.

28. The method of claim 24, wherein the first biological sample is obtained at least 10 days post vaccination.

29. The method of claim 24, further comprising performing multiplex PCR amplification of genomic templates comprising rearranged CDR3 regions to produce nucleic acid molecules for sequencing.

30. The method of claim 24, wherein identifying comprises calculating a false discovery rate, and wherein the calculating comprises performing a computation on a computer.

31. The method of claim 24, wherein the activated T cell clones are vaccine antigen-specific T cells.

32. The method of claim 24, wherein the activated T cell clones are CD8⁺ effector T cells.

33. The method of claim 24, wherein the vaccine is a vaccine for an infectious agent or a cancer vaccine.

34. The method of claim 24, further comprising:
performing high-throughput sequencing of nucleic acid molecules comprising rearranged CDR3 regions of TCR loci obtained from a second biological sample of the subject at a second time point post vaccination; and
identifying newly recruited memory T cell clones corresponding to the vaccine-induced responsive clones that have been recruited to a memory T cell population post vaccination.
35. The method of claim 34, wherein the identifying newly recruited memory T cell clones comprises sorting memory T cells by flow cytometry.
36. The method of claim 34, wherein identifying newly recruited memory T cell clones comprises comparing a first set of memory T cell clones in the first biological sample to a second set of memory T cell clones in the second biological sample to identify one or more newly recruited memory T cell clones that have been recruited to the memory T cell population post vaccination.
37. The method of claim 36, further comprising comparing the identified one or more newly recruited memory T cell clones with one or more vaccine-induced responsive clones from the set of activated T cells to find matches between the newly recruited memory T cell clones and the one or more vaccine-induced responsive clones.
38. The method of claim 37, wherein the matched memory T cell clones are a significant number of the vaccine-induced responsive clones and are identified as biomarkers for vaccine-specific response.
39. The method of claim 37, wherein the matched memory T cell clones are a significant proportion of total memory T cell population and are identified as biomarkers for vaccine-specific response.
40. The method of claim 34, wherein the memory T cell clones are CD8⁺CD45RO⁺CD62L^{lo} effector memory T cells.

41. The method of claim 34, wherein the memory T cell clones are CD8⁺CD45RO⁺CD62L^{hi} central memory T cells.

42. The method of claim 34, wherein the second time point is at least 30 days post vaccination.

43. A method for determining the effectiveness of a vaccine comprising:

performing high-throughput sequencing of nucleic acid molecules comprising rearranged CDR3 regions of TCR loci obtained from a first biological sample of the subject at a first time point prior to vaccination;

performing high-throughput sequencing of nucleic acid molecules comprising rearranged CDR3 regions of TCR loci obtained from a second biological sample of the subject at a second time point post vaccination;

identifying T cell clones having CDR3 regions of significantly higher proportional abundance in the second biological sample in comparison to the first biological sample, thereby identifying vaccine-induced responsive clones;

performing high-throughput sequencing of nucleic acid molecules comprising rearranged CDR3 regions of TCR loci obtained from a third biological sample of the subject at a third time point post vaccination;

identifying newly recruited memory T cell clones corresponding to the vaccine-induced responsive clones that have been recruited to a memory T cell population post vaccination; and

comparing a degree of recruitment of vaccine-induced responsive clones to immunological memory to a reference degree of recruitment, wherein the vaccine is effective when the degree of recruitment is greater than or equal to the reference degree of recruitment.

44. The method of claim 43, wherein identifying newly recruited memory T cell clones comprises comparing the identified one or more newly recruited memory T cell clones with one or more vaccine-induced responsive clones from the second biological sample to find matches between the newly recruited memory T cell clones and the one or more vaccine-specific responsive clones.

45. The method of claim 43, wherein the degree of recruitment is a percentage of vaccine-induced responsive clones that match newly recruited memory T cell clones.
46. The method of claim 43, wherein the reference degree of recruitment is a degree of recruitment following a candidate vaccine.
47. The method of claim 43, wherein the reference degree of recruitment is a degree of recruitment following a reference vaccine.
48. The method of claim 43, wherein the reference degree of recruitment is a degree of recruitment following an infection.
49. A method of measuring a T cell response to an infection in a subject, comprising:
performing high-throughput sequencing of nucleic acid molecules comprising rearranged CDR3 regions of TCR loci obtained from a first biological sample of the subject at a first time point prior to infection;
performing high-throughput sequencing of nucleic acid molecules comprising rearranged CDR3 regions of TCR loci obtained from a second biological sample of the subject at a second time point after infection; and
identifying T cell clones having CDR3 regions of significantly higher proportional abundance in the second biological sample in comparison to the first biological sample, thereby identifying infection-induced responsive clones.
50. The method of claim 49, further comprising:
performing high-throughput sequencing of nucleic acid molecules comprising rearranged CDR3 regions of TCR loci obtained from a third biological sample of the subject at a third time point post infection; and
identifying newly recruited memory T cell clones corresponding to the infection-induced responsive clones that are not present in the first biological sample and that have been recruited to a memory T cell population post infection.

51. The method of claim 49, wherein identifying newly recruited memory T cell clones comprises comparing a first set of memory T cell clones in the first biological sample to a second set of memory T cell clones in the second biological sample to identify one or more newly recruited memory T cell clones that have been recruited to the memory T cell population post infection.
52. The method of claim 49, wherein the infection is selected from the group consisting of viral infection, bacterial infection, and parasitic infection.
53. The method of claim 52, wherein the viral infection is an acute viral infection.
54. A method of measuring a T cell response to an infection in a subject, comprising:
performing high-throughput sequencing of nucleic acid molecules comprising rearranged CDR3 regions of TCR loci obtained from a first biological sample of the subject at a first time point post infection;
sorting activated T cells from a subset of the first biological sample using flow cytometry to generate a set of activated T cells;
performing high-throughput sequencing of nucleic acid molecules comprising rearranged CDR3 regions of TCR loci obtained from the set of activated T cells; and
identifying activated T cell clones in the set having CDR3 regions of significantly higher proportional abundance in the activated T cell population in comparison to the first biological sample, thereby identifying infection-induced responsive clones.
55. The method of claim 54, further comprising:
performing high-throughput sequencing of nucleic acid molecules comprising rearranged CDR3 regions of TCR loci obtained from a second biological sample of the subject at a second time point post infection; and
identifying newly recruited memory T cell clones corresponding to the infection-induced responsive clones that are not present in the first biological sample and that have been recruited to a memory T cell population post infection.

56. The method of claim 55, wherein identifying newly recruited memory T cell clones comprises comparing a first set of memory T cell clones in the first biological sample to a second set of memory T cell clones in the second biological sample to identify one or more newly recruited memory T cell clones that have been recruited to the memory T cell population post infection.
57. The method of claim 54, wherein the infection is selected from the group consisting of viral infection, bacterial infection, and parasitic infection.
58. The method of claim 57, wherein the viral infection is an acute viral infection.
59. A method for measuring B cell response to a vaccine in a subject, comprising:
performing high-throughput sequencing of nucleic acid molecules comprising rearranged CDR3 regions of immunoglobulin (Ig) loci obtained from a first biological sample of the subject at a first time point prior to vaccination;
performing high-throughput sequencing of nucleic acid molecules comprising rearranged CDR3 regions of Ig loci obtained from a second biological sample of the subject at a second time point post vaccination;
clustering groups of CDR3 sequences of common descent comprising clones having undergone somatic hypermutation, wherein said clustering employs a clustering algorithm using a string distance metric; and
identifying B cell clones having CDR3 sequence clusters of significantly higher proportional abundance in the second biological sample in comparison to the first biological sample, thereby identifying vaccine-induced responsive clones.
60. The method of claim 59, wherein the Ig loci are selected from the group consisting of the Ig heavy chain (IGH) locus, Ig kappa light chain (IGK) locus, and Ig lambda light chain (IGL) locus.
61. The method of claim 55, wherein the biological samples comprise PBMCs.
62. The method of claim 59, wherein the biological samples comprise memory B cells.

63. The method of claim 59, wherein the second biological sample is obtained at least 1 day post vaccination.

64. The method of claim 59, wherein the high-throughput sequencing comprises multiplex PCR amplification of the nucleic acid molecules comprising rearranged CDR3 regions.

65. The method of claim 59, wherein identifying comprises calculating a false discovery rate, and wherein the calculating comprises performing a computation on a computer.

66. The method of claim 59, wherein the activated B cell clones are vaccine antigen-specific B cells.

67. The method of claim 59, wherein the vaccine is a vaccine for an infectious agent or a cancer vaccine.

68. The method of claim 59, further comprising:
performing high-throughput sequencing of nucleic acid molecules comprising rearranged CDR3 regions of Ig loci obtained from a third biological sample of the subject at a third time point post vaccination; and
identifying newly recruited memory B cell clones corresponding to the vaccine-induced responsive clones that are not present in the first biological sample and have been recruited to a memory B cell population post vaccination.

69. The method of claim 68, wherein the identifying comprises sorting memory B cells by flow cytometry.

70. The method of claim 68, wherein identifying comprises comparing a first set of memory B cell clones in the first biological sample to a second set of memory B cell clones in the third biological sample to identify one or more newly recruited memory B cell clones that have been recruited to the memory B cell population post vaccination.

71. The method of claim 70, further comprising comparing the identified one or more newly recruited memory B cell clones with one or more vaccine-induced responsive clones from the second biological sample to find matches between the newly recruited memory B cell clones and the one or more vaccine-induced responsive clones.
72. The method of claim 71, wherein the matched memory B cell clones are identified as biomarkers for vaccine-specific response.
73. The method of claim 68, wherein the memory B cell clones are CD19⁺CD20⁺CD38⁻CD40⁺ memory B cells.
74. The method of claim 68, wherein the memory B cell clones are non-switched memory B cells.
75. The method of claim 68, wherein the memory B cell clones are switched memory B cells.
76. The method of claim 75, wherein the switched memory B cells are IgG⁺.
77. A method of measuring B cell response to a vaccine in a subject, comprising:
performing high-throughput sequencing of nucleic acid molecules comprising rearranged CDR3 regions of Ig loci obtained from a first biological sample of the subject at a first time point post vaccination;
sorting activated B cells from a subset of the first biological sample using flow cytometry to generate a set of activated B cells;
performing high-throughput sequencing of nucleic acid molecules comprising rearranged CDR3 regions of Ig loci obtained from the set of activated B cells;
clustering groups of CDR3 sequences of common descent comprising clones having undergone somatic hypermutation, wherein said clustering employs a clustering algorithm using a string distance metric; and
identifying activated B cell clones in the set having CDR3 sequence clusters of significantly higher proportional abundance in the activated B cell population in comparison to the first biological sample, thereby identifying vaccine-induced responsive clones.

78. The method of claim 77, wherein the Ig loci are selected from the group consisting of the IGH locus, IGK locus, and IGL locus.
79. The method of claim 77, wherein the biological samples comprise peripheral blood mononuclear cells (PBMCs).
80. The method of claim 77, wherein the biological samples comprise memory B cells.
81. The method of claim 77, wherein the first biological sample is obtained at least 1 day post vaccination.
82. The method of claim 77, further comprising performing multiplex PCR amplification of genomic templates comprising rearranged CDR3 regions to produce nucleic acid molecules for sequencing.
83. The method of claim 77, wherein identifying comprises calculating a false discovery rate, and wherein the calculating comprises performing a computation on a computer.
84. The method of claim 77, wherein the activated B cell clones are vaccine antigen-specific B cells.
85. The method of claim 77, wherein the vaccine is a vaccine for an infectious agent or a cancer vaccine.
86. The method of claim 77, further comprising:
performing high-throughput sequencing of nucleic acid molecules comprising rearranged CDR3 regions of Ig loci obtained from a second biological sample of the subject at a second time point post vaccination; and
identifying newly recruited memory B cell clones corresponding to the vaccine-induced responsive clones that have been recruited to a memory B cell population post vaccination.

87. The method of claim 86, wherein the identifying newly recruited memory B cell clones comprises sorting memory B cells by flow cytometry.

88. The method of claim 86, wherein identifying newly recruited memory B cell clones comprises comparing a first set of memory B cell clones in the first biological sample to a second set of memory B cell clones in the second biological sample to identify one or more newly recruited memory B cell clones that have been recruited to the memory B cell population post vaccination.

89. The method of claim 88, further comprising comparing the identified one or more newly recruited memory B cell clones with one or more vaccine-induced responsive clones from the set of activated B cells to find matches between the newly recruited memory B cell clones and the one or more vaccine-induced responsive clones.

90. The method of claim 89, wherein the matched memory B cell clones are a significant number of the vaccine-induced responsive clones and are identified as biomarkers for vaccine-specific response.

91. The method of claim 89, wherein the matched memory B cell clones are a significant proportion of total memory B cell population and are identified as biomarkers for vaccine-specific response.

92. The method of claim 86, wherein the second time point is at least 30 days post vaccination.

93. A method for determining the effectiveness of a vaccine comprising:
performing high-throughput sequencing of nucleic acid molecules comprising rearranged CDR3 regions of immunoglobulin (Ig) loci obtained from a first biological sample of the subject at a first time point prior to vaccination;
performing high-throughput sequencing of nucleic acid molecules comprising rearranged CDR3 regions of Ig loci obtained from a second biological sample of the subject at a second time point post vaccination;

clustering groups of CDR3 sequences of common descent comprising clones having undergone somatic hypermutation, wherein said clustering employs a clustering algorithm using a string distance metric; and

identifying B cell clones having CDR3 sequence clusters of significantly higher proportional abundance in the second biological sample in comparison to the first biological sample, thereby identifying vaccine-induced responsive clones;

performing high-throughput sequencing of nucleic acid molecules comprising rearranged CDR3 regions of Ig loci obtained from a third biological sample of the subject at a third time point post vaccination;

identifying newly recruited memory B cell clones corresponding to the vaccine-induced responsive clones that are not present in the first biological sample and have been recruited to a memory B cell population post vaccination; and

comparing a degree of recruitment of vaccine-induced responsive clones to immunological memory to a reference degree of recruitment, wherein the vaccine is effective when the degree of recruitment is greater than or equal to the reference degree of recruitment.

94. The method of claim 93, wherein identifying comprises comparing the identified one or more newly recruited memory B cell clones with one or more vaccine-induced responsive clones from the second biological sample to find matches between the newly recruited memory B cell clones and the one or more vaccine-specific responsive clones.

95. The method of claim 93, wherein the degree of recruitment is a percentage of vaccine-induced responsive clones that match newly recruited memory B cell clones.

96. The method of claim 95, wherein the reference degree of recruitment is a degree of recruitment following a candidate vaccine.

97. The method of claim 93, wherein the reference degree of recruitment is a degree of recruitment following a reference vaccine.

98. The method of claim 93, wherein the reference degree of recruitment is a degree of recruitment following an infection.

99. A method of measuring a B cell response to an infection in a subject, comprising:
- performing high-throughput sequencing of nucleic acid molecules comprising rearranged CDR3 regions of immunoglobulin (Ig) loci obtained from a first biological sample of the subject at a first time point prior to infection;
 - performing high-throughput sequencing of nucleic acid molecules comprising rearranged CDR3 regions of Ig loci obtained from a second biological sample of the subject at a second time point post infection;
 - clustering groups of CDR3 sequences of common descent comprising clones having undergone somatic hypermutation, wherein said clustering employs a clustering algorithm using a string distance metric; and
 - identifying B cell clones having CDR3 sequence clusters of significantly higher proportional abundance in the second biological sample in comparison to the first biological sample, thereby identifying vaccine-induced responsive clones.
100. The method of claim 99, further comprising:
- performing high-throughput sequencing of nucleic acid molecules comprising rearranged CDR3 regions of Ig loci obtained from a third biological sample of the subject at a third time point post infection; and
 - identifying newly recruited memory B cell clones corresponding to the infection-induced responsive clones that are not present in the first biological sample and have been recruited to a memory B cell population post infection.
101. The method of claim 100, wherein identifying newly recruited memory B cell clones comprises comparing a first set of memory B cell clones in the first biological sample to a second set of memory B cell clones in the second biological sample to identify one or more newly recruited memory T cell clones that have been recruited to the memory B cell population post infection.
102. The method of claim 99, wherein the infection is selected from the group consisting of viral infection, bacterial infection, and parasitic infection.
103. The method of claim 102, wherein the viral infection is an acute viral infection.

104. A method of measuring B cell response to an acute viral infection in a subject, comprising:

- performing high-throughput sequencing of nucleic acid molecules comprising rearranged CDR3 regions of Ig loci obtained from a first biological sample of the subject at a first time point post infection;

- sorting activated B cells from a subset of the first biological sample using flow cytometry to generate a set of activated B cells;

- performing high-throughput sequencing of nucleic acid molecules comprising rearranged CDR3 regions of Ig loci obtained from the set of activated B cells;

- clustering groups of CDR3 sequences of common descent comprising clones having undergone somatic hypermutation, wherein said clustering employs a clustering algorithm using a string distance metric; and

- identifying activated B cell clones having CDR3 sequence clusters of significantly higher proportional abundance in the activated B cell population in comparison to the first biological sample, thereby identifying infection-induced responsive clones.

105. The method of claim 104, further comprising:

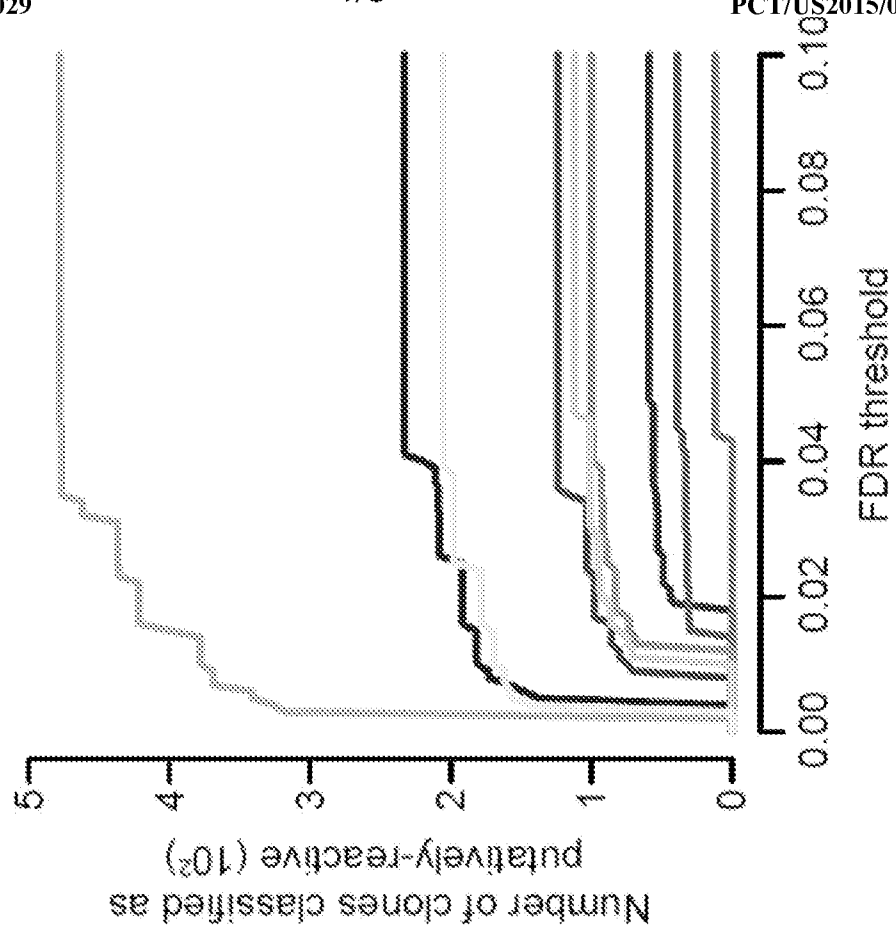
- performing high-throughput sequencing of nucleic acid molecules comprising rearranged CDR3 regions of Ig loci obtained from a second biological sample of the subject at a second time point post infection; and

- identifying newly recruited memory B cell clones corresponding to the infection-induced responsive clones that have been recruited to a memory B cell population post infection.

106. The method of claim 105, wherein identifying newly recruited memory B cell clones comprises comparing a first set of memory B cell clones in the first biological sample to a second set of memory B cell clones in the third biological sample to identify one or more newly recruited memory B cell clones that have been recruited to the memory B cell population post infection.

107. The method of claim 104, wherein the infection is selected from the group consisting of viral infection, bacterial infection, and parasitic infection.

108. The method of claim 107, wherein the viral infection is an acute viral infection.



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FIG. 2

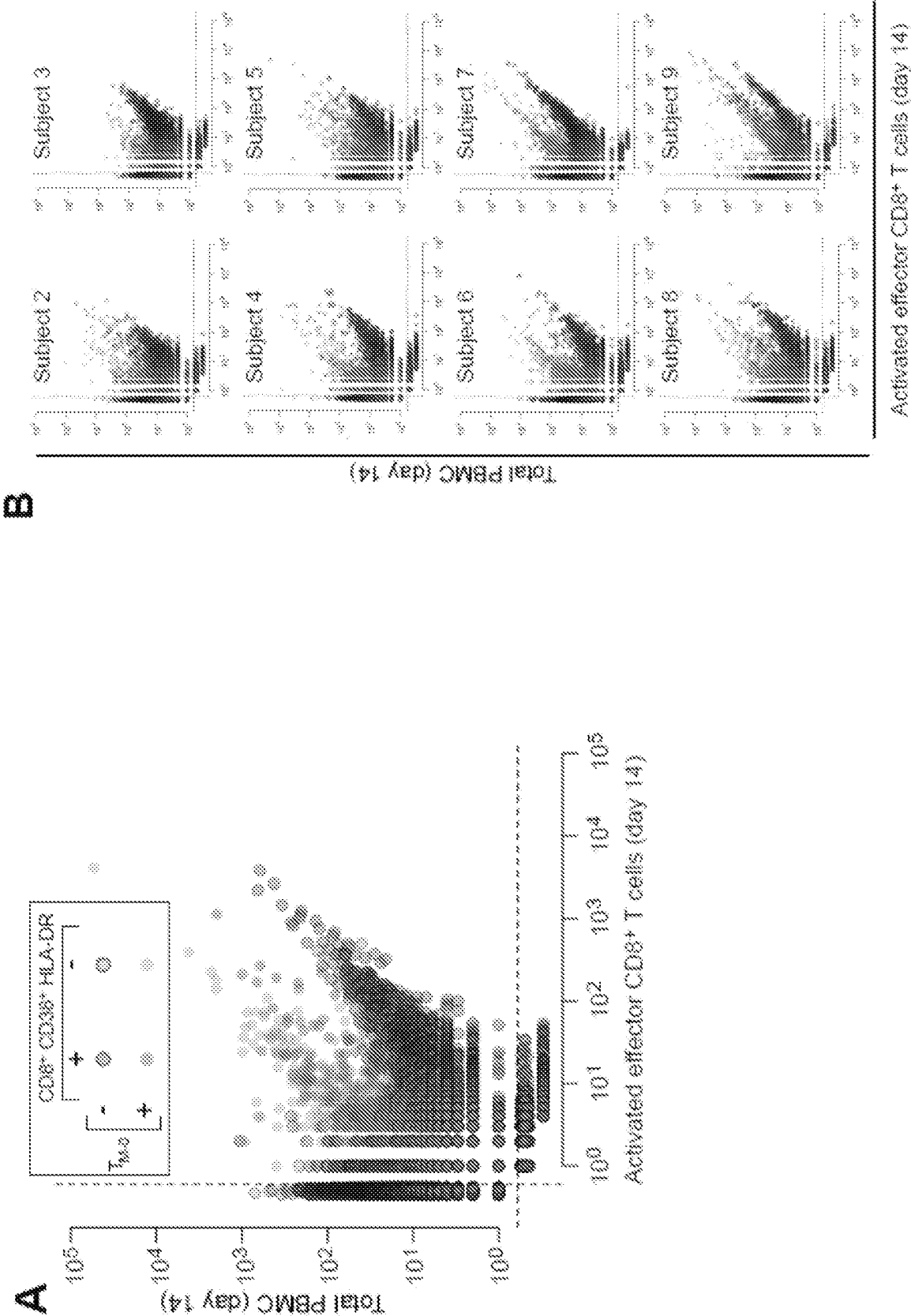


FIG. 3

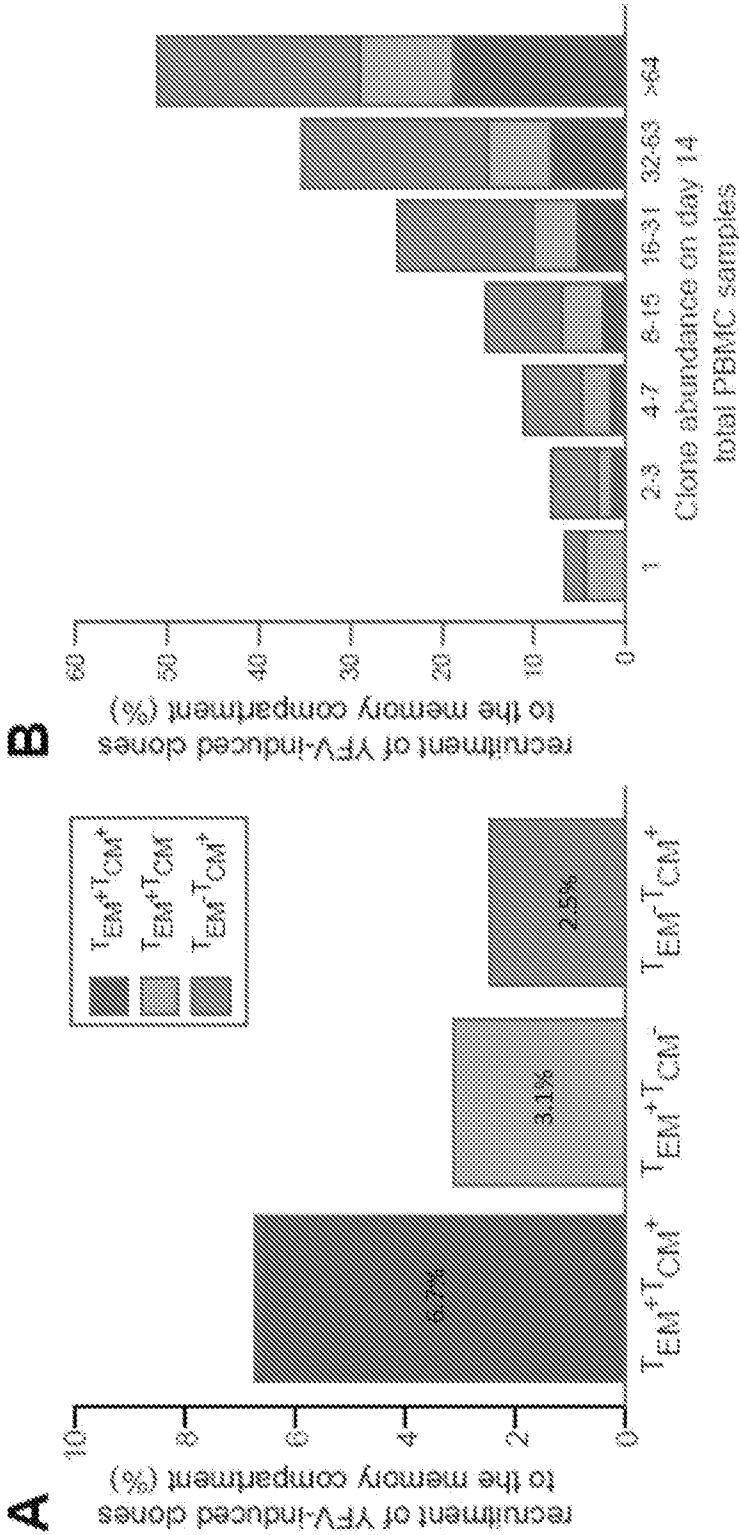


FIG. 4

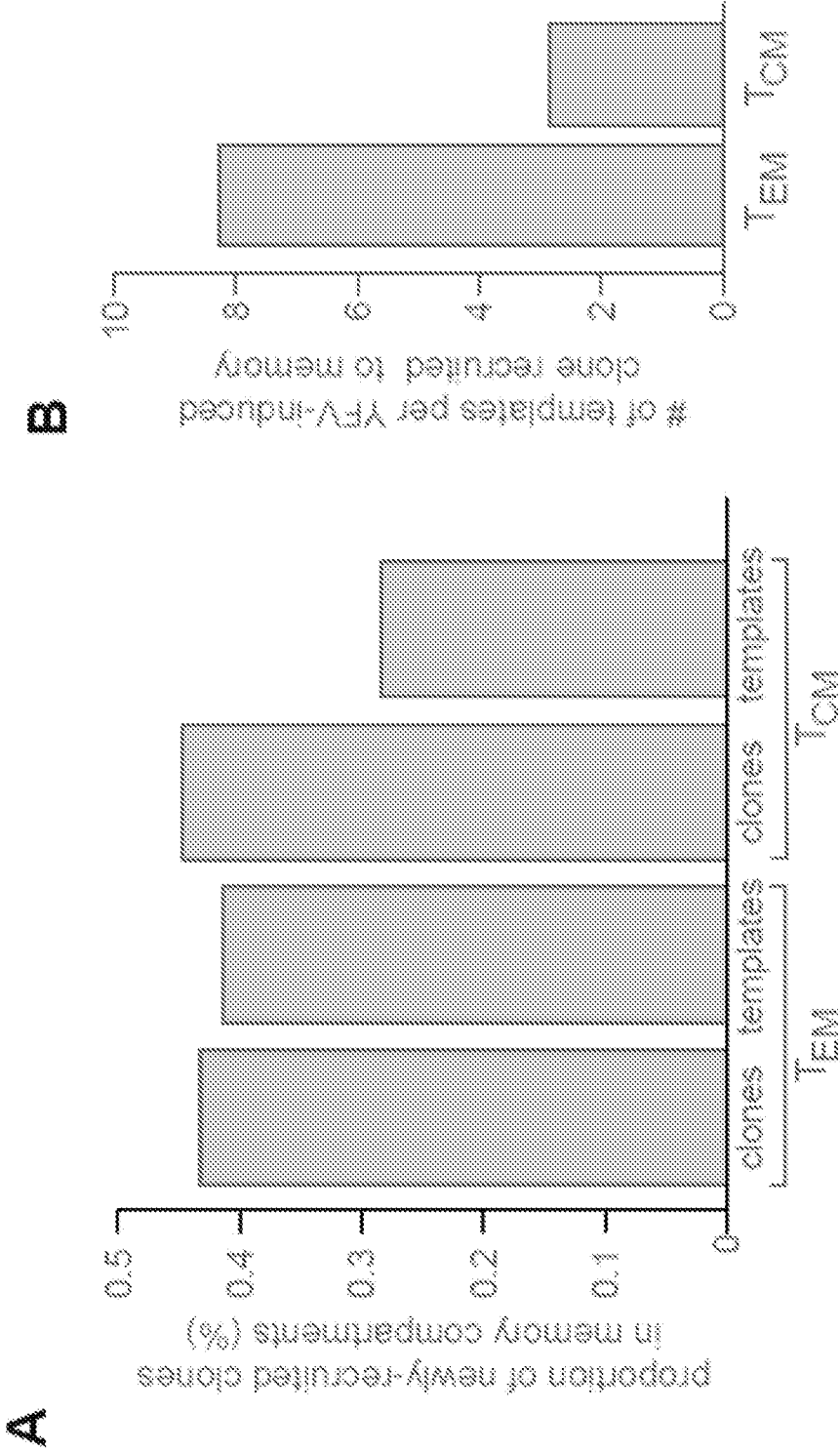
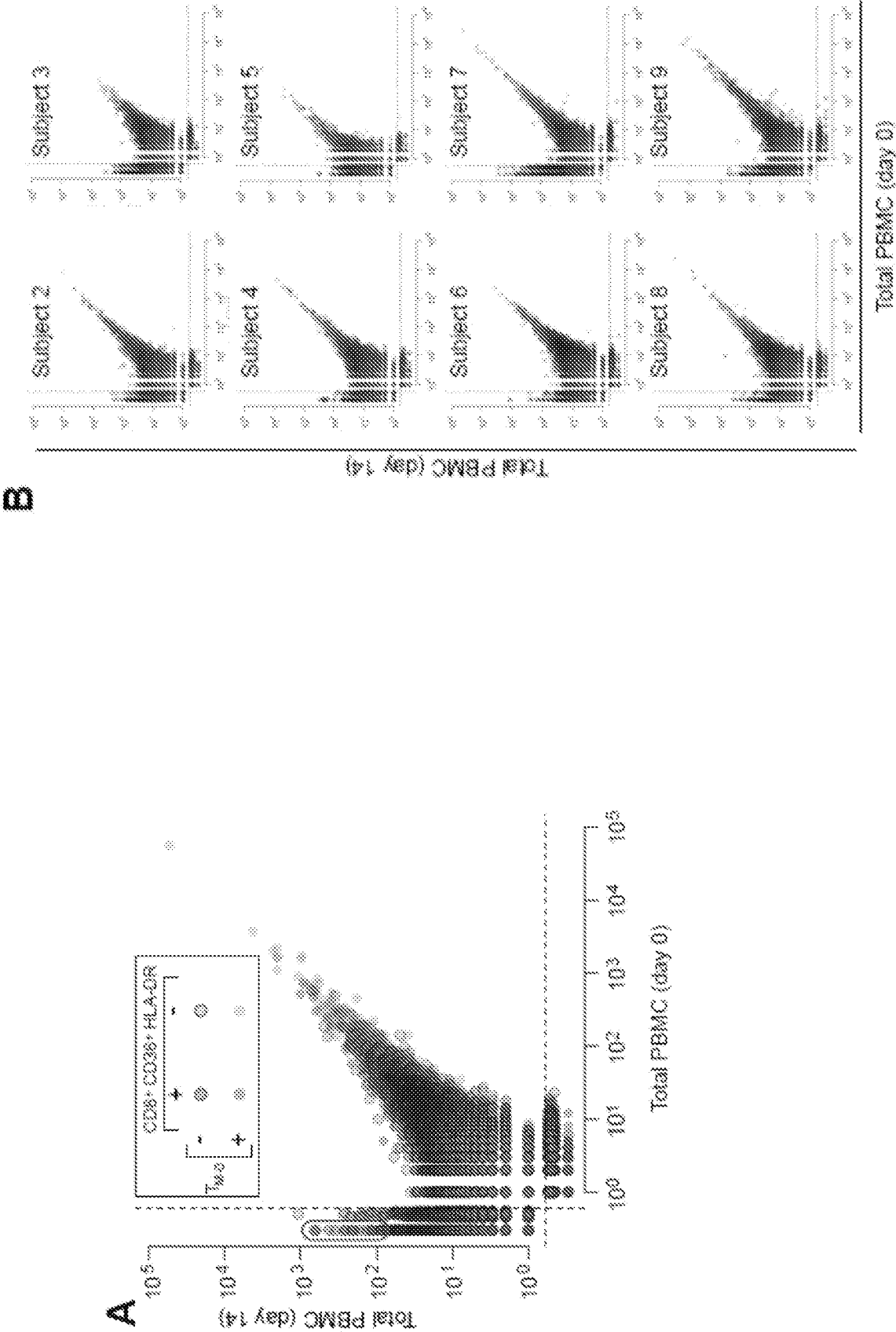


FIG. 5



INTERNATIONAL SEARCH REPORT

International application No.

PCT/US 15/62494

A. CLASSIFICATION OF SUBJECT MATTER

IPC(8) - C12Q 1/68, G01N 33/53, G06F 19/22 (2016.01)

CPC - C12Q 1/6869, C12Q 2600/106, G06F 19/22

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC(8) - C12Q 1/68, G01N 33/53, G06F 19/22 (2016.01)

CPC - C12Q 1/6869, C12Q 2600/106, G06F 19/22

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

CPC - C12Q 1/68, G01N 33/53, C12Q 2600/156

(keyword limited; terms below)

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

PatBase, Google Patents, Google Scholar

Search terms: T cell, T lymphocyte, TCR, T cell receptor, CDR3, rearrange, vaccine, abundance, clone, clonality, memory, vaccine-induced, vaccine-elicited, induce, elicit, recruit, repertoire, cluster, clustering, infection, high-throughput sequencing, time point

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X --- Y	WO 2014/055561 A1 (ADAPTIVE BIOTECHNOLOGIES CORP et al.) 10 April 2014 (10.04.2014) para [0003], [0005], [0044], [0047], [0048], [0068], [0069], [0070], [0073], [00124], [00127], [00128], [00131], [00144], [00145], [00157], [00226]	1-16, 19-22, 24-36, 40-43, 49-58 ----- 17-18, 23, 37-39, 44-48
Y	SPEISER et al., A novel approach to characterize clonality and differentiation of human melanoma-specific T cell responses: spontaneous priming and efficient boosting by vaccination. J Immunol. 10 July 2006, Vol 177, No 2, pp 1338-48. Especially abstract; p 1339, col 1, para 2.	17-18, 23, 37-39, 44-48

☐ Further documents are listed in the continuation of Box C.

* Special categories of cited documents:

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier application or patent but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

"&" document member of the same patent family

Date of the actual completion of the international search

19 march 2016

Date of mailing of the international search report

31 MAR 2016

Name and mailing address of the ISA/US

Mail Stop PCT, Attn: ISA/US, Commissioner for Patents
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Facsimile No. 571-273-8300

Authorized officer:

Lee W. Young

PCT Helpdesk: 571-272-4300
PCT OSP: 571-272-7774

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US 15/62494

Box No. II Observations where certain claims were found unsearchable (Continuation of item 2 of first sheet)

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claims Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box No. III Observations where unity of invention is lacking (Continuation of item 3 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

This application contains the following inventions or groups of inventions which are not so linked as to form a single general inventive concept under PCT Rule 13.1. In order for all inventions to be examined, the appropriate additional examination fees must be paid.

Group I: Claims 1-58, drawn to methods of measuring T cell response to a vaccine or infection, or determining vaccine effectiveness

Group II: Claims 59-108, drawn to methods of measuring B cell response to a vaccine or infection, or determining vaccine effectiveness

-----please see continuation on extra sheet-----

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying additional fees, this Authority did not invite payment of additional fees.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:
1-58

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest and, where applicable, the payment of a protest fee.
- ☐ The additional search fees were accompanied by the applicant's protest but the applicable protest fee was not paid within the time limit specified in the invitation.
- ☐ No protest accompanied the payment of additional search fees.

Continuation of: Box No. III Observations where unity of invention is lacking
The inventions listed as Groups I and II do not relate to a single general inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons:

Special Technical Features

Group I requires analysis of T cells, sequencing of TCR loci, and sorting activated T cells from a subset of the first biological sample using flow cytometry to generate a set of activated T cells; not required by Group II.

Group II requires analysis of B cells, sequencing of Ig loci, and clustering groups of CDR3 sequences of common descent comprising clones having undergone somatic hypermutation, wherein said clustering employs a clustering algorithm using a string distance metric; not required by Group I.

Common Technical Features

The feature shared by Groups I and II is [claims 1, 59] a method of measuring T or B cell response to a vaccine in a subject, comprising: performing high-throughput sequencing of nucleic acid molecules comprising rearranged CDR3 regions of TCR or immunoglobulin (Ig) loci obtained from a first biological sample of the subject at a first time point prior to vaccination; performing high-throughput sequencing of nucleic acid molecules comprising rearranged CDR3 regions of TCR or Ig loci obtained from a second biological sample of the subject at a second time point post vaccination; and identifying T or B cell clones having CDR3 regions of significantly higher proportional abundance in the second biological sample in comparison to the first biological sample, thereby identifying vaccine-induced responsive clones.

Another feature shared by Groups I and II is [claims 24, 77] a method of measuring T or B cell response to a vaccine in a subject, comprising: performing high-throughput sequencing of nucleic acid molecules comprising rearranged CDR3 regions of TCR or Ig loci obtained from a first biological sample of the subject at a first time point post vaccination; sorting activated T or B cells from a subset of the first biological sample using flow cytometry to generate a set of activated T or B cells; performing high-throughput sequencing of nucleic acid molecules comprising rearranged CDR3 regions of TCR or Ig loci obtained from the set of activated T or B cells; and identifying activated T cell or B cell clones in the set having CDR3 regions of significantly higher proportional abundance in the activated T or B cell population in comparison to the first biological sample, thereby identifying vaccine-induced responsive clones.

Another feature shared by Groups I and II is [claims 43, 93] a method for determining the effectiveness of a vaccine comprising: performing high-throughput sequencing of nucleic acid molecules comprising rearranged CDR3 regions of TCR or Ig loci obtained from a first biological sample of the subject at a first time point prior to vaccination; performing high-throughput sequencing of nucleic acid molecules comprising rearranged CDR3 regions of TCR or Ig loci obtained from a second biological sample of the subject at a second time point post vaccination; performing high-throughput sequencing of nucleic acid molecules comprising rearranged CDR3 regions of TCR or Ig loci obtained from a third biological sample of the subject at a third time point post vaccination; identifying newly recruited memory T or B cell clones corresponding to the vaccine-induced responsive clones that are not present in the first biological sample and have been recruited to a memory T or B cell population post vaccination; and comparing a degree of recruitment of vaccine-induced responsive clones to immunological memory to a reference degree of recruitment, wherein the vaccine is effective when the degree of recruitment is greater than or equal to the reference degree of recruitment.

Another feature shared by Groups I and II is [claims 49, 99] a method of measuring a T or B cell response to an infection in a subject, comprising: performing high-throughput sequencing of nucleic acid molecules comprising rearranged CDR3 regions of TCR or Ig loci obtained from a first biological sample of the subject at a first time point prior to infection; performing high-throughput sequencing of nucleic acid molecules comprising rearranged CDR3 regions of TCR or Ig loci obtained from a second biological sample of the subject at a second time point after infection; and identifying T or B cell clones having CDR3 regions of significantly higher proportional abundance in the second biological sample in comparison to the first biological sample, thereby identifying infection-induced responsive clones.

Another feature shared by Groups I and II is [claims 54, 104] a method of measuring a T or B cell response to an infection in a subject, comprising: performing high-throughput sequencing of nucleic acid molecules comprising rearranged CDR3 regions of TCR or Ig loci obtained from a first biological sample of the subject at a first time point post infection; sorting activated T or B cells from a subset of the first biological sample using flow cytometry to generate a set of activated T cells; performing high-throughput sequencing of nucleic acid molecules comprising rearranged CDR3 regions of TCR or Ig loci obtained from the set of activated T or B cells; and identifying activated T or B cell clones in the set having CDR3 regions of significantly higher proportional abundance in the activated T or B cell population in comparison to the first biological sample, thereby identifying infection-induced responsive clones.

However, these shared technical features do not represent a contribution over prior art, because the shared technical features are taught by WO 2014/055561 A1 (Adaptive Biotechnologies Corp et al., 10 April 2014, to Robins) (hereinafter 'Robins').

Robins discloses [for claims 1, 59] a method of measuring T or B cell response to a vaccine in a subject (para [0048] "the method includes steps for managing a treatment of said test subject who is undergoing immunotherapy based on a determination of said immunological status of said test subject. In one embodiment, the immunotherapy comprises ?.. a vaccine"; para [0068] "determining the immunological status of a subject or of a plurality of subjects, including by qualitatively (e.g., by T cell receptor or immunoglobulin sequence diversity) and quantitatively (e.g., by TCR or IG sequence distribution) characterizing adaptive immune cell (e.g., T cell or B cell) clonality, from which immunocompetence of an individual's adaptive immune system can be assessed"; para [0003] "assessment of immunocompetence of a subject's adaptive immune system by highly sensitive, high throughput DNA sequence-based quantification of the diversity and frequency of occurrence (e.g., clonal expansion) of adaptive immune cells having a particular rearranged T cell receptor (TCR) or immunoglobulin (IG or Ig) encoding gene sequence. Information about the immunological status of a subject or a population of subjects can be used, for example, to characterize ... likelihood of responding to immunotherapy"), comprising:
performing high-throughput sequencing of nucleic acid molecules comprising rearranged CDR3 regions of TCR or immunoglobulin (Ig) loci (para [0068]; para [0069] "The present embodiments for the first time permit high resolution, large-scale, high throughput assessment of immunocompetence by characterization at the DNA sequence level of (i) TCR and IG repertoire diversity, and (ii) TCR and IG repertoire distribution"; para [00157] "A multiplex PCR system can be used to amplify rearranged adaptive immune cell receptor loci from genomic DNA, preferably from a CDR3 region. In certain embodiments, the CDR3 region is amplified from a TCRA, TCRP,

-----please see continuation on next extra sheet-----

Continuation of: Box No. III Observations where unity of invention is lacking

TCRgamma or TCR5 CDR3 region or similarly from an IgH or IgL (lambda or kappa) locus"; para [0070] "The multiplex PCR amplification products are amenable to rapid, high throughput, high quality quantitative DNA sequencing. Structural TCR or IG repertoire diversity in the sample is determined by identifying a plurality of unique rearranged DNA sequences from the DNA sequence information, and therefrom determining the total number of unique sequences in the sample") obtained from a first biological sample of the subject at a first time point prior to vaccination (para [0047] "In another aspect, the plurality of time points comprise time points prior to immunotherapy"; para [00128] "immunotherapy can comprise treatment with an immunotherapy agent, such as ... a vaccine");

performing high-throughput sequencing of nucleic acid molecules comprising rearranged CDR3 regions of TCR or Ig loci (para [0068]-[0070], [00157]) obtained from a second biological sample of the subject at a second time point post vaccination (para [0047] "In other aspects, the plurality of time points comprise timepoints during or after immunotherapy"; para [00128] "immunotherapy can comprise treatment with an immunotherapy agent, such as ... a vaccine"); and

identifying T or B cell clones having CDR3 regions of significantly higher proportional abundance in the second biological sample in comparison to the first biological sample, thereby identifying vaccine-induced responsive clones (para [0073] "By way of non-limiting theory, this sequence distribution can represent the degree of T cell or B cell clonality in each sample from a patient (e.g., quantitative degree of representation, or relative abundance) ... The distribution and diversity values can be used in a rating step to rate individual samples and compare them to a control sample and/or to one another"; para [00226] "In Figure 8, the dynamics of individual TCR clonal representations were investigated as a function of time in blood samples and in tumor samples obtained prior to immunotherapy ... The arrow at timepoint CT indicates a single clone that was unremarkable in its relative abundance prior to therapy, but that increased in relative frequency in tumor samples post-therapy, to account for 10 percent of the repertoire at timepoint CT. Two clones (X1 and X2) that each accounted for 7-9 percent of TCR sequences in blood at timepoints A and B subsequently declined significantly in relative abundance, while several T cell receptor sequences that initially had very low frequencies in blood increased significantly by timepoint C"; para [00128] "immunotherapy can comprise treatment with an immunotherapy agent, such as ... a vaccine").

Robins further discloses [for claims 24, 77] a method of measuring T or B cell response to a vaccine in a subject (para [0048] "the method includes steps for managing a treatment of said test subject who is undergoing immunotherapy based on a determination of said immunological status of said test subject. In one embodiment, the immunotherapy comprises ... a vaccine"; para [0068] "determining the immunological status of a subject or of a plurality of subjects, including by qualitatively (e.g., by T cell receptor or immunoglobulin sequence diversity) and quantitatively (e.g., by TCR or IG sequence distribution) characterizing adaptive immune cell (e.g., T cell or B cell) clonality, from which immunocompetence of an individual's adaptive immune system can be assessed"; para [0003] "assessment of immunocompetence of a subject's adaptive immune system by highly sensitive, high throughput DNA sequence-based quantification of the diversity and frequency of occurrence (e.g., clonal expansion) of adaptive immune cells having a particular rearranged T cell receptor (TCR) or immunoglobulin (IG or Ig) encoding gene sequence. Information about the immunological status of a subject or a population of subjects can be used, for example, to characterize ... likelihood of responding to immunotherapy"), comprising:

performing high-throughput sequencing of nucleic acid molecules comprising rearranged CDR3 regions of TCR or Ig loci (para [0069] "The present embodiments for the first time permit high resolution, large-scale, high throughput assessment of immunocompetence by characterization at the DNA sequence level of (i) TCR and IG repertoire diversity, and (ii) TCR and IG repertoire distribution"; para [00157] "A multiplex PCR system can be used to amplify rearranged adaptive immune cell receptor loci from genomic DNA, preferably from a CDR3 region. In certain embodiments, the CDR3 region is amplified from a TCRA, TCRP, TCRgamma or TCR5 CDR3 region or similarly from an IgH or IgL (lambda or kappa) locus"; para [0070] "The multiplex PCR amplification products are amenable to rapid, high throughput, high quality quantitative DNA sequencing. Structural TCR or IG repertoire diversity in the sample is determined by identifying a plurality of unique rearranged DNA sequences from the DNA sequence information, and therefrom determining the total number of unique sequences in the sample") obtained from a first biological sample of the subject at a first time point post vaccination (para [0047] "In another aspect, the plurality of time points comprise timepoints prior to immunotherapy"; para [00128] "immunotherapy can comprise treatment with an immunotherapy agent, such as ... a vaccine").

Robins does not specifically teach further sorting activated T or B cells from a subset of the first biological sample using flow cytometry to generate a set of activated T or B cells; performing high-throughput sequencing of nucleic acid molecules comprising rearranged CDR3 regions of TCR or Ig loci obtained from the set of activated T or B cells; and identifying activated T or B cell clones in the set having CDR3 regions of significantly higher proportional abundance in the activated T or B cell population in comparison to the first biological sample, thereby identifying vaccine-induced responsive clones.

However, Robins does teach that T or B cell samples can be prepared by flow cytometry sorting that uses antibodies specific to known T and B cell surface markers (para [00144] "In certain related embodiments, preparations that comprise predominantly lymphocytes (e.g., T and B cells) or that comprise predominantly T cells or predominantly B cells, can be prepared for use as a biological sample as provided herein ... Various methods and commercially available kits for isolating different subpopulations of T and B cells are known in the art and include, but are not limited to subset selection immunomagnetic bead separation or flow immunocytometric cell sorting using antibodies specific for one or more of any of a variety of known T and B cell surface markers ... [Markers are used to] determine T, B, and monocyte lineages and subpopulations in flow cytometry"), and further teaches that a marker indicative of activated T cells is known (para [00136] "LAG-3 (CD223) is a cell surface molecule expressed on activated T cells"). Thus, sorting activated T or B cells from a subset of the first biological sample using flow cytometry to generate a set of activated T or B cells would have been obvious in view of the teaching of Robins.

Further, Robins teaches performing high-throughput sequencing of nucleic acid molecules comprising rearranged CDR3 regions of TCR or Ig loci (para [0068]-[0070], [00157]) to identify T or B cell clones having CDR3 regions of significantly higher proportional abundance in a second biological sample in comparison to a first biological sample (para [0073] "By way of non-limiting theory, this sequence distribution can represent the degree of T cell or B cell clonality in each sample from a patient (e.g., quantitative degree of representation, or relative abundance) ... The distribution and diversity values can be used in a rating step to rate individual samples and compare them to a control sample and/or to one another"; para [00226] "In Figure 8, the dynamics of individual TCR clonal representations were investigated as a function of time in blood samples and in tumor samples obtained prior to immunotherapy ... The arrow at time point CT indicates a single clone that was unremarkable in its relative abundance prior to therapy, but that increased in relative frequency in tumor samples post-therapy, to account for 10 percent of the repertoire at timepoint CT. Two clones (X1 and X2) that each accounted for 7-9 percent of TCR sequences in blood at timepoints A and B subsequently declined significantly in relative abundance, while several T cell receptor sequences that initially had very low frequencies in blood increased significantly by timepoint C"; para [00128] "immunotherapy can comprise treatment with an immunotherapy agent, such as ... a vaccine"). One of ordinary skill in the art would have readily appreciated that the set of activated T or B cells obtained by flow cytometry sorting as discussed above can -----please see continuation on next extra sheet-----

Continuation of: Box No. III Observations where unity of invention is lacking

be subjected to the high-throughput sequencing step in order to identify clones having rearranged CDR3 regions of TCR or Ig loci that are indicative of activated T or B cells in order to assess the subject's immunocompetence to respond to a vaccine. Thus, one of ordinary skill in the art in view of the teaching of Robins would have found it obvious to perform high-throughput sequencing of nucleic acid molecules comprising rearranged CDR3 regions of TCR or Ig loci obtained from the set of activated T or B cells; and identify activated T or B cell clones in the set having CDR3 regions of significantly higher proportional abundance in the activated T or B cell population in comparison to the first biological sample, thereby identifying vaccine-induced responsive clones.

Robins further discloses [for claims 43, 93] a method for determining the effectiveness of a vaccine (para [0048] "the method includes steps for managing a treatment of said test subject who is undergoing immunotherapy based on a determination of said immunological status of said test subject. In one embodiment, the immunotherapy comprises ? a vaccine"; para [0068] "determining the immunological status of a subject or of a plurality of subjects, including by qualitatively (e.g., by T cell receptor or immunoglobulin sequence diversity) and quantitatively (e.g., by TCR or IG sequence distribution) characterizing adaptive immune cell (e.g., T cell or B cell) clonality, from which immunocompetence of an individual's adaptive immune system can be assessed"; para [0003] "assessment of immunocompetence of a subject's adaptive immune system by highly sensitive, high throughput DNA sequence-based quantification of the diversity and frequency of occurrence (e.g., clonal expansion) of adaptive immune cells having a particular rearranged T cell receptor (TCR) or immunoglobulin (IG or Ig) encoding gene sequence. Information about the immunological status of a subject or a population of subjects can be used, for example, to characterize ... likelihood of responding to immunotherapy") comprising: performing high-throughput sequencing of nucleic acid molecules comprising rearranged CDR3 regions of TCR or Ig loci (para [0068]; para [0069] "The present embodiments for the first time permit high resolution, large-scale, high throughput assessment of immunocompetence by characterization at the DNA sequence level of (i) TCR and IG repertoire diversity, and (ii) TCR and IG repertoire distribution"; para [00157] "A multiplex PCR system can be used to amplify rearranged adaptive immune cell receptor loci from genomic DNA, preferably from a CDR3 region. In certain embodiments, the CDR3 region is amplified from a TCR α , TCR β , TCR γ or TCR δ CDR3 region or similarly from an IgH or IgL (lambda or kappa) locus"; para [0070] "The multiplex PCR amplification products are amenable to rapid, high throughput, high quality quantitative DNA sequencing. Structural TCR or IG repertoire diversity in the sample is determined by identifying a plurality of unique rearranged DNA sequences from the DNA sequence information, and therefrom determining the total number of unique sequences in the sample") obtained from a first biological sample of the subject at a first time point prior to vaccination (para [0047] "In another aspect, the plurality of time points comprise timepoints prior to immunotherapy"; para [00128] "immunotherapy can comprise treatment with an immunotherapy agent, such as ... a vaccine");

performing high-throughput sequencing of nucleic acid molecules comprising rearranged CDR3 regions of TCR or Ig loci (para [0068]-[0070], [00157]) obtained from a second biological sample of the subject at a second time point post vaccination (para [0047] "In other aspects, the plurality of time points comprise timepoints during ... immunotherapy"; para [00128] "immunotherapy can comprise treatment with an immunotherapy agent, such as ... a vaccine");

performing high-throughput sequencing of nucleic acid molecules comprising rearranged CDR3 regions of TCR or Ig loci (para [0068]-[0070], [00157]) obtained from a third biological sample of the subject at a third time point post vaccination (para [0047] "In other aspects, the plurality of time points comprise timepoints ... after immunotherapy"; para [00128] "immunotherapy can comprise treatment with an immunotherapy agent, such as ... a vaccine");

identifying newly recruited memory T or B cell clones corresponding to the vaccine-induced responsive clones that are not present in the first biological sample and have been recruited to a memory T cell or B cell population post vaccination (para [00226] "In Figure 8, the dynamics of individual TCR clonal representations were investigated as a function of time in blood samples and in tumor samples obtained prior to immunotherapy ... The arrow at timepoint CT indicates a single clone that was unremarkable in its relative abundance prior to therapy, but that increased in relative frequency in tumor samples post-therapy, to account for 10 percent of the repertoire at timepoint CT. Two clones (X1 and X2) that each accounted for 7- 9 percent of TCR sequences in blood at timepoints A and B subsequently declined significantly in relative abundance, while several T cell receptor sequences that initially had very low frequencies in blood increased significantly by timepoint C"; para [00128] "immunotherapy can comprise treatment with an immunotherapy agent, such as ... a vaccine"); and

comparing a degree of recruitment of vaccine-induced responsive clones to immunological memory to a reference degree of recruitment, wherein the vaccine is effective when the degree of recruitment is greater than or equal to the reference degree of recruitment.

(para [0073] "By way of non-limiting theory, this sequence distribution can represent the degree of T cell or B cell clonality in each sample from a patient (e.g., quantitative degree of representation, or relative abundance) ... The distribution and diversity values can be used in a rating step to rate individual samples and compare them to a control sample and/or to one another"; para [0075] "In blood samples obtained from patients before and after immunotherapy ... a high TCR sequence diversity and low clonality in the blood of the patient correlated with positive clinical outcomes. On the other hand, a TCR repertoire that was characterized by a low TCR sequence diversity (high clonality) and a lower entropy of TCR sequence distribution was associated with poorer clinical outcomes that were attributable to compromised adaptive immune capability").

Robins further discloses [for claims 49, 99] a method of measuring a T cell or B cell response to an infection in a subject (para [0003] "The present disclosure relates generally to assessment of immunocompetence of a subject's adaptive immune system by highly sensitive, high throughput DNA sequence-based quantification of the diversity and frequency of occurrence (e.g., clonal expansion) of adaptive immune cells having a particular rearranged T cell receptor (TCR) or immunoglobulin (IG or Ig) encoding gene sequence. Information about the immunological status of a subject or a population of subjects can be used, for example, to characterize an individual or to stratify a patient population with respect to ability to mount an immune response"), comprising:

performing high-throughput sequencing of nucleic acid molecules comprising rearranged CDR3 regions of TCR or Ig loci obtained from a first biological sample of the subject at a first time point prior to infection (para [00190] "Blood samples were collected at 0, 28, 56, 100, 180, and 360 days post transplant. ... T cell clonal expansion and contraction of hundreds of thousands of T cell clones were tracked over time and TCR repertoire diversity was directly measured ... diversity of the T cell repertoire is a measure of immunocompetence, as a clinical application of high-throughput sequencing. Of the 34 patients, six patients died between Day 100 and Day 360 of infectious cause. At both Day 56 and Day 100, the diversity of the T cell repertoire of each of these six patients was far lower than the average of the remaining patients (P -value = 0.015). By two months after transplant, TCR diversity accurately predicted risk of death due to infection"; para [0068] "determining the immunological status of a subject or of a plurality of subjects, including by qualitatively (e.g., by T cell receptor or immunoglobulin sequence diversity) and quantitatively (e.g., by TCR or IG sequence distribution) characterizing adaptive immune cell (e.g., T cell or B cell) clonality, from which immunocompetence of an individual's adaptive immune system can be

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Continuation of: Box No. III Observations where unity of invention is lacking

assessed"; para [0069] "The present embodiments for the first time permit high resolution, large-scale, high throughput assessment of immunocompetence by characterization at the DNA sequence level of (i) TCR and IG repertoire diversity, and (ii) TCR and IG repertoire distribution");

performing high-throughput sequencing of nucleic acid molecules comprising rearranged CDR3 regions of TCR or Ig loci obtained from a second biological sample of the subject at a second time point after infection (para [00190], [0068]-[0069]); and identifying T or B cell clones having CDR3 regions of significantly higher proportional abundance in the second biological sample in comparison to the first biological sample, thereby identifying infection-induced responsive clones (para [0073] "By way of non-limiting theory, this sequence distribution can represent the degree of T cell or B cell clonality in each sample from a patient (e.g., quantitative degree of representation, or relative abundance) ... The distribution and diversity values can be used in a rating step to rate individual samples and compare them to a control sample and/or to one another"; para [0074] "a relatively low degree of TCR repertoire diversity in patients following the cord blood transplant was shown to be a predictor of the relative likelihood of susceptibility to infection and of the immunological inability to clear the infection (e.g., poor response). On the other hand, a relatively high degree of TCR repertoire diversity in human patients following cord blood transplant to treat hematologic malignancies was shown to be a predictor of the relative likelihood of resistance to infection and of immunocompetence, i.e., the immunological ability to clear the infection").

Robins further discloses [for claims 54, 104] a method of measuring a T or B cell response to an infection in a subject (para [0003] "The present disclosure relates generally to assessment of immunocompetence of a subject's adaptive immune system by highly sensitive, high throughput DNA sequence-based quantification of the diversity and frequency of occurrence (e.g., clonal expansion) of adaptive immune cells having a particular rearranged T cell receptor (TCR) or immunoglobulin (IG or Ig) encoding gene sequence. Information about the immunological status of a subject or a population of subjects can be used, for example, to characterize an individual or to stratify a patient population with respect to ability to mount an immune response"), comprising:

performing high-throughput sequencing of nucleic acid molecules comprising rearranged CDR3 regions of TCR or Ig loci obtained from a first biological sample of the subject at a first time point post infection (para [00190] "Blood samples were collected at 0, 28, 56, 100, 180, and 360 days post transplant. ... T cell clonal expansion and contraction of hundreds of thousands of T cell clones were tracked over time and TCR repertoire diversity was directly measured ... diversity of the T cell repertoire is a measure of immunocompetence, as a clinical application of high-throughput sequencing. Of the 34 patients, six patients died between Day 100 and Day 360 of infectious cause. At both Day 56 and Day 100, the diversity of the T cell repertoire of each of these six patients was far lower than the average of the remaining patients (P-value = 0.015). By two months after transplant, TCR diversity accurately predicted risk of death due to infection"; para [0068] "determining the immunological status of a subject or of a plurality of subjects, including by qualitatively (e.g., by T cell receptor or immunoglobulin sequence diversity) and quantitatively (e.g., by TCR or IG sequence distribution) characterizing adaptive immune cell (e.g., T cell or B cell) clonality, from which immunocompetence of an individual's adaptive immune system can be assessed"; para [0069] "The present embodiments for the first time permit high resolution, large-scale, high throughput assessment of immunocompetence by characterization at the DNA sequence level of (i) TCR and IG repertoire diversity, and (ii) TCR and IG repertoire distribution").

Robins does not specifically teach further sorting activated T or B cells from a subset of the first biological sample using flow cytometry to generate a set of activated T or B cells; performing high-throughput sequencing of nucleic acid molecules comprising rearranged CDR3 regions of TCR or Ig loci obtained from the set of activated T or B cells; and identifying activated T cell clones in the set having CDR3 regions of significantly higher proportional abundance in the activated T or B cell population in comparison to the first biological sample, thereby identifying infection-induced responsive clones.

However, Robins does teach that T or B cell samples can be prepared by flow cytometry sorting that uses antibodies specific to known T and B cell surface markers (para [00144] "In certain related embodiments, preparations that comprise predominantly lymphocytes (e.g., T and B cells) or that comprise predominantly T cells or predominantly B cells, can be prepared for use as a biological sample as provided herein ... Various methods and commercially available kits for isolating different subpopulations of T and B cells are known in the art and include, but are not limited to subset selection immunomagnetic bead separation or flow immunocytometric cell sorting using antibodies specific for one or more of any of a variety of known T and B cell surface markers ... [Markers are used to] determine T, B, and monocyte lineages and subpopulations in flow cytometry"), and further teaches that a marker indicative of activated T cells is known (para [00136] "LAG-3 (CD223) is a cell surface molecule expressed on activated T cells"). Thus, sorting activated T or B cells from a subset of the first biological sample using flow cytometry to generate a set of activated T or B cells would have been obvious in view of the teaching of Robins.

Further, Robins teaches performing high-throughput sequencing of nucleic acid molecules comprising rearranged CDR3 regions of TCR or Ig loci (para [0068]-[0070], [00157]) to identify T or B cell clones having CDR3 regions of significantly higher proportional abundance in a second biological sample in comparison to a first biological sample (para [0073] "By way of non-limiting theory, this sequence distribution can represent the degree of T cell or B cell clonality in each sample from a patient (e.g., quantitative degree of representation, or relative abundance) ... The distribution and diversity values can be used in a rating step to rate individual samples and compare them to a control sample and/or to one another"; para [00190]). One of ordinary skill in the art would have readily appreciated that the set of activated T or B cells obtained by flow cytometry sorting as discussed above can be subjected to the high-throughput sequencing step in order to identify clones having rearranged CDR3 regions of TCR or Ig loci that are indicative of activated T or B cells in order to assess the subject's immunocompetence to respond to an infection. Thus, one of ordinary skill in the art in view of the teaching of Robins would have found it obvious to perform high-throughput sequencing of nucleic acid molecules comprising rearranged CDR3 regions of TCR or Ig loci obtained from the set of activated T or B cells; and identify activated T cell clones in the set having CDR3 regions of significantly higher proportional abundance in the activated T or B cell population in comparison to the first biological sample, thereby identifying infection-induced responsive clones.

As the technical features were known in the art at the time of the invention, they cannot be considered special technical features that would otherwise unify the groups. Groups I and II therefore lack unity of invention under PCT Rule 13 because they do not share a same or corresponding special technical feature.