

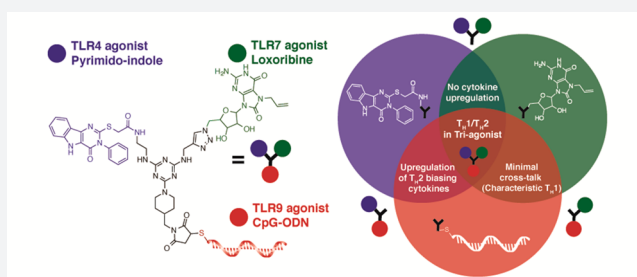
# Modulation of Innate Immune Responses *via* Covalently Linked TLR Agonists

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## Supporting Information

**ABSTRACT:** We present the synthesis of novel adjuvants for vaccine development using multivalent scaffolds and bio-conjugation chemistry to spatially manipulate Toll-like receptor (TLR) agonists. TLRs are primary receptors for activation of the innate immune system during vaccination. Vaccines that contain a combination of small and macro-molecule TLR agonists elicit more directed immune responses and prolong responses against foreign pathogens. In addition, immune activation is enhanced upon stimulation of two distinct TLRs. Here, we synthesized combinations of TLR agonists as spatially defined tri- and di-agonists to understand how specific TLR agonist combinations contribute to the overall immune response. We covalently conjugated three TLR agonists (TLR4, 7, and 9) to a small molecule core to probe the spatial arrangement of the agonists. Treating immune cells with the linked agonists increased activation of the transcription factor NF- $\kappa$ B and enhanced and directed immune related cytokine production and gene expression beyond cells treated with an unconjugated mixture of the same three agonists. The use of TLR signaling inhibitors and knockout studies confirmed that the tri-agonist molecule activated multiple signaling pathways leading to the observed higher activity. To validate that the TLR4, 7, and 9 agonist combination would activate the immune response to a greater extent, we performed *in vivo* studies using a vaccinia vaccination model. Mice vaccinated with the linked TLR agonists showed an increase in antibody depth and breadth compared to mice vaccinated with the unconjugated mixture. These studies demonstrate how activation of multiple TLRs through chemically and spatially defined organization assists in guiding immune responses, providing the potential to use chemical tools to design and develop more effective vaccines.



## INTRODUCTION

Vaccines are powerful and effective tools for disease prevention, treatment, and even elimination.<sup>1,2</sup> Many effective, whole pathogen vaccines activate the innate immune system through synergistic interactions of multiple immune cell receptors, where Toll-like receptor (TLR) synergies are the most established.<sup>1,3,4</sup> TLR agonists are defined molecular entities, ranging from oligonucleotides to heterocyclic small molecules, which are used as vaccine adjuvants that enhance the immune response against a coadministered antigen.<sup>5–11</sup> However, individual TLR agonists are not as effective as whole pathogens. Many TLR agonists combinations influence immune signaling pathways both spatially and temporally.<sup>12–19</sup> Until recently, understanding how the spatial organization of multiple TLR agonists affects TLR activation and the overall immune response has been difficult, as probing synergies has been limited to combining mixtures of TLR agonists in solution. Therefore, removing the defined spatial arrangement of native agonists in a pathogen.<sup>3,12,15,16,20–23</sup>

To determine how spatial arrangement affects immune synergies and to eliminate diffusion issues, a single molecular entity that activates multiple receptors is needed. Here, we

covalently conjugated three TLR agonists *via* a tri-functional, small molecule core and correlated how the specific spatial arrangement directly controlled innate immune cell activation. We observed that treatment with the tri-agonist compound produced a distinct array of cytokines *in vitro*, and this activity translated *in vivo* to generate a wider set of antibodies against a model vaccinia vaccine.

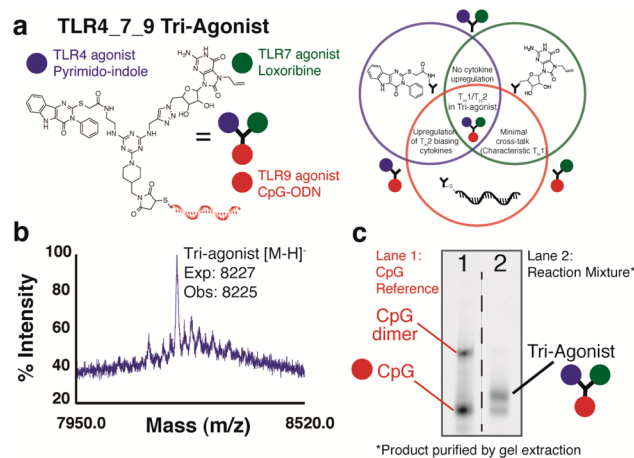
In recent years, the conjugation of up to two TLR agonists has been explored, where treatment with covalently conjugated TLR agonists can generate immune responses that are synergistic or repressive.<sup>24–27</sup> However, the components of many vaccines activate three to five TLRs. A prime example is the Yellow Fever Vaccine, one of the most successful vaccines, which activates four different TLRs (2, 7, 8, and 9).<sup>1,28,29</sup> Some of these enhanced synergies are postulated to result from cooperation between MyD88 and TRIF adaptor proteins that are downstream from TLR activation and modulate changes in transcription.<sup>30–35</sup> As a result, our working hypothesis was that stimulating a specific set of TLRs on one cell *via* covalent

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linkage of three TLR agonists would activate a distinct pattern of cell-signaling molecules as measured by transcription. If each molecular combination yields a distinct immune response profile, then the synthetic, spatial manipulation of TLR agonists could guide a particular immune response. To gain a better understanding of TLR synergies, we covalently attached three agonists together allowing spatially defined activation of three distinct TLRs.

Here, we present the conjugation of pyrimido[5,4-*b*]indole, loxoribine, and CpG-ODN1826, TLR4, 7, and 9 agonists, respectively, into a single tri-agonist compound. TLR7 and 9 are endosomal receptors, while TLR4 is located on the cell surface and in the endosome. Once stimulated, each TLR activates a specific immune signaling pathway.<sup>36,37</sup> TLR4, 7, and 9 agonists were chosen on the basis of these agonists' previously reported synergistic effects on the immune response (Figure 1a).<sup>15,38–40</sup> Using these agonists, the tri-agonist would



**Figure 1.** Schematic and characterization of tri-agonist compound, Indole\_Lox\_CpG. (a) Chemical structure of covalently conjugated tri-agonist compound (Indole\_Lox\_CpG) (left). Diagram illustrating how each TLR agonist (pyrimido-indole, loxoribine, or CpG-ODN) and the corresponding combinations (Indole\_Lox, Lox\_CpG, or Indole\_CpG) contributed to innate immune activation (right). (b) Confirmation of synthesized Indole\_Lox\_CpG via MALDI-TOF. (c) Analysis of Indole\_Lox\_CpG via gel electrophoresis: CpG-ODN1826 reference (lane 1) and Indole\_Lox\_CpG reaction mixture (lane 2). Tri-agonist was extracted from the gel and isolated as purified Indole\_Lox\_CpG.

activate multiple signaling pathways from the endosome or from both the endosome and cell surface, instead of a single pathway, which could result in a modulated cytokine and chemokine immune response. Immune activation with our tri-agonist was determined by measurement of NF- $\kappa$ B activation in RAW264.7 macrophage cells (RAW-Blue) and cytokine transcription levels in bone marrow-derived dendritic cells (BMDCs). Immune cells incubated with the covalently conjugated TLR4, 7, and 9 agonists exhibited an increase in NF- $\kappa$ B activation and changes in cytokine expression profiles relative to a mixture of the three unconjugated agonists. Additionally, using gene expression profiling, we observed that the covalent tri-agonist displayed a shift from a characteristic T<sub>H</sub>1 biased response (cellular response) toward a balanced response with upregulation of genes linked to a T<sub>H</sub>2 type response (humoral/antibody response), B cell activation, and innate and adaptive immune cell recruitment. Subsequently, we

used the corresponding TLR signaling inhibitors to confirm contribution from TLR4 and TLR9 activation pathways. Additional studies comparing the effect of the tri-agonist on wild-type, *MyD88*, and *TRIF* knockout mice verified activation of *MyD88* and *TRIF* pathways, thus contributing to a synergistic increase in the immune response. Taking our studies into an *in vivo* vaccination model demonstrated that covalent conjugation of TLR agonists changes antibody production in terms of antibody breadth and depth, showing how synthetic chemical tools can shape the immune response. By chemically linking the three agonists in close proximity, we can begin to decipher how spatial arrangement contributes to immune agonist synergies at the molecular, cytokine, and gene expression levels.

## RESULTS AND DISCUSSION

To covalently probe TLR synergies, we first synthesized a tri-agonist compound using three agonists exhibiting synergistic activity through specific TLRs (Scheme 1, for additional synthetic details see Schemes S1–S5). The agonists were linked using orthogonal coupling chemistries on a tri-functional small molecule core. The triazine based molecule was synthesized by treating cyanuric chloride with amines containing alkyne, amine, and maleimide functional handles.<sup>41</sup> Increasing the reaction temperature with the addition of each moiety resulted in a modular asymmetric core. This approach allows many three-TLR agonist combinations to be synthesized and tested in future studies.

With a core that could be conjugated to three different bioactive molecules, we attached three TLR agonists, a pyrimido[5,4-*b*]indole (Indole, TLR4 agonist), loxoribine (Lox, TLR7 agonist), and CpG-ODN1826 (CpG, TLR9 agonist) to our core.<sup>42–46</sup> We chose these TLR agonists based on previous studies reporting synergies activating two of the three TLRs together.<sup>15,38–40</sup> A pyrimido[5,4-*b*]indole compound was used to activate TLR4.<sup>42</sup> The carboxylic acid precursor of the pyrimido[5,4-*b*]indole compound was conjugated to the primary amine functionality on the core. Next, to activate TLR7, we attached an azide-modified loxoribine to the alkyne handle using copper-catalyzed Huisgen cycloaddition chemistry. Finally, to conjugate the TLR9 agonist CpG, the protected maleimide was revealed via a retro-Diels–Alder reaction and conjugated to a 5'-C6 linked thiol modified CpG-ODN1826 providing the tri-agonist conjugate, Indole\_Lox\_CpG (TLR4\_7\_9). 89.5% conversion was achieved when treating CpG with compound 9 to provide the tri-agonist, as determined by gel electrophoresis using ImageJ software. The tri-agonist was extracted from the gel and isolated as the purified tri-agonist before analysis and use. Synthesis of the tri-agonist was confirmed by MALDI-TOF and quantified via UV–vis spectroscopy using the fluorescent 6-FAM tag on CpG (Figures 1b, 1c, and S1). In parallel reactions, the corresponding di-agonist compounds, Indole\_Lox (TLR4\_7), Lox\_CpG (TLR7\_9), and Indole\_CpG (TLR4\_9), were also synthesized to determine how each agonist contributed to immune activation (Schemes S4 and S5).

First, to determine how covalent attachment of the three agonists affected synergistic activity, we measured NF- $\kappa$ B activation, one of the main transcription pathways involved in immune-related cytokine transcription, using the colorimetric macrophage reporter cell line, RAW-Blue. The tri- and di-agonist compounds were incubated with RAW-Blue cells for 18 h, where Indole\_Lox\_CpG activity (0.5  $\mu$ M) was compared to

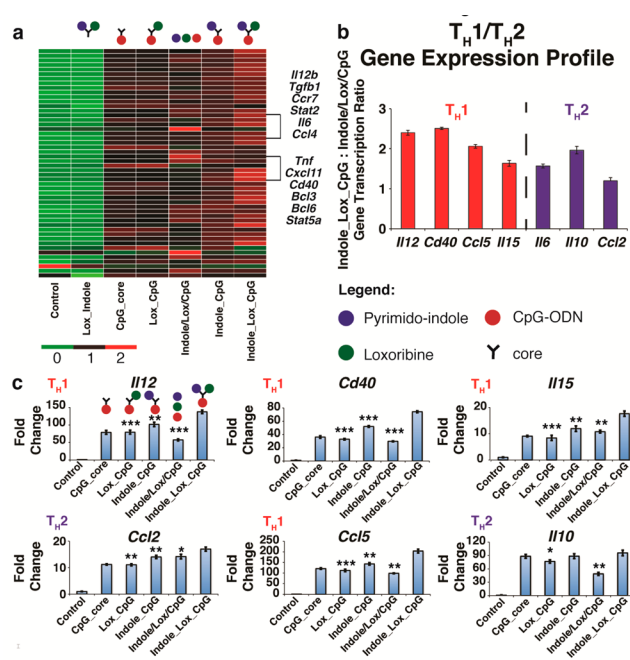


results correlated with our RAW-Blue studies that Indole\_Lox\_CpG resulted in increased immune activation compared to Indole/Lox/CpG. By placing the agonists in closer proximity due to covalent conjugation, Indole\_Lox\_CpG possibly achieves more effective stimulation of multiple TLRs, resulting in the observed synergy. In contrast, when the three agonists are in solution, the molecules freely diffuse through the cellular environment. This diffusion could prevent localization of the TLR agonists and subsequent activation of TLR4, 7, and 9 in a spatial manner.

To further examine how each agonist contributed to immune activation, we also compared covalently conjugated di-agonist combinations that activated only two TLRs. IL-12 production of Indole\_CpG, Lox\_CpG, and CpG\_core treated cells was comparable to that of Indole/Lox/CpG. On the other hand, Indole\_Lox\_CpG displayed nearly 1.5-fold higher IL-12 production than Indole\_CpG, and Indole\_CpG exhibited nearly 1.5-fold higher IL-12 production relative to CpG\_core. Although both results were not significant, this data alluded to Lox's contribution to the upregulation of TLR activation in the tri-agonist and Indole's (TLR4) contribution to the upregulation of TLR activation when presented to immune cells with CpG (TLR9). These observations were confirmed with significant results in the gene expression profile experiments. In contrast, the activity of Lox\_CpG was similar to that of CpG\_core, demonstrating that Lox (TLR7) did not affect CpG (TLR9) activity and thus resulted in no change in IL-12 production. These results suggest how each agonist added to the overall activity of Indole\_Lox\_CpG, implying that particular agonist combinations give distinct responses.

Since these covalent synergies were suggestive of specific changes in the cytokine levels based on the covalent conjugation and agonist combinations, we examined the global influence of these two parameters on dendritic cell gene expression profiles. Using microarray gene expression profiling, we measured changes in the transcription level of 561 genes associated with an immune response using a NanoString Immunology Assay (Figure 3a, for a complete list of genes see the Supporting Information gene list spreadsheet). BMDCs were incubated with tri- and di-agonist constructs at 0.5  $\mu$ M for 18 h. Then, total RNA was extracted (Qiagen RNeasy kit) and subsequently analyzed in triplicate using the microarray technology (UC Irvine Genomics High Throughput Facility). We mapped the activity of our compounds to gene expression for specific immune-related functions, such as  $T_H1$  and  $T_H2$  linked responses, to observe if activating specific agonist combinations in close proximity upregulated a response and to what extent. We validated that the gene expression of *Il12* agreed with our intracellular flow cytometry experiments (Figure 3c).

Additionally, we observed two main trends in the gene profile data: one in which a subset of gene expression related to  $T_H2$  and T- and B-cell development was upregulated and a second in which a subset of gene expression related to inflammation and chemotaxis was upregulated, but to a lesser extent. The first trend corresponded to what we observed for *Il12* gene expression where Indole\_Lox\_CpG expressed the highest gene count, followed by Indole\_CpG and last, Lox\_CpG, CpG\_core, and Indole/Lox/CpG, which were typically comparable (Figures 3b and 3c). This major trend of upregulation was observed not only with *Il12* expression, which is associated with a  $T_H1$  polarized response, but also with a subset of gene expression related to  $T_H2$  responses and

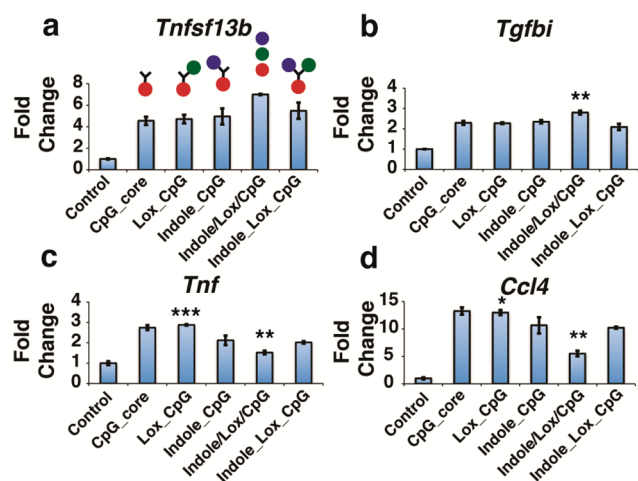


**Figure 3.** BMDC gene expression profile data. (a) Heat map of immune function related genes. Each figure represents the average of three independent experiments. BMDCs were incubated with each compound for 18 h at 37 °C. Total RNA was then isolated using RNeasy kit (Qiagen) and analyzed using NanoString Technology. (b) Graph illustrating  $T_H1/T_H2$  gene expression profile comparing the gene transcription level of Indole\_Lox\_CpG to Indole/Lox/CpG. (c) BMDC gene profile illustrating the main trend: Indole\_Lox\_CpG treated cells elicited the most upregulation in a subset of gene expression. Each figure illustrates the fold change of the specified agonist compared to the no agonist control and is the result of three independent experiments, where \* $p$  < 0.05, \*\* $p$  < 0.01, and \*\*\* $p$  < 0.001. All statistics represent the asterisked compound compared to Indole\_Lox\_CpG.

activation of innate and adaptive immunity, which included *Il6*, *Il10*, *Il15*, *Cd40*, *Ccl2*, and *Ccl5* (Figure 3c).<sup>49,50</sup>

Comparing CpG\_core to the di-agonists, Indole\_CpG and Lox\_CpG, showed that Indole (TLR4) upregulated CpG (TLR9) activity as exemplified by the 1.3-fold increase in *Il12* gene expression of Indole\_CpG compared to CpG\_core (Figure 3c, \*\* $p$  < 0.01). Lox (TLR7), on the other hand, did not change CpG (TLR9) activity in Lox\_CpG, and Indole\_Lox still did not activate immune cells. However, the addition of Lox (TLR7) to the TLR4\_9 combination in Indole\_Lox\_CpG was associated with upregulation of the immune response expression profile. This upregulation correlated with our previous observations, signifying the importance of activating specific TLR agonist combinations in close proximity and the effect of synergistic interactions on innate immune cells.

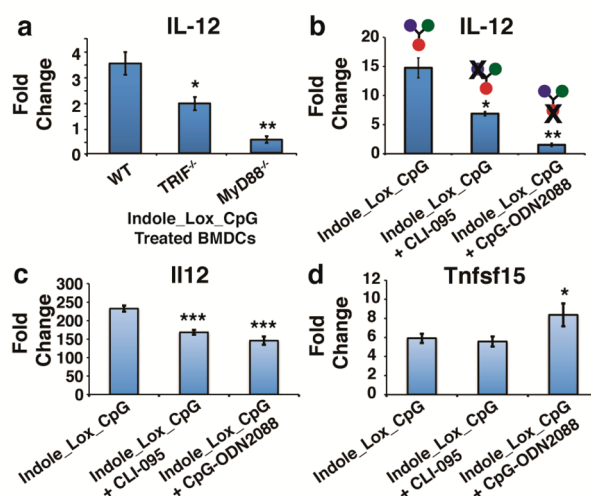
Interestingly, Indole\_Lox\_CpG activity also exhibited a lower level of gene upregulation with a subset of genes compared to the agonists in solution (Figure 4). Regulatory genes and those in the TNF ligand family were upregulated to a lower degree by our covalent compound Indole\_Lox\_CpG compared to Indole/Lox/CpG (\*\* $p$  < 0.01). This subset of genes included *Tnfsf14*, *Tgfb1*, and *Tnfsf13b*.<sup>51,52</sup> In other cases, when compared to Lox\_CpG, the tri-agonist compound exhibited a decrease in gene upregulation, with genes such as *Tnf* and *Ccl4* (\*\*\* $p$  < 0.001 and \* $p$  < 0.05, respectively), related to inflammation and immune cell chemoattraction. In



**Figure 4.** BMDC gene expression profile data. (a–d) BMDC gene expression profile illustrating second main trend observed, where Indole contributed to a decrease in CpG immune activity exhibited by Indole\_Lox\_CpG. BMDCs were incubated with each compound for 18 h at 37 °C. Total RNA was then isolated using RNeasy kit (Qiagen) and analyzed using NanoString Technology. Each figure illustrates the fold change of the specified agonist compared to the no agonist control and is the result of three independent experiments, where  $*p < 0.05$ ,  $**p < 0.01$ , and  $***p < 0.001$ . All statistics represent the asterisked compound compared to Indole\_Lox\_CpG.

general, this repressive trend showed that Indole\_CpG and Indole\_Lox\_CpG exhibited lower gene expression compared to Lox\_CpG and CpG\_core. This result suggested that Indole (TLR4) caused less upregulation of a subset of genes related to the TNF ligand family and inflammation, which contributed to the lower fold change in gene expression observed with Indole\_Lox\_CpG treated cells. Comparing the tri- and di-agonist compounds demonstrated how each TLR agonist affected specific families of genes. Thus, particular agonist combinations upregulated defined subsets of gene expression to different extents, possibly affecting downstream signaling and adaptive immune responses.

To understand what signaling pathways were involved in Indole\_Lox\_CpG activation, we used BMDCs harvested from *MyD88* knockout (*MyD88*<sup>-/-</sup>) and *TRIF* knockout (*TRIF*<sup>-/-</sup>) mice. MyD88 and TRIF are adaptor proteins downstream of TLR activation and control transcription of immune-signaling molecules. Research has shown that MyD88 and TRIF work together to synergistically activate cytokine production and enhance the immune response.<sup>30,31</sup> We treated each group of BMDCs with Indole\_Lox\_CpG for 6 h and then assessed IL-12 production using ICS. When treated with the tri-agonist, both *TRIF*<sup>-/-</sup> and *MyD88*<sup>-/-</sup> BMDCs showed decreases in IL-12 production compared to treated wild-type (WT) BMDCs, nearly two-fold and seven-fold decreases ( $*p < 0.05$  and  $**p < 0.01$ ), respectively (Figure 5a). These results demonstrated that Indole\_Lox\_CpG activated the TRIF pathway, probably originating from Indole, since TLR4 agonists can signal *via* both MyD88 and TRIF pathways.<sup>31,36,53</sup> Activation was heavily dependent on MyD88 activation, as shown by the seven-fold decrease in IL-12 production, which was likely due to CpG (TLR9) being a strong MyD88 activator.<sup>54</sup> The difference in TRIF and MyD88 activation levels may also be due to a temporal component of immune pathway activation that will require further investigation.<sup>12</sup> With the ability to change



**Figure 5.** BMDC cytokine and gene expression profile mechanistic studies using *TRIF* and *MyD88* knockout mice or TLR signaling inhibitors. (a) IL-12 cytokine profile of wild-type (WT), *TRIF* knockout (*TRIF*<sup>-/-</sup>), and *MyD88* knockout (*MyD88*<sup>-/-</sup>) BMDCs treated with Indole\_Lox\_CpG, represented as the fold change of median fluorescent intensity (MFI) of IL-12 expressing cells compared to the no agonist control. BMDCs were incubated with Indole\_Lox\_CpG for 6 h at 37 °C, where Brefeldin A was added for the last 4 h of incubation. Each figure represents three independent experiments, where  $*p < 0.05$  and  $**p < 0.01$ . (b) BMDC IL-12 cytokine profile with TLR signaling inhibitors, represented as the fold change of median fluorescent intensity (MFI) of IL-12 expressing cells compared to the no agonist control. BMDCs were incubated with the designated inhibitor for 1 h at 37 °C and then each compound for 6 h at 37 °C. Brefeldin A was added for the last 4 h of incubation. Each figure represents three independent experiments, where  $*p < 0.05$  and  $**p < 0.01$ . (c, d) Gene expression profile representative of the two main trends observed when BMDCs were treated with TLR signaling inhibitors: (c) *Il12* expression of Indole\_Lox\_CpG treated cells incubated with CLI-095 (TLR4 inhibitor) and CpG-ODN2088 (TLR9 antagonist), showing contributions from TLR4 and TLR9 pathways, and (d) upregulation of gene expression profile when TLR9 signaling was inhibited. Each figure illustrates the fold change of the specified agonist compared to the no agonist control and represents three independent experiments, where  $*p < 0.05$  and  $***p < 0.001$ . All statistics represent the asterisked compound compared to Indole\_Lox\_CpG.

*MyD88* and *TRIF* activation levels using tri-agonist constructs, we can synthesize other multi-agonist adjuvants that potentially provide tailored immune responses.

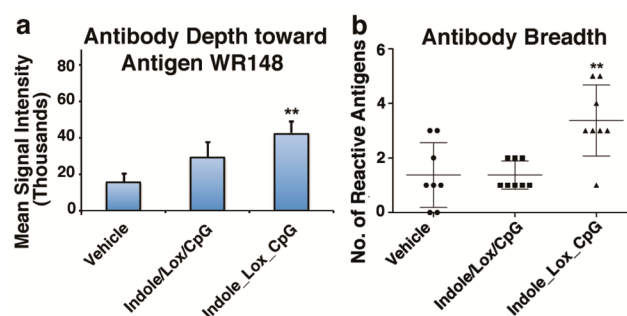
In order to identify the precise role of each agonist/receptor set in directing BMDCs, we used a TLR inhibitor and antagonist to perform mechanistic studies. Our hypothesis was that inhibiting activation of a single type of TLR would lead to a subsequent change in cytokine levels and gene expression, confirming that receptor's role in the response elicited from Indole\_Lox\_CpG. A TLR4 intracellular domain inhibitor, CLI-095,<sup>55,56</sup> and a TLR9 antagonist oligonucleotide, CpG-ODN2088,<sup>57</sup> were used to selectively inhibit TLR signaling or block TLR agonist binding, respectively. The inhibitor or the antagonist was used along with the tri-agonist compound, Indole\_Lox\_CpG. Resulting cytokine production allowed us to determine the contribution of each agonist and TLR activation pathway.

First, we examined whether each signaling inhibitor reduced IL-12 production. BMDCs were incubated with a designated

inhibitor for 1 h before adding in Indole\_Lox\_CpG. The cells were then incubated for an additional 6 h, and ICS was performed to assess IL-12 production. Using CLI-095 (100 nM), a minimal, but significant, decrease in IL-12 (20% decrease of Indole\_Lox\_CpG IL-12 production with CLI-095 compared to Indole\_Lox\_CpG,  $*p < 0.05$ ) was observed (Figures 5b and S9 for flow cytometry histograms). When incubating with CpG-ODN 2088 (100 nM), greater inhibition of IL-12 production (80% decrease of Indole\_Lox\_CpG IL-12 production with CpG-ODN2088 compared to Indole\_Lox\_CpG,  $**p < 0.01$ ) was observed, confirming that TLR9 was the main contributor of IL-12 production when treating cells with Indole\_Lox\_CpG. The TLR9 antagonist, CpG-ODN2088, was used to synthesize an antagonist version of the tri-agonist compound (Indole\_Lox\_CpG2088). Incubating Indole\_Lox\_CpG2088 with BMDCs reduced IL-12 production to near resting state (Figure S10,  $**p < 0.01$ ). The low amount of cytokine production without CpG was attributed to the potency of CpG, also showing that the incorporation of CpG was necessary to observe synergistic activity between TLR4, 7, and 9.

Expanding our studies to a broader range of cytokines and proteins *via* the NanoString assay, we analyzed gene expression of BMDCs after exposure to CLI-095 or CpG-ODN2088 and Indole\_Lox\_CpG (Figures 5c and 5d). We observed two main trends that correlated to the two trends observed in the previous tri- and di-agonist comparisons: first, that activation of all three receptors is important for the upregulation of genes to elicit a more balanced response, and second, that defined agonist combinations control the specific direction of the activity. The ICS experiment matched the main trend observed in the gene studies. *Il12* gene expression was reduced by CLI-095 (28% decrease of Indole\_Lox\_CpG *Il12* expression with CLI-095 compared to Indole\_Lox\_CpG,  $***p < 0.001$ ) and further by CpG-ODN2088 (38% decrease of Indole\_Lox\_CpG *Il12* expression with CpG-ODN2088 compared to Indole\_Lox\_CpG,  $***p < 0.001$ ), confirming contribution from TLR4 and TLR9 signaling pathways. This trend applied to the majority of genes, including proinflammatory genes *Il6* and *Il15* as well as adaptive immune-related genes *Ccl2* and *Ccl5*. The second trend observed resulted in gene upregulation relative to Indole\_Lox\_CpG when TLR9 inhibition occurred and minimal to no decrease in gene expression with TLR4 inhibition. This was observed for genes related to CD4<sup>+</sup> cell chemotaxis and development as well as the TNF ligand family. This confirmed how close agonist proximity through covalent modifications resulted in contribution from multiple TLR activation pathways, which altered and directed innate immune responses.

After studying how our compounds changed the immune response *in vitro*, we wanted to observe how Indole\_Lox\_CpG performed *in vivo* using a model vaccination system, vaccinia virus (small pox). C57BL/6 mice were immunized *via* im injection with heat-inactivated vaccinia virus ( $2.5 \times 10^7$  pfu/mL) and adjuvanted with either phosphate buffered saline (PBS) as the vehicle, Indole/Lox/CpG (0.05 nmol of each agonist), or Indole\_Lox\_CpG (0.05 nmol). Mice were boosted on day 14 with the designated vaccine. Serum was drawn from the mice on day 0, 7, 14, 21, and 28, and analyzed using a vaccinia protein microarray<sup>58</sup> to determine antibody depth and breadth. Looking at the immunodominant vaccinia antigen (WR148), Indole\_Lox\_CpG displayed the greatest depth in IgG1 antibody response (Figure 6a). Additionally, Indole\_Lox\_CpG elicited the broadest breadth in antigen-specific



**Figure 6.** Effect of Indole\_Lox\_CpG on IgG1 immune response in heat-inactivated vaccinia virus immunized mice. Mice were vaccinated *via* im injection on day 0 with heat inactivated vaccinia virus ( $2.5 \times 10^7$  pfu/mL) adjuvanted with PBS (Vehicle), Indole/Lox/CpG, or Indole\_Lox\_CpG with a total injection volume of 50  $\mu$ L. Mice were boosted on day 14. At day 28, the experiment end point, serum was collected from mice and probed on a vaccinia protein microarray. (a) Mean signal intensities of sera toward vaccinia immunodominant antigen WR148 at day 28, where  $**p < 0.01$ . (b) Number of reactive antigens in sera of immunized mice at day 28, where  $**p < 0.01$ . Results are expressed as mean  $\pm$  SEM;  $n = 8$ /group; unpaired, two-tailed *t* test. All statistics represent the asterisked compound compared to the no adjuvant vehicle.

antibody response compared to the no adjuvant vehicle or Indole/Lox/CpG (Figure 6b,  $**p < 0.01$ ). In contrast, Indole/Lox/CpG did not significantly change antibody depth or breadth compared to the vehicle. These results demonstrated that delivering a single, spatially defined tri-agonist compound *in vivo* can control antibody responses. The difference in antibody response between the tri-agonist, Indole\_Lox\_CpG, and Indole/Lox/CpG may be attributed to the different immune signaling pathways that are activated and the order in which the TLRs are stimulated, as a result of the covalent linkage and spatial arrangement of the TLR agonists. We are currently working on performing more *in vivo* studies to understand the mechanism and effect of different agonist combinations. These experiments show the utility and influence covalently linked multi-agonists might have on immunotherapy development.

## CONCLUSIONS

Here, we present evidence that the spatial arrangement of TLR agonists and the specific combinations of stimulated receptors resulted in defined activation patterns of dendritic cells. We detailed the synthesis of a tri-agonist construct, expanding recent two agonist synergistic studies to the use of three agonists. Through conjugation of a third agonist and in close proximity, we created a distinctive, more balanced response, shifting the immune response from T<sub>H</sub>1 polarization to a more balanced T<sub>H</sub>1/T<sub>H</sub>2 response and activation of innate and adaptive immunity. By comparing the tri-agonist compound to di-agonist constructs, we observed how each agonist shaped the innate immune response. Mechanistic studies were performed with adaptor protein knockout mice and the corresponding TLR inhibitor and antagonist to show the specific receptors and pathways through which the tri-agonist compound proceeded. We also observed that Indole\_Lox\_CpG increased antibody breadth and signal intensity toward a specific antigen when compared to the mixture of three agonists. In future studies, we plan to synthesize other TLR agonist combinations. These molecules will aid in determining how covalent synergies direct

antigen presentation and the types of cell populations that become activated. The covalently linked Indole<sub>Lox</sub>CpG aided in elucidating how TLR4, 7, and 9 synergies contributed to the observed changes in innate immune responses. Chemically controlling the spatial organization of innate immune agonists and specific agonist combinations can be used as a tool to direct immune responses and further understand how the immune system responds to pathogens. From this, researchers can potentially start to develop more effective immunotherapies using adjuvants designed to elicit targeted responses.

## METHODS

**General Materials and Methods.** Reagents were purchased from Sigma-Aldrich and used as is unless otherwise noted. Single stranded CpG-ODN1826 (Thio-C6-5'-TCCAT-GACGTTCCCTGACGTT-3'-6-FAM) with a phosphorothioated backbone was purchased from IDT. Centrifugal Filter Devices (3k) and ZipTip<sub>C18</sub> for MALDI-MS were purchased from Millipore. Compounds were filtered using 0.22  $\mu\text{M}$  syringe filters (Restek). Anti-mouse antibodies CD16/32 (93), APC anti-mouse IL-12 (C15.6), and Rat Isotype IgG1 (RTK2071) were purchased from BioLegend. BD Cytotfix/Cytoperm Kit for intracellular cytokine flow cytometry and GolgiPlug were purchased from BD Biosciences. Bone marrow-derived dendritic cells (BMDCs) were harvested from 6-week-old C57BL/6, B6.129P2(SJL)-Myd88<sup>tm1.1D<sup>efr</sup>/J</sup> (MyD88<sup>-/-</sup>), and C57BL/6J-Ticam1<sup>Lps2</sup>/J (TRIF<sup>-/-</sup>) mice (Jackson Laboratory). BMDCs were cultured in BMDC primary medium: RPMI 1640 (Life Technologies), 10% heat inactivated fetal bovine serum (FBS), 20 ng/mL granulocyte-macrophage colony-stimulating factor (GM-CSF) (produced from "66" cell line), 2 mM L-glutamine (Life Technologies), antibiotic-antimycotic (1 $\times$ ) (Life Technologies), and 50  $\mu\text{M}$  beta-mercaptoethanol (all components were 0.2  $\mu\text{M}$  sterile filtered together before use). RAW264.7 macrophage cells (RAW-Blue) were cultured in D-MEM High Glucose medium (Life Technologies), 10% FBS, 2 mM L-glutamine, 200  $\mu\text{g}/\text{mL}$  Zeocin (InvivoGen), and antibiotic-antimycotic (1 $\times$ ). Experiments were run in D-MEM High Glucose medium (Life Technologies), 10% heat inactivated FBS, 2 mM L-glutamine, and antibiotic-antimycotic (1 $\times$ ). Sterile phosphate buffered saline (PBS) buffer was obtained from Life Technologies. Fluorescence-activated cell sorting (FACS) buffer contained PBS (1 $\times$ ), 10% FBS, and 0.1% sodium azide. Mass spectra were obtained using MALDI-TOF (AB SCIEX TOF/TOF 5800). Flow cytometry data was acquired using a BD Accuri C6 Flow Cytometer and analyzed using the BD Accuri C6 software. RAW-Blue absorbances were measured on a Fisher Scientific MultiSkan FC. UV-vis spectra were obtained using NanoDrop 2000c spectrophotometer. Gel images were obtained using a GE Typhoon scanner. ImageJ was used to quantify percent conversion of the tri-agonist. Total RNA isolation was performed using an RNeasy Kit (Qiagen), according to the provided manufacturer's instructions. Total RNA samples were analyzed by the UC Irvine Genomics High Throughput Facilities using a NanoString Immunology Assay (NanoString Technologies) to obtain gene expression profiles. Semi-preparative high performance liquid chromatography was performed on a 1260 Infinity HPLC (Agilent). Gel electrophoresis was carried out using 10% TBE-urea gels in a Mini-PROTEAN tetra cell (BIO-RAD). All animal studies and mice maintenance were approved by the Institutional Animal Care

and Use Committee (IACUC). Data was analyzed using a two-tailed *t* test. All values were reported as mean  $\pm$  SD, unless stated otherwise.

**RAW264.7 Macrophage (RAW-Blue) NF- $\kappa$ B Assay.** RAW-Blue cells were plated at  $55 \times 10^4$  cells/mL density (180  $\mu\text{L}$ ) in 96-well plates using testing media as described in [General Materials and Methods](#). RAW-Blue cells were incubated with 20  $\mu\text{L}$  of each agonist for 18 h at 37  $^\circ\text{C}$  in a CO<sub>2</sub> incubator. Cell medium (50  $\mu\text{L}$ ) from the stimulated RAW-Blue cells was removed, placed into a 96-well plate, and incubated with QUANTI-Blue solution (InvivoGen) (150  $\mu\text{L}$ ) for 1–5 h at 37  $^\circ\text{C}$  in a CO<sub>2</sub> incubator. The absorbance (620 nm) was measured using a Fisher Scientific MultiSkan FC.

**In Vitro Bone Marrow-Derived Dendritic Cell Culture and Intracellular Cytokine Staining.** Monocytes were harvested from 6-week-old C57BL/6, B6.129P2(SJL)-Myd88<sup>tm1.1D<sup>efr</sup>/J</sup> (MyD88<sup>-/-</sup>), or C57BL/6J-Ticam1<sup>Lps2</sup>/J (TRIF<sup>-/-</sup>) mice.<sup>59</sup> Monocytes were differentiated into dendritic cells (BMDCs) using supplemented culture medium: RPMI 1640 (Life Technologies), 10% heat inactivated fetal bovine serum (Sigma), 20 ng/mL granulocyte-macrophage colony-stimulating factor (produced using "66" cell line), 2 mM L-glutamine (Life Technologies), antibiotic-antimycotic (1 $\times$ ) (Life Technologies), and 50  $\mu\text{M}$  beta-mercaptoethanol (Sigma). After 5 days of culture, BMDCs were incubated with each agonist (0.5  $\mu\text{M}$ ) in culture medium for 6 h at 37  $^\circ\text{C}$  in a CO<sub>2</sub> incubator. GolgiPlug (BD Biosciences), containing Brefeldin A, was added to cell culture for the final 4 h of culture. Cells were stained for intracellular IL-12 cytokine production and analyzed using BD Accuri C6.

**Immunization.** C57BL/6 mice were vaccinated intramuscularly (im) at day 0 with heat-inactivated vaccinia virus Western Reserve (VVWR) strain ( $2.5 \times 10^7$  pfu/mL) adjuvanted with specified multi-agonist compound(s) (0.05 nmol) or PBS as a control in a total injection volume of 50  $\mu\text{L}$ . Mice received vaccine boost at day 14. Serum samples were collected from mice *via* saphenous vein at day 0, 7, 14, 21, and 28 postvaccination.

**Viruses.** VVWR stocks were grown on HeLa cells in T175 flasks, infecting at a multiplicity of infection of 0.5. Cells were harvested at 60 h, and virus was isolated by rapidly freeze-thawing the cell pellet three times in a volume of 2.3 mL of RPMI plus 1% fetal calf serum (FCS). Cell debris was removed by centrifugation. Clarified supernatant was frozen at  $-80$   $^\circ\text{C}$  as virus stock. VVWR stocks were titered on Vero cells ( $2 \times 10^8$  pfu/mL). Heat-inactivated VVWR stock was prepared by incubating virus on a water bath at 65  $^\circ\text{C}$  for 1 h.

**Gel Electrophoresis.** CpG-ODN containing compounds were purified using Mini-PROTEAN TBE-Urea Precast Gels (BIO-RAD) and Mini-PROTEAN Tetra Cell system. Compounds were loaded into gels in TBE urea buffer (7:20 compound:loading buffer). Gels were run in TBE buffer at 100 V for 1 h. The resulting gels were imaged using a GE Typhoon gel scanner. The desired band was excised, crushed, and eluted into HPLC grade water overnight at 37  $^\circ\text{C}$ . The resulting solution was concentrated using 3k Amicon Centrifugal Filter Units (EMD Millipore) and filtered using 0.2  $\mu\text{M}$  cellulose acetate syringe filter (Restek). The resulting product was desalted using ZipTip<sub>C18</sub>, analyzed by MALDI-TOF using 3-hydroxypicolinic acid matrix, and quantified using a NanoDrop spectrophotometer.

**MALDI-TOF.** The reaction mixture was passed through ZipTip<sub>C18</sub> (Millipore) according to Millipore protocol:

ZipTip<sub>C18</sub> was equilibrated with 50% acetonitrile/water ( $2 \times 10 \mu\text{L}$ ) and subsequently 0.1 M triethylammonium acetate (TEAA) ( $3 \times 10 \mu\text{L}$ ). The oligonucleotide-containing compound was passed through the ZipTip<sub>C18</sub> ( $10 \times 10 \mu\text{L}$ ). The ZipTip<sub>C18</sub> was washed with 0.1 M TEAA buffer ( $3 \times 10 \mu\text{L}$ ) followed by nanopure water ( $3 \times 10 \mu\text{L}$ ). The desired product was eluted using 50% acetonitrile/water ( $3 \times 10 \mu\text{L}$ ). The eluted product was concentrated using a speed-vacuum and mixed with 0.36 M 3-hydroxypicolinic acid matrix (1:1 acetonitrile:300 mM ammonium citrate solution in 50% acetonitrile/water) ( $2 \mu\text{L}$ ). The sample was spotted directly onto the MALDI plate and analyzed in negative ion mode. For small molecules, the sample was spotted with  $\alpha$ -cyano-4-hydroxycinnamic acid matrix (in 1:1 acetonitrile:water with 0.1% TFA) and analyzed in positive ion mode.

**Production and Probing of Vaccinia Protein Microarray.** The cloning and expression platform is described in detail previously.<sup>58</sup> Briefly, custom PCR primers comprising 20 bp of gene-specific sequence with 33 bp of “adapter” sequences were used in PCRs with vaccinia virus WR strain genomic DNA as a template. The adapter sequences, which become incorporated into the termini flanking the amplified gene, were homologous to the cloning site of the T7 expression vector pNHsCHA (Gene Therapy Systems, San Diego, CA) and allowed the PCR products to be cloned by homologous recombination in competent DH5 $\alpha$  cells. The adapters also incorporated a 5'-polyhistidine epitope, an ATG translation start codon, and a 3'-hemagglutinin epitope and T7 terminator. Sequence-confirmed plasmids were expressed in 5 h *in vitro* transcription-translation reactions (RTS 100 kits from Roche) according to the manufacturer's instructions. Protein expression was monitored either by dot blot or by microarray using both monoclonal anti-polyhistidine (clone His-1 from Sigma) and monoclonal anti-hemagglutinin (clone 3F10 from Roche) antibodies, followed by appropriate secondary antibodies. Microarrays were printed onto nitrocellulose coated glass slides (FAST from Schleicher & Schuell Bioscience) using an Omni Grid 100 microarray printer (Gene Machines). Prior to array staining, the sera were diluted to 1/100 in Protein Array Blocking Buffer (Schleicher & Schuell Bioscience) containing *Escherichia coli* lysate at a final concentration of 10% and incubated at room temperature for 1 h with constant mixing. The arrays were rehydrated in blocking buffer for 30 min and probed with the pretreated sera for 2 h at room temperature with constant agitation. The slides were then washed 3 times in Tris buffer containing 0.05% Tween-20 and incubated with biotin conjugated anti-mouse IgG1 secondary antibodies at 1:200 in blocking buffer for 1 h. The slides were then washed 3 times with Tris buffer containing 0.05% Tween-20 followed by incubation with streptavidin-Surelight P-3 conjugated at 1:200 in blocking buffer for 45 min. After washing, the slides were air-dried under brief centrifugation and stored in a desiccator at room temperature. The microarrays were scanned using a Gene Pix 4100A scanner (Molecular Devices, Sunnyvale, CA), and image analysis was performed with Genepix Pro 5.0 software (Molecular Devices). The spot intensity was calculated as the median spot value minus local spot background. A secondary correction for background binding to *E. coli* proteins in the reaction mixture was done by subtracting an average of the no-DNA spots from the background-corrected spot value.

## ■ ASSOCIATED CONTENT

### 📄 Supporting Information

The Supporting Information is available free of charge on the ACS Publications website at DOI: [10.1021/acscentsci.5b00274](https://doi.org/10.1021/acscentsci.5b00274).

Synthetic protocols and schemes and *in vitro* cell data (PDF)

Gene list (XLSX)

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### Notes

The authors declare no competing financial interest.

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