Characterization of host responses during *Pseudomonas aeruginosa* acute lung infection in the lungs and blood and after treatment with the synthetic immunomodulatory peptide IDR-1002

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Abstract

Pseudomonas aeruginosa is an opportunistic pathogen that causes nosocomial pneumonia and infects patients with cystic fibrosis. *P. aeruginosa* lung infections are difficult to treat due to bacterial resistance to antibiotics, and strains with multi-drug resistance are becoming more prevalent. Here we examined the use of a small host defense peptide, innate defense regulator 1002 (IDR-1002), in an acute *P. aeruginosa* lung infection in vivo. IDR-1002 significantly reduced the bacterial burden in the bronchoalveolar lavage fluid (BALF) as well as MCP-1 in the BALF and serum, KC in the serum, and IL-6 in the BALF. RNA-Seq was conducted on lungs and whole blood and the effects of *P. aeruginosa*, IDR-1002, or the combination of *P. aeruginosa* and IDR-1002 were evaluated. Differential gene expression analysis showed that *P. aeruginosa* increased multiple inflammatory and innate immune pathways as well as affected hemostasis, matrix metalloproteinases, collagen biosynthesis, and various metabolism pathways in the lungs and/or blood. Infected mice treated with IDR-1002 had significant changes in gene expression compared to untreated infected mice, with fewer differentially expressed genes associated with the inflammatory and innate immune responses to microbial infection, and treatment also affected morphogenesis, certain metabolic pathways, and lymphocyte activation. Overall, these results show that IDR-1002 was effective in treating *P. aeruginosa* acute lung infections and associated inflammation.

43
44 **Introduction**

45 *Pseudomonas aeruginosa* is a common source of infections caused by medical devices,
46 such as catheters, and also frequently infects burns and wounds (1, 2). However, its roles in lung
47 infections are among the most concerning incidents. *P. aeruginosa* is one of the leading causes
48 of ventilator-associated pneumonia and hospital-acquired pneumonia, particularly in the
49 intensive care unit or in late-onset cases (3-5). *P. aeruginosa* has also been found in patients with
50 chronic obstructive pulmonary disease (COPD) (6). Critically, it chronically infects the lungs of
51 patients with cystic fibrosis (CF), with the majority of patients becoming infected by their mid-
52 twenties, and *P. aeruginosa* is associated with increased hospitalization and mortality in CF
53 patients (7, 8). Treatment of *P. aeruginosa* lung infections is difficult due to its inherent,
54 adaptive, and acquired antibiotic resistance mechanisms as well as challenges in delivering drugs
55 to the lung environment (9, 10). Multi-drug resistance in *P. aeruginosa* is increasing,
56 necessitating a search for new treatment options (11).

57 Host defense peptides (HDPs), also called antimicrobial peptides (AMPs), are small,
58 amphipathic peptides (10-50 amino acids) that are typically cationic (charge +2 to +9). They
59 demonstrate numerous anti-inflammatory and anti-infective effects against microbial infections,
60 but previous work using HDPs against in vivo *P. aeruginosa* respiratory tract infections has had
61 only limited success (12-18). Many of the peptides demonstrated toxicity in vivo or their effects
62 on inflammation, a key feature of *P. aeruginosa* lung infections, were not fully examined (12-
63 18). None of these peptides has advanced to clinical trials for the treatment of *P. aeruginosa*
64 infections. Recently, we showed that one HDP, innate defense regulator 1002 (IDR-1002), was
65 effective against the inflammatory sequelae of *P. aeruginosa* infections in a model using the
66 polysaccharide alginate to mimic a chronic infection without showing toxicity (19). Here, the

aim was to explore the mechanisms underlying IDR-1002 activities in an acute *P. aeruginosa* lung infection model as well as to examine the effects of the *P. aeruginosa* infection itself using systems biology methods.

IDR-1002 (VQRWLIVWRIRK-NH_2) is a synthetic derivative of the bovine HDP bactenecin (RLCRIVVIRVCR-NH_2), with amino acid substitutions used to create a linearized peptide that shows improved immunomodulatory activity compared to bactenecin (20, 21). Previous work on IDR-1002 in a *Staphylococcus aureus* intraperitoneal infection model demonstrated that it helped to recruit leukocytes to the infection site, with an increase seen in both neutrophils and the neutrophil chemokine KC (20). Increased numbers of monocytes were also observed, although no changes in MCP-1 expression were seen (20). Eliminating macrophages with liposomal clodronate eliminated the protective effect of IDR-1002 (20). This indicates that a key factor in IDR-1002-mediated protection in the *S. aureus* IP model was the recruitment of macrophages, although there are some reports indicating that liposomal clodronate also depletes dendritic cells (DCs) (22, 23). Similar results were achieved for another peptide, IDR-1, against *S. aureus* infection, with macrophages and monocytes required for protection, while it was additionally shown that depleting neutrophils, T cells, or B cells had no effect (24). In vitro studies with human monocytes showed that IDR-1002 can promote cell adhesion to fibronectin in the presence of chemokines due to its increased activation of β-integrins and the PI3K-Akt pathway, and this peptide also increased the expression of the chemokine receptor CCR5 (25, 26). IDR-1002 also reduced inflammation in a sterile ear inflammation model, which was attributed to its repression of class A/1 rhodopsin-like G protein-coupled receptors, the IFN-γ response, and regulation by IRF8 (27). Therefore, while some aspects of IDR-1002 mechanisms have been uncovered and indicate its involvement in leukocyte recruitment, IDR-

1002 has not been thoroughly examined in the context of infections, especially lung infections by *P. aeruginosa*. Additionally, it was decided to take a more comprehensive approach to the evaluation of its mechanisms of action. Therefore, RNA-Seq was utilized in conjunction with advanced bioinformatics appraisal of the host immune response both locally at the lungs and systemically in the blood. RNA-Seq is a powerful method for evaluating the transcriptome of an organism. It uses sequencing by synthesis and does not require the use of probes as with microarray technology, thereby allowing for the more efficient and accurate discovery of dysregulated transcripts, without substantial and variable backgrounds as seen for hybridization methods such as microarrays (28).

While the host response to murine *P. aeruginosa* lung infections has been evaluated using microarrays (29, 30), the use of RNA-Seq has been limited. To the best of our knowledge, only one study has used (dual) RNA-Seq for a *P. aeruginosa* lung infection model and it examined only the response in the lungs and utilized a weakly virulent isolate PAO1 at very high input doses (2×10^8 colony forming units (CFUs)) to define only 702 host genes changing expression (31). In contrast, here we performed RNA-Seq on both the lungs and blood from infected mice after infection with lower input doses ($\sim 8 \times 10^5$) of a highly virulent isolate strain, PA103, to provide new insights into the effects of acute, rapidly-progressing *P. aeruginosa* infections and possibly uncover new drug targets.

The RNA-Seq results showed that *P. aeruginosa* caused >4700 genes to change expression in the lungs, with profound inflammatory and immune responses in both the lungs and the blood, and also demonstrated the involvement of novel biological processes. While the mice given IDR-1002 alone showed few changes in gene expression compared to the negative control group, differences in hemostasis and other processes among the infected mice after IDR-

1002 treatment of PA103 infected mice provide new leads for understanding IDR mechanisms of action. Critically, in these experiments IDR-1002 led to reductions in the CFU burden, the inflammatory cytokine and chemokine levels, and the associated inflammatory pathways.

Results

IDR-1002 reduced *P. aeruginosa* burden and inflammation in the lungs and did not itself produce inflammatory cytokines

To examine the effects of IDR-1002, *P. aeruginosa*, or their combination, an acute *P. aeruginosa* lung model was used. Female C57Bl/6J mice 6-8 weeks of age were given 8 mg/kg IDR-1002 or the vehicle (endotoxin-free water) intranasally (IN) 24 h prior to infection with ~8 x 10^5 CFU/mouse of the virulent *P. aeruginosa* strain PA103 or the vehicle (endotoxin-free saline), and then euthanized and all samples collected at 18 h post-infection. Prophylactic treatment was used to eliminate any direct antimicrobial effects of IDR-1002 on the bacteria, since our goal was to focus on characterizing the immunomodulatory activities of IDR-1002. The groups of mice are hereafter referred to as the negative control (received only vehicles), IDR-1002 control (received IDR-1002 and saline), PA103 infected (received water and PA103), and IDR-1002 treatment (received IDR-1002 and PA103), with the underlined nomenclature subsequently used in figures.

Prophylactic treatment with IDR-1002 significantly decreased the PA103 CFU burden in the lungs by more than two log orders of magnitude when compared to PA103 infected mice (Fig. 1). Infection with PA103 significantly increased leukocyte infiltration into the lungs compared to either the negative control or IDR-1002 control mice, whereas the IDR-1002 treatment mice showed a leukocyte count that was lower than that of the PA103 infected but higher than the negative or IDR-1002 control mice, although none of the comparisons involving

IDR-1002 treatment mice was significant. The increase in the total leukocyte count of IDR-1002 treatment mice was not significant compared to negative control or IDR-1002 control mice (Fig. 1B). As expected, the PA103 infected mice showed a very strong increase in neutrophils compared to the uninfected control mice (Fig. 1C), while monocytes became a relatively minor proportion of leukocytes. In contrast, the treatment mice showed similar proportions of neutrophils and monocytes/macrophages that favored neutrophils in sicker mice, while mice that had few signs of infection showed more monocytes/macrophages. Both the PA103 and treatment groups had slight but significant weight loss compared to the negative control mice (Fig. 1D), and although the health scores showed improvement in the IDR-1002 treatment group at both 3 and 18 h post-infection compared to the PA103 infected mice, these differences were not significant (Fig. 1E and 1F).

The expression of cytokines and chemokines in the bronchoalveolar lavage fluid (BALF) and serum was also examined (Fig. 2). MCP-1, KC, and IL-6 showed significant increases in the BALF and serum of the PA103 infected mice compared to either negative control or IDR-1002 control mice, while the IDR-1002 treatment mice had significant decreases in most of these outputs compared to the PA103 mice. TNF-α also showed similar trends. Notably, there were no significant increases for IDR-1002 control compared to negative control mice for any of the tested cytokines or chemokines.

P. aeruginosa lung infection induced profound changes in the transcriptome of both the lungs and blood

The lungs and whole blood from one of two experiments, consisting of 4-5 mice per condition, were used to isolate RNA and run RNA-Seq to characterize the differentially expressed (DE) genes of the host transcriptome during the infection and treatment with IDR-

1002. The total number of host DE genes for several comparisons is shown in Table 1. Infection with PA103 led to the differential expression of 4,739 genes in the lungs and 1,327 in the blood when compared to the negative control samples. In the lungs, there were 2,360 upregulated DE genes and 2,379 downregulated DE genes after PA103 infection compared to the negative control mice. The upregulated DE genes in the PA103-infected lungs included multiple genes encoding innate immune and inflammatory response proteins, including the mouse cathelicidin CRAMP, acute phase serum amyloid A proteins, and numerous chemokines. There were also genes for several matrix metalloproteinases (MMPs) upregulated (MMP-3, -8, -9, -12, -14, and -25). The genes for the cytokines and chemokines examined in the ELISAs, IL-6, TNF-α, MCP-1, and KC, were all upregulated in the PA103 infected mice similar to the results seen at the protein level in Fig. 2, with these genes showing greater than 32-fold changes compared to the control mice. The downregulated DE genes in the lungs were more varied in function but notably included several genes encoding subunits of various types of collagen, which is a major component of the extracellular matrix (ECM) (32).

While the top DE genes according to fold-change provide some interesting insights, it is important to take a systemic approach to the data. Therefore, over-represented pathways were discerned among DE genes using Signature Overrepresentation Analysis (SIGORA), a gene-pair over-representation analysis tool that is designed to reveal specific processes that are relevant to the model under consideration (33). Unlike many other pathway tools, SIGORA limits repetition of pathways (i.e., reduces the identification of certain pathways due to genes annotated to multiple pathways) by performing gene-pair-based pathway enrichment. For PA103 infected vs. negative control mice, 59 pathways were enriched among the DE genes (Table 2). The top two pathways identified were hemostasis and axon guidance, which have not been identified in most

182 previous infection studies. Hemostasis is often associated with sepsis and can be targeted by
183 inflammatory mediators (34). While axon guidance is associated with the nervous system, the
184 proteins in this pathway are also involved in the development of other tissues, including the
185 lungs and blood vessels, and have roles in cell migration (35). Other highly dysregulated
186 pathways included many involved in inflammation and innate immune responses including
187 chemokine receptor binding; interferon gamma signaling; TLR5 and MyD88-independent
188 TLR3/4 cascades; and interleukin-1 and other cytokine signaling (Table 2). These results were in
189 agreement with the strong immune response expected as a consequence of an infection, and the
190 roles of both MyD88-dependent and MyD88-independent pathways have been noted in other *P.*
191 *aeruginosa* infection models (36, 37).

192 To gain further insights into the genes and molecular interactions involved in some of
193 these pathways, NetworkAnalyst was used to create and visualize protein-protein interaction
194 networks (38). Since the genes for multiple chemokines were upregulated, and the chemokine
195 receptors bind chemokines pathway was dysregulated (Table 2), a zero-order network was
196 created showing the interactions of DE genes associated with leukocyte migration (Fig. 3).
197 Almost all of the genes in the network were upregulated (red-colored nodes) in the PA103
198 infected mice compared to the negative control mice, and numerous chemokines from both the
199 CXC and CC families were observed and interconnected with various transcription factors
200 including three NFκB subunits, Jun, and Fos. In agreement with these observations, *P.*
201 *aeruginosa* lung infections are known to lead to an influx of leukocytes, particularly neutrophils
202 (39, 40) as confirmed here by an increase in neutrophils in the BALF (Fig. 1).

203 The pathway analysis also showed multiple pathways related to cell and tissue
204 differentiation or structure, including collagen, integrins, and ECM organization (Table 2).

Therefore, genes involved in ECM organization were also used to create a protein:protein interaction network (Fig. 4). The upregulated DE genes included *Mmp9*, which encodes a matrix metalloproteinase that is upregulated and released during numerous lung injury models and which decreases ECM integrity (41). Downregulated DE genes included several for chains of types of collagen, the major fibrous component of the ECM (32). These data are consistent with the breakdown of tissues in the lung.

The RNA-Seq results for the lungs also pointed to substantial changes in metabolism or nutrient acquisition, including metabolism of water-soluble vitamins and cofactors, iron uptake and transport (also noted in (31)), pyruvate metabolism, and mitochondrial fatty acid beta-oxidation (Table 2). Many of these pathways involve genes that were downregulated in the PA103 infected mice compared to the control mice.

In the blood, there were 686 upregulated and 641 downregulated DE genes in the PA103 infected mice compared to the negative control mice. As with the lungs, several of the most upregulated DE genes in the blood were associated with infection and inflammation, such as *Lcn2*, *Cd177*, and *Ngp* and other genes associated with neutrophil-induced inflammation, and the genes for host defense peptide CRAMP and iron-sequestering lactotransferrin. There were 729 genes that were differentially expressed in the blood but not the lungs, which included *Cd72*, *Tnfrsf3*, and complement-associated genes such as *C1qa* and *C4b*. These differences between the local (lung) and distant (blood) gene expression responses were reflected in the dysregulated pathways (Table 3), with fewer inflammatory pathways involved and the observation of novel pathways. While IL-6, MCP-1, and KC were significantly upregulated in the serum and TNF-α showed a trend towards upregulation, only the genes for MCP-1 and TNF-α were significantly upregulated in the blood, probably reflecting differences in kinetics for these cytokines and

chemokines and/or mobilization of some cytokines from the lung into the blood. Amongst the downregulated DE genes, there were several involved with B-cell signaling responses, activation, and antigen presentation. Similarly, the SIGORA over-representation analysis also demonstrated pathways related to an immune response including TLR, interferon, and chemokine signaling, as well as MHC class II antigen presentation and B cell signaling pathways (Table 3).

A zero-order interaction network for the blood (Fig. 5) showed a mixture of up- and downregulated genes. Prominent hubs for upregulated genes included *Rela*, a subunit of the transcription factor NF-κB; *MyD88*; and *Cebpa* and *Cebpb*, two members of the CCAAT/enhancer binding proteins (C/EBP) transcription factor family that are involved in lung inflammation (42). The downregulated gene *Sp3*, which encodes a proteinase inhibitor, was also a hub.

Administration of IDR-1002 reduced innate immune and inflammatory responses induced by *P. aeruginosa* in the lungs and blood

The application of IDR-1002 to uninfected mice led to only two DE genes in the lungs, *Csf3* and *Saa2*, the genes encoding G-CSF and serum amyloid A2, which were upregulated and downregulated, respectively, compared to the negative control mice. However, while the response in uninfected mice was limited, the prophylactic administration of IDR-1002 in combination with PA103 infection had a large impact on the transcriptome. The comparison between the IDR-1002 treatment and PA103 infected groups showed 2,111 DE genes in the lungs, with 1,110 upregulated and 1,001 downregulated DE genes. The genes for the four proteins examined in ELISAs, namely MCP-1, KC, IL-6, and TNF-α, showed a trend towards downregulation in the IDR-1002 treatment mice but were not significantly differentially

expressed. When compared to the PA103 infected mice, the IDR-1002 treatment mice had the genes for several chemokines downregulated, including *Ccl4*, *Cxcl10*, *Ccl11*, and *Cxcl13*, along with many other inflammatory response genes. In contrast, the upregulated genes were more diverse. In the over-representation analysis, 20 pathways were dysregulated in the IDR-1002 treatment mice compared to PA103 infected mice (Table 4). Four of these pathways, prolonged ERK activation events, IRF3-mediated induction of type I IFN, CRMPs in Sema3A signaling, and hyaluronan uptake and degradation, were not observed in the PA103 infected vs. negative control comparison, while the other 16 pathways were also found in this comparison. The common pathways between these two comparisons indicated that the IDR-1002 treatment mice had similarities to the negative control mice and therefore showed that the IDR-1002 treatment mice generally mitigated (reduced) the effects of infection. Indeed, a zero-order interaction network (Fig. 6) demonstrated that a large number of the downregulated genes in the IDR-1002 treatment mice compared to PA103 infected mice were associated with the inflammatory response, including *Myd88*, *Traf6*, *Rela*, *Nfkb2*, and many chemokines. Overall, these results indicated that, while the IDR-1002 treated mice were still showing an immune response to infection, this response was muted when compared to that of the PA103 infected mice.

In the blood, no DE genes were detected for IDR-1002 control mice compared to negative control mice. There was also only one DE gene related to IDR-1002 treatment vs. PA103 infected in the blood, *Ighd*, a gene encoding a heavy constant region of IgD, which was upregulated in the treatment group.

Discussion

Given our interests in characterizing the host immunomodulatory activities of IDR-1002, RNA-Seq analysis was performed on mice with prophylactic treatment of IDR-1002 prior to *P.*

aeruginosa infection to eliminate any potential direct antimicrobial effects of the peptide on the bacteria. Infection with *P. aeruginosa* PA103 alone led to 4,739 DE host genes in the lungs and 1,327 DE host genes in the blood when compared to the uninfected negative control group. These numbers were greatly reduced by treatment with IDR-1002 in both the lungs and the blood when compared to PA103 infection alone, indicating greater similarity of treatment mice with the uninfected negative control mice. This was in agreement with the reduction in bacterial CFU burden and the ELISA results indicating reduced cytokine and chemokine expression in the IDR-1002 treatment mice compared to the PA103 infected mice; however levels still remained above those seen in the negative or IDR-1002 control mice. The prophylactic use of IDR-1002 to treat PA103 infections led to a range of results with regards to individual mice, with some mice showing either a complete or partial elimination of bacterial CFUs and signs of inflammation, while a few showed results similar to those of the untreated PA103 infected mice. It is possible that this diversity might reflect the heterogeneity implicit in biological systems in response to both bacteria and peptide, microheterogeneity in the diet or microbiota of mice, or perhaps minor differences in bacterial infectious doses. Indeed such variation in response to the immune modulator IDR-1002 has been observed with IDRs in other in vivo models, including IDR-1018 in a malaria model and IDR-1002 in IP-administered *Escherichia coli* and *S. aureus* models (20, 43). Increasing the IDR-1002 dose or formulating it to improve delivery might improve its effectiveness in individual mice. Regardless of this heterogeneity, there were still 2,111 DE genes in the lungs when comparing the IDR-1002 treatment to PA103 infected but untreated mice, with the IDR-1002 treatment vs. PA103 infected comparison showing almost the opposite results to PA103 infected vs. control, indicating that the treatment with IDR-1002 reduced the overwhelming inflammatory response induced by PA103, as seen with both the ELISA and the

RNA-Seq results. Selected genes identified by RNA-Seq were also validated using qPCR (Fig. S1) and showed similar trends to the RNA-Seq results, such as increases in chemokines with PA103 infection that were reduced by treatment with IDR-1002.

There were only two DE genes in IDR-1002 control vs. negative control for the lungs and none for the blood. Since the samples were collected 42 h after IDR-1002 administration it was arguably unsurprising that few changes were seen at the transcriptional level. This indicates that the effect of IDR-1002 is likely to involve priming or polarizing the immune/protective response and that these changes were then potentiated by the additional stimulus of PA103 infection, whereas in the mice given only IDR-1002 the mice did not receive an additional signal to the immune system, which then returned essentially to baseline levels. For example, the anti-inflammatory cytokine IL-10 decreases signaling through MHC class II, and IDR-1002 has been shown to increase IL-10 secretion by peritoneal mouse macrophages stimulated ex vivo, although the overexpression of IL-10 in *P. aeruginosa* lung infections could have both beneficial and deleterious effects (20, 44, 45), which might also partly explain the differences in responses in individual IDR-1002 treatment mice.

The RNA-Seq results showed that multiple innate immunity and inflammation pathways were upregulated in the lungs and blood in response to *P. aeruginosa*. The large number of chemokine genes upregulated was consistent with the increased number of leukocytes seen in the BALF with PA103 infection. Intriguingly, *P. aeruginosa* lung infection, even in chronic conditions such as CF, is associated with increased neutrophils in the lungs (40), a feature that was also seen in this acute *P. aeruginosa* lung infection model, together with the upregulation of many genes associated with neutrophil activation. The upregulation of numerous MMP genes and the decreased expression of genes involved in ECM organization pathways, as observed with

the mice infected with PA103, also occurs with the early stages of lung disease such as CF and COPD (46-49). As these diseases progress, the deposition of certain classes of collagen (particularly I and III) leads to fibrosis and decreases patient respiratory capacity (46, 49).

In conclusion, prophylactic treatment with IDR-1002 reduced bacterial counts and inflammation caused by *P. aeruginosa* infection. Interestingly we recently showed that IDR-1002 could also suppress inflammation in an alginate model used to represent chronic lung infection but had no effect on bacterial counts in the lung (19). The RNA-Seq results here revealed the differential expression of 4,739 host genes in the lungs (nearly 20% of all of the genes in a mouse) and 1,327 host genes in the blood in response to *P. aeruginosa* acute lung infection, while the treatment of *P. aeruginosa* infections with IDR-1002 led to a more muted response compared to infection alone, with only a few hundred DE genes compared to uninfected controls. Finally, the combination of IDR-1002 and PA103 compared to PA103 alone indicated 2,111 DE genes that were influenced by peptide treatment, in particular revealing a muted innate immune/inflammatory response. These data provided additional insights into *P. aeruginosa* infection, revealing several new elements not observed previously, and possible mechanisms of IDR-1002 protection. Together, these results suggest that IDR-1002 could potentially be used as an adjuvant (perhaps together with antibiotics) to prime the host immune system by modulating the inflammatory response, cytokine production and immune cell recruitment. Given that IDRs have been shown to have additional activities such as anti-biofilm activity and demonstrate synergistic effects when used in combination with conventional antibiotics, our future work will focus on identifying the appropriate synergistic combinations to develop ~~Most importantly, these results provided evidence supporting the potential use of~~ IDRs as agents for use against *P. aeruginosa* acute lung infections (50-52).

Materials and methods

Mice and ethics statement

Female C57Bl/6J mice were purchased from Jackson Laboratory or were bred at the Modified Barrier Facility (University of British Columbia, Vancouver, Canada) and used between 6-8 weeks of age. Animals were housed at the Modified Barrier Facility and kept on a standard 12 h/12 h light/dark timed schedule with ad libitum access to food and water. All experiments were approved by the UBC Animal Care Committee.

Reagents

IDR-1002 (VQRWLIVWRIRK-NH_2) was synthesized by F-moc chemistry (Kinexus, Vancouver, British Columbia, Canada) and stored at -20°C as a desiccated powder. For experiments, peptide was resuspended in endotoxin-free water and stored at -20°C.

Preparation of bacteria and acute *Pseudomonas* lung infection

The culture was prepared and mice infected as previously described (19). Briefly, a frozen stock of bacterial strain *P. aeruginosa* PA103 was streaked onto LB plates and grown overnight at 37°C, then individual CFUs from the plates were used in LB and grown overnight at 37°C with shaking. Overnight cultures were diluted 1:50 and grown to an OD_{600} reading of approximately 0.5. After washing with endotoxin-free 0.9% sodium chloride solution (saline), the cultures were centrifuged and the supernatant discarded, then the bacteria were resuspended in endotoxin-free saline to an OD_{600} of 0.5. Bacteria were then diluted to the final concentration for immediate instillation in vivo at ~8 x 10^5 CFU/mouse.

Mice were anesthetized with isoflurane (2-5%), placed on an intubation stand (BrainTree Scientific, Braintree, Massachusetts, USA), and given IDR-1002 (10-20 µl depending on mouse weight) or endotoxin-free water, then after 24 h the mice were again anesthetized, placed on the

intubation stand, and given either *P. aeruginosa* (20 µl) or endotoxin-free saline (20 µl). The solutions were instilled dropwise into the left nostril of each mouse using a micropipette, with periodic administration of isoflurane to maintain a steady respiratory rate. After instillation, mice were kept on the intubation stand under isoflurane for 2-3 minutes to ensure absorption of the liquid. Mice were monitored at 3 and 18 h post-infection and assigned health scores based on a scoring sheet approved by the UBC Animal Care Committee (Table S1).

Mice were euthanized with an intraperitoneal injection of sodium pentobarbital (120 mg/kg). Blood was collected from the inferior vena cava and 100 µl was placed in RNAprotect animal blood tubes (Qiagen, Hilden, Germany) for RNA isolation according to the manufacturer's protocol. The remaining blood was allowed to clot, then centrifuged and the serum was collected and stored at -20°C until used for ELISAs. For BALF collection, the chest cavity and trachea were exposed and an incision was made in the trachea. A cannulated needle was then inserted and used to slowly fill the lungs with sterile PBS (600 µl), which was then slowly withdrawn through the cannulated needle and saved. This procedure was repeated twice for a total of three washes. After the lavage, the smallest lobe of the lung was placed in RNAlater (Qiagen) and saved for RNA-Seq according to the manufacturer's protocol.

The first BALF wash was used for CFU enumeration by spread-plating undiluted BALF or ten-fold dilutions made in PBS onto LB agar plates in duplicate. Plates were incubated overnight at 37°C and CFUs were enumerated the following day. The remaining first BALF wash was centrifuged and the supernatant saved at -20°C until used for ELISAs. The pellet from the first BALF wash was combined with the pellet from BALF washes 2 and 3 and resuspended in PBS, then leukocytes were counted on a hemocytometer using Turk's stain.

The leukocytes were also used in a StatSpin Cytofuge 2 (Beckman-Coulter) and the resulting slides were air-dried overnight, stained with the Diff-Quik Staining Kit (VWR, Radnor, Pennsylvania, USA) according to the manufacturer's protocol, and then 200 cells/slide were counted.

ELISAs

The levels of cytokines and chemokines were measured using antibodies and standards from eBioscience (San Diego, California, USA) for TNF-α and IL-6, eBioscience or R&D Systems (Minneapolis, Minnesota, USA) for MCP-1, and Fitzgerald (Acton, Massachusetts, USA) or R&D Systems for KC. The ELISAs were performed as per the manufacturer protocols, with optimization of antibody and sample dilutions, washes, and incubation times. ELISAs were developed with TMB (eBioscience) and the enzymatic reactions stopped with 2 N sulfuric acid. The plates were read on a Power Wave X340 plate-reader (Bio-Tek Instruments, Winooski, Vermont, USA) and data were fitted to a 4-parameter standard curve using KC4 software (Bio-Tek).

RNA isolation and RNA-Seq

Total RNA was isolated from the lungs and blood from one experiment (n = 5 per condition) using the RNAeasy Plus Mini kit (Qiagen). The quality of the RNA was analyzed using an RNA 6000 Nano Chip (Agilent Technologies, Santa Clara, California, USA) on an Agilent 2100 Bioanalyzer, with all samples showing excellent quality with RNA integrity number (RIN) values of greater than 8. An enrichment with poly d(T) beads (New England Biolabs, Ipswich, Massachusetts, USA) was then used to isolate the mRNA, and a KAPA Stranded Total RNA-Seq kit (Kapa Biosystems, Wilmington, Massachusetts, USA) was used to create the cDNA libraries. In brief, first strand cDNA was synthesized, following by second

strand synthesis and blunt-end formation. After 3' adenylation, adapters (Bioo Scientific, Austin, Texas, USA) for multiplexing were ligated, followed by amplification and then purification using Agencourt Ampure XP beads (Beckman Coulter). The quality of the library was checked using a High Sensitivity DNA chip (Agilent, Santa Clara, California, USA) on an Agilent 2100 Bioanalyzer and all samples were shown to have optimal fragment size distribution. The libraries were sequenced on an Illumina (San Diego, California, USA) GAIIx (lungs) or HiSeq 2500 Rapid Run (blood).

After demultiplexing, the resulting FASTQ files were aligned to the Ensembl murine reference genome GRCm38.p5 (build 86) using STAR aligner (version 2.5.2B) (53). Read count tables were generated using HTSeq-count (version 0.6.1p1) (54). DESeq2 (1.14.1) in R (3.3.2) was used for finding differentially expressed (DE) genes, with cutoffs for DE genes set as a fold-change of ± 1.5, equivalent to a $\log_2$ FC of ± 0.58, and an adjusted p-value (false discovery rate) of < 0.05 (55, 56). One mouse in the PA103 group was inadequately infected and was removed from the analysis for lungs and blood. All remaining lung samples had excellent quality and number of read counts. For the blood, samples with < 800,000 read counts were excluded, leaving n = 3 per condition except for the PA103 group which had n = 4. The DE genes were analyzed with Signature Overrepresentation Analysis (SIGORA) for pathway enrichment analysis using the Reactome gene annotation system, using an adjusted p-value cutoff of < 0.001 as recommended by the SIGORA manual (33). The DE genes were used in NetworkAnalyst for network visualization using the Imex database (38).

The RNA transcriptomic data have been submitted to the National Center for Biotechnology Information Gene Expression Omnibus under accession number GSE110415.

Lung samples were also used for validation in qPCR. The RNA isolated for RNA-Seq was transcribed into cDNA using the cDNA synthesis kit from Quanta Biosciences (Beverly, Massachusetts, USA). The cDNA was used for real time qPCR using the two-step SYBR Green qPCR master mix from Roche (Basel, Switzerland) and primers (Table S2) from Thermofisher (Waltham, Massachusetts, USA). Fold-changes were calculated based on the Ct value method using the average Ct value of two housekeeping genes, *Eef2* and *B2m*, and values compared to the control group.

Statistical analysis

Data from the lung model were analyzed using Microsoft Excel 2013 and GraphPad Prism version 7. GraphPad Prism was used to perform an unpaired two-tailed t-test or one-way ANOVA with Tukey's multiple comparisons tests. A value of $p \leq 0.05$ was considered statistically significant.

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Peptide IDR-1002 is the subject of a pending patent granted to REWH and 3 other inventors in the US and Europe, assigned to their employer the University of British Columbia, and licensed to ABT Innovations, Inc., Victoria, British Columbia, Canada, which is partly owned by REWH.

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613
614 **Figure legends**
615

616 **Fig. 1: IDR-1002 treatment reduced CFU burden and in mice infected with *P. aeruginosa***
617 **PA103.** Mice were given water or IDR-1002 at -24 h, given saline or *P. aeruginosa* PA103 at 0
618 h, then euthanized and samples processed at 18 h. (A) CFU counts from the BALF. (B)
619 Leukocyte counts in the BALF. (C) Distribution of leukocytes in the BALF represented as mean
620 ± SEM. (D) Percentage of weight loss. (E, F) Health scores at 3 h or 18 h post-infection. Data
621 represent n = 9 or 10 mice per condition from the combination of two experiments and were
622 analyzed using an unpaired two-tailed t-test for the CFUs (A), a one-way ANOVA and Tukey's
623 multiple comparisons test for the total leukocytes (B), and Kruskal-Wallis with Dunn's multiple
624 comparisons test (C-F). *: $p \leq 0.05$, **: $p \leq 0.01$.
625

626 **Fig. 2: IDR-1002 treatment reduced cytokines and chemokines in the BALF and serum that**
627 **were induced by *P. aeruginosa* PA103.** Mice were given water or IDR-1002 at -24 h, given
628 saline or *P. aeruginosa* PA103 at 0 h, then euthanized and samples processed at 18 h. ELISAs
629 were performed for MCP-1 in BALF (A) and serum (B); KC in BALF (C) and serum (D); IL-6
630 in BALF (E) and serum (F); and TNF-α in BALF (G) and serum (H). Data represent mean ±
631 SEM for n = 9 or 10 mice per condition from the combination of two experiments and were
632 analyzed using one-way ANOVA and Tukey's multiple comparisons test. *: $p \leq 0.05$, **: $p \leq$
633 0.01, ***: $p \leq 0.001$.
634

635 **Fig. 3: Zero-order protein-protein interaction network of DE genes in the lungs for PA103**
636 **infected vs. negative control mice that are associated with leukocyte migration and their**

interacting partners. Red nodes were upregulated in the PA103 group and green nodes were downregulated in the PA103 group. A darker color indicates a stronger fold-change. Chemokines are highlighted with blue circles.

Fig. 4: Zero-order protein-protein interaction network of DE genes in the lungs for PA103 infected vs. negative control mice that are associated with ECM organization and their interacting partners. Red nodes were upregulated in the PA103 group and green nodes were downregulated in the PA103 group. A darker color indicates a stronger fold-change. The gene for matrix metalloproteinase MMP-9 and components of collagen are highlighted with blue circles.

Fig. 5: Zero-order protein-protein interaction network of DE genes in the blood for PA103 infected vs. negative control mice. Red nodes were upregulated in the PA103 group and green nodes were downregulated in the PA103 group. A darker color indicates a stronger fold-change. Several key genes involved in the immune response to an infection are highlighted with blue circles.

Fig. 6: Zero-order protein-protein interaction network of DE genes in the lungs for IDR-1002 treatment vs. PA103 infected mice. Red nodes were upregulated in the treatment group and green nodes were downregulated in the treatment group. A darker color indicates a stronger fold-change. Several key genes involved in the immune response to an infection are highlighted with blue circles.

Tables

Table 1: Number of host DE genes for different comparisons in the lungs and blood.

Comparison	Lungs	Blood
IDR-1002 control vs. Negative control	2	0
PA103 infected vs. Negative control	4739	1327
IDR-1002 treatment vs. Negative control	813	294
IDR-1002 treatment vs. IDR-1002 control	638	271
IDR-1002 treatment vs. PA103 infected	2111	1

Table 2: Host pathways dysregulated in the lungs for PA103 infected vs. negative control mice.

Pathway description	Corrected p value
Hemostasis	4.07E-88
Axon guidance	4.39E-77
Chemokine receptors bind chemokines	3.57E-70
Interferon gamma signaling	1.99E-68
Signaling by PDGF	4.83E-58
Metabolism of water-soluble vitamins and cofactors	1.07E-41
Cytokine Signaling in Immune system	2.25E-39
MyD88-independent TLR3/TLR4 cascade	2.14E-36
Extracellular matrix organization	4.85E-29
Basigin interactions	1.82E-26
Toll Like Receptor 5 (TLR5) Cascade	2.18E-22
Collagen degradation	3.64E-21
Interleukin-1 signaling	1.38E-20
Iron uptake and transport	6.24E-20
Collagen biosynthesis and modifying enzymes	8.06E-20
Integrin alphaIIb beta3 signaling	3.60E-17
Cell surface interactions at the vascular wall	1.77E-16
Signaling by ERBB2	1.93E-15
Signaling by FGFR	2.33E-14
SHC-mediated cascade:FGFR2	4.66E-14
Pyruvate metabolism	5.00E-14
Mitochondrial Fatty Acid Beta-Oxidation	1.58E-13
Intraflagellar transport	2.83E-13
Molecules associated with elastic fibres	2.93E-13
Integrin cell surface interactions	3.02E-13
Association of TriC/CCT with target proteins during biosynthesis	9.11E-13
Signaling by the B Cell Receptor (BCR)	1.34E-12
Biotin transport and metabolism	1.58E-12
Other semaphorin interactions	2.94E-12

Activated TLR4 signalling	3.64E-12
TNF receptor superfamily (TNFSF) members mediating non-canonical NF-kB pathway	5.66E-12
Signaling by Interleukins	2.13E-11
Toll Like Receptor TLR1:TLR2 Cascade	3.41E-10
Binding and Uptake of Ligands by Scavenger Receptors	1.85E-09
PI3K Cascade	2.89E-09
Amino acid transport across the plasma membrane	2.20E-08
Frs2-mediated activation	2.83E-08
FRS-mediated FGFR3 signaling	3.08E-08
Transport of inorganic cations/anions and amino acids/oligopeptides	3.20E-08
Kinesins	6.55E-08
ARMS-mediated activation	1.47E-07
Erythrocytes take up oxygen and release carbon dioxide	2.16E-07
p130Cas linkage to MAPK signaling for integrins	3.14E-07
Toll Like Receptor 10 (TLR10) Cascade	1.13E-06
TNFR2 non-canonical NF-kB pathway	1.19E-06
Scavenging by Class A Receptors	2.93E-06
Assembly of the primary cilium	8.91E-06
Toll Like Receptor 4 (TLR4) Cascade	1.16E-05
Energy dependent regulation of mTOR by LKB1-AMPK	1.41E-05
C-type lectin receptors (CLRs)	2.29E-05
RAF-independent MAPK1/3 activation	9.34E-05
PD-1 signaling	0.000123
GPVI-mediated activation cascade	0.000158
Tetrahydrobiopterin (BH4) synthesis, recycling, salvage and regulation	0.000163
Activation of SMO	0.000193
Semaphorin interactions	0.000248
Metal ion SLC transporters	0.000354
NCAM1 interactions	0.000747
Effects of PIP2 hydrolysis	0.000969

Table 3: Host pathways dysregulated in the blood for PA103 infected vs. negative control mice.

Pathway description	Corrected p value
C-type lectin receptors (CLRs)	2.08E-09
Immunoregulatory interactions between a Lymphoid and a non-Lymphoid cell	5.56E-09
Interferon Signaling	4.76E-08
Antigen activates B Cell Receptor (BCR) leading to generation of second messengers	9.27E-08
Hemostasis	5.21E-07
MHC class II antigen presentation	1.27E-06
Chromatin organization	1.97E-06
Transcriptional Regulation of Adipocyte Differentiation in 3T3-L1 Pre-adipocytes	3.00E-06
Respiratory electron transport	3.37E-06
Cellular responses to stress	6.14E-06
Signaling by the B Cell Receptor (BCR)	9.93E-05
Chemokine receptors bind chemokines	0.000111
Negative regulators of RIG-I/MDA5 signaling	0.000196
Interferon gamma signaling	0.000201
Respiratory electron transport, ATP synthesis by chemiosmotic coupling, and heat production by uncoupling proteins.	0.000204
Toll Like Receptor 4 (TLR4) Cascade	0.000876
Purine catabolism	0.000892
MyD88-independent TLR3/TLR4 cascade	0.000952

Table 4: Host pathways dysregulated in the lungs for IDR-1002 treatment vs. PA103 infected mice.

Pathway description	Corrected p value
Axon guidance	6.24E-26
Hemostasis	1.97E-25
Transport of inorganic cations/anions and amino acids/oligopeptides	3.08E-21
Collagen degradation	2.50E-13
Basigin interactions	8.71E-10
Prolonged ERK activation events	9.18E-08
Iron uptake and transport	1.05E-06
Cell surface interactions at the vascular wall	2.06E-06
IRF3-mediated induction of type I IFN	2.42E-06
Amino acid transport across the plasma membrane	3.65E-06
Extracellular matrix organization	4.73E-06
Integrin cell surface interactions	5.76E-06
Biotin transport and metabolism	8.36E-06
CRMPs in Sema3A signaling	9.03E-06
Hyaluronan uptake and degradation	2.45E-05
Signaling by FGFR	0.0001352
Activation of SMO	0.000139
Semaphorin interactions	0.0001657
Activated TLR4 signalling	0.0001719
Kinesins	0.0003253