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Kinase Activity Profiling of Pneumococcal Pneumonia

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Abstract

Background: Pneumonia represents a major health burden. Previous work demonstrated that although the induction of inflammation is important for adequate host defense against pneumonia, an inability to regulate the host's inflammatory response within the lung later during infection can be detrimental. Intracellular signaling pathways commonly rely on activation of kinases, and kinases play an essential role in the regulation of the inflammatory response of immune cells.

Methodology/Principal Findings: Pneumonia was induced in mice via intranasal instillation of Streptococcus (S.) pneumoniae. Kinomics peptide arrays, exhibiting 1024 specific consensus sequences for protein kinases, were used to produce a systems biology analysis of cellular kinase activity during the course of pneumonia. Several differences in kinase activity revealed by the arrays were validated in lung homogenates of individual mice using western blot. We identified cascades of activated kinases showing that chemotoxic stress and a T helper 1 response were induced during the course of pneumococcal pneumonia. In addition, our data point to a reduction in WNT activity in lungs of S. pneumoniae infected mice. Moreover, this study demonstrated a reduction in overall CDK activity implying alterations in cell cycle biology.

Conclusions/Significance: This study utilizes systems biology to provide insight into the signaling events occurring during lung infection with the common cause of community acquired pneumonia, and may assist in identifying novel therapeutic targets in the treatment of bacterial pneumonia.

Introduction

Due to its unique relationship with the environment, the lung must defend itself from infection by numerous inhaled microorganisms. Although in general the lung is successful in doing so, bacterial pneumonia remains a major health burden. The Gram-positive bacterium S. pneumoniae is the main causative pathogen in community-acquired pneumonia (CAP), responsible for an estimated ten million deaths annually worldwide [1,2,3]. Increasing resistance of this common pathogen to antibiotics is a great concern [4,5,6].

Recognition of invading bacteria by the host is considered to occur mainly through toll-like receptors (TLRs). After interacting with their ligands, TLRs signal via adaptor proteins and kinases to activate Nuclear factor-kB (NF-kB) inducing inflammatory responses [7]. However, the interactions between bacteria and host cells are not confined to TLRs and ongoing intracellular signaling cascades may be much more extensive and complex than generally thought. Many studies on host pathogen interactions concentrate mainly on isolated pathways [8,9,10,11]. Although elegant in emphasizing the importance of these single pathways, such studies do not address the synergy of the multitude of signal-cascades, activated upon recognition of pathogens. Systems biology provides tools to enable understanding of such complex matters.

Kinases comprise an important part of the intracellular responses mediated by a variety of receptors. Although it is highly likely that kinases mediate lung inflammation during pneumonia, knowledge about the activation of kinases during pneumonia is limited. Microarray-based kinase profiling approaches have been subject of development over the last years and an interesting tool to integral study signaling events [12,13,14]. Unraveling the complexities of the host-pathogen interactions during pneumococcal pneumonia can be of great value in finding new targets of therapy. Here we use a radio-kinome substrate array to determine kinase activities in the lungs during S. pneumoniae pneumonia in mice and furthermore attempt to elucidate complex interactions occurring during the course of the infection. To our surprise, we did not detect signaling pathways belonging to the TLR signaling cascades. In contrast, we detected pathways that induce chemotoxic stress and promoted the T helper 1 (Th1) response. In addition we found an overall reduction in WNT signaling. Canonical WNT signaling, named after the homology of WNT-genes with int-1 and wingless in Drosophila, is important in...
developmental signaling [13,16]. However more roles of this signaling cascade have emerged (e.g. development of cancer)[17]. Moreover, we found a reduction in cell cycle activity during the course of S. pneumoniae pneumonia. This study is the first to apply kinome profiling using kinomics chip arrays in infectious diseases.

Results

Bacterial pneumonia

First, we determined the course of bacterial infection. After instillation of S. pneumoniae bacterial loads remained similar at 3 and 6 hours (Figure 1a). Between 6 and 24 hours bacterial loads in the lung increased exponentially (up to 5 logs increase). At this time an apparent maximum number of bacteria had been reached in the lung compartment, as no further increase was detected at 48 hours. The induction of lung inflammation was illustrated by increases in the pulmonary levels of all measured cytokines (cytokine-induced neutrophil chemoattractant (KC), interleukin (IL)-1β, IL-6, and chemokines (cytokine-induced neutrophil chemoattractant (KC)), Macrophage inflammatory protein (MIP)-2) during the course of bacterial pneumonia (Figures 1b–f).

Kinome profile overview

To determine the relation between each data-set of obtained kinome profiles we performed hierarchical clustering according to Johnson (Figure 2a) [18]. During S. pneumoniae infection the distance to the control increased throughout the course of infection and with increasing bacterial loads, indicating increased divergence from the initial kinase activity profile. Interestingly, 6 hours after infection, the kinome profile resembled that of the control more than the profile at 3 hours. This suggested that strong changes occurred in phosphorylation patterns early in infection. As the infection progressed more changes in the kinome profile were detected, creating a greater distance in the cluster. The greatest distance to the control was found at 24 and 48 hours, which cluster outside of the control and 3 and 6 hours group. Overall, a total of 153 kinases were found to be activated significantly different from uninfected control lungs. In Figure 2b a multi-dimensional Venn diagram represents distribution of phosphorylation events in time. When studied at separate time points the following patterns were observed: 53 spots were detectible by western blot assay (Figure 7). The total kinase A (PKA) and mitogen-activated protein kinase (MAPK) activation differed from uninfected lungs at all time points studied. Of note, the MAPK spot (960) is a MAPK_group phosphorylation site, thus does not indicate which pathway is implicated.

S. pneumoniae impact on signaling in the lung

Infection with S. pneumoniae induced a multitude of changes in kinome activity. Figure 3 shows an overview of ongoing processes during infection. Kinome chip analysis revealed that during pneumonia a Th1 associated signaling was induced as illustrated by the reduced activity of B-cell receptor (BCR, spot 68) at 3 hours, nuclear factor of activated T-cells (NFAT, spot 89) at 3 and 48 hours [19] and v-abl Abelson murine leukemia viral oncogene homolog 1 (ABL, spots 660 and 672) at 3, 24 and 48 hours [20]. Furthermore, increased activities of Ataxia telangiectasia mutated (ATM, spot 36) and DNA-dependent protein kinase (DNApK, spots 495 and 553) at 6 hours revealed the emergence of chemotoxic stress. ATM was upregulated likely due to presence of reactive oxygen species and DNA damage [21,22]. DNApK activation occurs in response to DNA damage signals [23,24]. In contrast to induction of chemotoxic stress, downstream insulin-receptor (INS-R) signaling was inhibited, as demonstrated by the reduced activity of pyruvate dehydrogenase kinase (PDK, spot 226) at 6, 24 and 48 hours, AMP-activated protein kinase (AMPK, spot 572) at 48 hours and the dynamic profiles of AKT (spots 46, 105, 361, 397, 557 and 901), which has events at all time points, and glycogen synthase kinase-3β (GSK-3β, spots 2, 116, 157 and 959) at 3 and 24 hours with both an increase and decrease in activity early during infection and a subsequent decrease/stabilization in the late phases of pneumococcal pneumonia. A decrease in transforming growth factor-β (TGF-β, spot 870) activity was seen at 3 hours. Casein kinase-2 (CK2, spots 60, 173, 256, 573, 618, 792 and 1005) is involved and needed for WNT activation [25], while casein kinase-1 (CK1, spot 310) inhibits WNT signaling [26].

The found GSK-3β primary activation and reduction could also attribute to WNT signaling. In line, we found overall reduced activity of ephrin (EHP1, spot 12) at 3 hours and β-catenin/spots (137 and 321) at 3, 24 and 48 hours. Interestingly, kinome array analysis revealed reduced activity for numeral kinases involved in regulation of the cell cycle (Cyclin-dependent kinase (CDK):1: spots 105, 3112, 542, 796, 554, 615/CDK2 spot 309/CDK4 spots: 274, 374, 668/CDK5 spot 420).

Western blots of selected kinases confirm kinomics chip kinome profile data

In order to validate the phosphorylation-states of AMPK-α both phosphorylated and unphosphorylated AMPK-α were detected in lung homogenates from S. pneumoniae infected animals (Figure 4b). When comparing AMPK-α activity on the kinomics chip (Figure 4a) with the results from the western blots, a similar pattern emerged: decreased phosphorylation of AMPK-α at later time points of infection (Figure 4c).

To investigate if phosphorylation status of substrates on the kinomics chip mirrors that of more upstream kinases the phosphorylation state of Ser9, an inhibitory site of GSK-3β was measured. GSK-3β phosphorylates the substrate glycogen synthase 1 (GS-1). However inhibition of GSK-3β at Ser9 results in reduced GS-1 phosphorylation. Indeed, GS-1 on the kinomics chip showed reduced phosphorylation at all time points except for 24 hours after infection. As demonstrated by Figure 5a, GSK-3β activity was enhanced during the first 6 hours of infection. Activation pattern of the substrate GS-1 matched the activity of upstream kinase closely; the ratio of the inverted p-GSK-3β signal closely resembled the ratio of the kinomics chip signal of GS-1. In general, CDK activity was decreased over time during pneumonia (Table 1). Since antibodies for the different CDK substrates (cyclins) are not available, we set out to validate these findings by using a pan CDK p-substrate western blot. By this approach we can detect activity of all CDKs at once. Semi-quantitative analysis of the blots validated the results obtained by the kinomics chip kinome profiles (Figure 6a, b): overall CDK activity in S. pneumoniae infection was decreased.

Upon phosphorylation, β-catenin is rapidly degraded, reflecting the off state of WNT [27]. Unsurprisingly, only β-catenin levels were detectible by western blot assay (Figure 7). The total β-catenin amounts decreased over time. This, indirectly, represents a decrease of potentially active β-catenin.

Discussion

Current mass spectrometry techniques and novel proteomics approaches like antibody microarrays determine protein phosphorylation levels rather than the enzymatic activity resulting from
it, while measurement of kinase activity using the peptide microarray provides a direct view on the extent of enzymatic activity leading to specific signal transduction. We here utilized kinome substrate arrays to obtain insight in alterations in kinase activity in the lungs during respiratory tract infection caused by the most common causative agent in CAP, *S. pneumoniae*. The most strongly affected pathways identified during pneumococcal pneumonia were associated with enhanced chemotoxic stress, a developing Th1 response, reduced WNT signaling and downregulated cell cycle activity.

The infectious dose of *S. pneumoniae* chosen causes lethality in mice from 48 hours onward with an overall mortality rate of 90%--
Pneumococcal pneumonia was induced, as demonstrated by a profound bacterial outgrowth and a strong induction
of inflammatory cytokines and chemokines. We obtained lung samples between 3 and 48 hours after infection, thus
presenting the entire dynamics of the host response during pneumococcal pneumonia from shortly after
infection until shortly before death. As such, kinases activities found in the kinomics analysis are representative of
severe pneumococcal pneumonia.

The kinome profile dendogram (Figure 2a) generated from lung samples harvested 6 hours after infection was more closely related
to control than the kinome profile obtained after 3 hours. We hypothesize that this is the effect of early and rapid changes
occurring in response to the introduction of the pathogen. Of note, cells migrating into lung tissue in response to
S. pneumoniae entering the airways likely affect kinome profiling patterns, since these were generated from whole lung homogenates. Kinome studies on
specific leukocyte subsets purified from lung tissue at several time points after induction of pneumonia might circumvent this
shortcoming. However, cell isolation procedures potentially influence phosphorylation states and thus we chose to utilize total
lung lysates, generated from snap frozen material. One also has to consider that, when searching for new therapies, it is the
whole lung that will be exposed to a potential drug, e.g. administered via nebulization. Therefore, we chose to determine
kinase profiles of total lung lysates without isolating different cell types.

Analysis of our chip data revealed several significant ongoing processes in pneumonia. Much to our surprise specific MAPKs
and other kinases classically related with the immune response, like those involved with TLR signaling (e.g. inhibitory κB (IKK)-α/
IKKβ), TANK-binding kinase 1 and MAPK-kinase 1 (MEK-1)) were not prominently present in the results obtained from the
kinomics chip, not even at the earliest time point. A general MAPK substrate however was shared between time points, but no
links to its specific contexts could be made. Ex vivo stimulation of bone marrow derived macrophages with serotype 2 S. pneumoniae
gave rise to p38MAPK/c-Jun N-terminal kinase and extracellular signal-regulated kinase (ERK) phosphorylation [30]. Moreover, in
a murine model of pneumococcal pneumonia p38MAPK inhibition resulted in enhanced bacterial loads [31], thus
indicating that MAPKs may play a role in pneumococcal pneumonia.

PKA was also shared in all time points. This kinase is involved
in regulation of proliferation and differentiation, microtubule
dynamics, chromatin condensation and decondensation, nuclear
envelope disassembly and reassembly, as well as regulation of
intracellular transport mechanisms and ion fluxes [32]. Thus, its
overall presence is not surprising.

In context of an immune response to bacterial infection, the
Th1 response signaling was the only prominent pathway that
appeared in our analysis. Th1 responses were mirrored by the
decreased activity of BCR and NFAT. De-phosphorylation of
NFAT (as a substrate) enables its translocation to the nucleus
inducing IL-2 transcription [33]. Contrary to NFAT and BCR,
ABL activation was decreased reducing its Th1 inducing responses
[34]. Although in this model of acute respiratory tract infection, the
innate immune response plays an important role, T cell
immune function is important for generating an adaptive immune
response and memory building.

Moreover, in recent studies CD8 knockout mice or CD8+ T-cell
depleted wild type mice displayed an increased susceptibility to
serotype 3 pneumococcal pneumonia, while adoptive transfer of
CD8+ T-cell to knockout mice improved survival [35]. Our Th1
results combined with this study demonstrate that T cells play a
role in serotype 3 pneumococcal pneumonia.

A variety of CDKs and CDK associated kinases displayed a
reduced activity during the course of pneumococcal pneumonia.
These kinases regulate the progression through the cell cycle [36].
However, recent studies demonstrate that utilizing a CDK inhibitor
reduced cerebrospinal fluid leukocyte count, hemorrhagic events
and improved recovery in a mouse model of antibiotic treated S.
puernoeae meningitis [37]. It is proposed that the inhibition of
CDKs in effect facilitates induction of caspase dependent apoptosis
via myeloid cell leukemia sequence 1 (MCL-1) [38,39]. The
functional role of CDKs during S. pneumoniae pneumonia remains to
be established.

Several kinases not primarily associated with inflammation or
infection, were abundant in our findings. Nonetheless, most of these
kinases have been implicated to also contribute to an inflammatory
Figure 3. Provisional signal transduction scheme of active signaling pathways during pneumonia. Activation is depicted in green and inhibition in red, direction of events is calculated in relation to the noninfected control. Events from all timepoints (3, 6, 24 and 48 hours) were used to construct this scheme representing the entire host response dynamics of pneumococcal pneumonia. Important are the overall increment of chemotoxic stress and the initiation of the Th1 response. Spot numbers and activities (up ↑ or down ↓) are presented with corresponding kinases and timepoints. WNT signaling and the cell cycle are reduced throughout S. pneumoniae pneumonia.

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AMPK-α and GSK-3β mainly are known in metabolic context, specifically in insulin and glucose signaling [40,41], but also have strong connections with inflammation. AMPK activation results in reduced TLR4 dependent lung inflammation [42]. GSK3 inhibition reduced IL-12p40, IL-6 and TNF-α in a mouse model of tularemia [43]. Furthermore, TLR induced pro-inflammatory cytokine production was reduced in monocytes by GSK-3β inhibition [44]. TGF-β is known to have strong anti-inflammatory effects [45]. Both GSK-3β and TGF-β, via CK2, are implicated in WNT signaling [46]. Our kinome analysis demonstrated that WNT signaling is overall reduced during pneumonia. To our knowledge, the role of WNT signaling in pneumococcal pneumonia has not been clearly defined yet, although β-catenin signaling has been...
associated with MAPK-signaling and modulation of NFκB function [46,47]. WNT5 was described to contribute to the inflammatory response of human macrophages[48].

It should be noted, however, that differences in pneumococcal serotype can illicit differential immune responses. Serotype 11a (M10) murine pneumococcal pneumonia resulted in an early local levels of TNF-α and IL-6 in the pulmonary compartment, whereas

| Kinase | Protein | Motif | Signal | Event time |
|--------|---------|-------|--------|-----------|
| CDK1   | RAP1GAP | IVPGKSPTTXK | Down | 24 h |
| CDK1   | MYOD1   | GDSASSPR5N  | Down | 3 h |
| CDK1   | CALD1   | PTAAGTPNKT | Down | 48 h |
| CDK1   | DAB1    | APRQSSPKSS  | Down | 3 h |
| CDK2-cyclin E | COIL | EAKRSPKKE    | Down | 24, 48 h |

Figure 6. Decrease in CDK activity with increasing pneumonia.

Western blot (a) and quantification (b) revealed a decrease in CDK activity. Quantification was performed for all positive signals on the blot and corrected for β-actin. Data are represented as mean ± SD of n=3. doi:10.1371/journal.pone.0018519.g006

Table 1. Kinome chip analysis of cyclin-dependent kinase activity.

Figure 7. β-catenin levels decrease over time.

Western blot (a) and quantification (b) of β-catenin. β-catenin protein levels decrease during S. pneumoniae pneumonia. Indirectly, represent a decrease of potentially active β-catenin. Data are represented as mean ± SD of n=3. doi:10.1371/journal.pone.0018519.g007

Materials and Methods

Ethics Statement

This study was carried out in accordance with the Dutch Experiment on Animals Act. The Animal Care and Use Committee of the University of Amsterdam approved all experiments (Permit number: DIX100121).
Animals
For all experiments female C57Bl/6 mice (aged 10 weeks) were purchased from Charles River (Maastricht, The Netherlands). The Animal Care and Use Committee of the University of Amsterdam approved all experiments.

Induction of pneumonia/inflammation
Pneumonia was induced as previously described [28,29]. S. pneumoniae serotype 3 (ATCC 6303) was grown to a mid-logarithmic phase at 37°C in Todd-Hewitt broth supplemented with 0.5% Yeast extract (both Difco, Detroit, MI). Bacteria were harvested by centrifugation at 4000 rpm for 15 minutes; washed twice and resuspended in sterile saline at a concentration of 5 x 10⁸ colony forming units (CFU)/μl. Mice were inoculated with 50 μl of bacterial suspensions intranasally under isoflurane inhalation anesthesia (Ujoh, Ede, The Netherlands).

Determination of bacterial load
Three, six, 24 and 48 hours after infection, 3 mice per time point were sacrificed by cardiac puncture under Domitor (Pfizer Animal Health Care, Capelle aan de Ijssel, The Netherlands: active ingredient medetomidine) anesthesia. Left lungs were harvested and homogenized in 4 volumes of sterile saline with a tissue homogenizer (Proscience, Oxford, CT, USA). CFUs were determined from serial dilutions of samples, plated on blood agar plates and incubated at 37°C for 16 hours before colonies were counted.

Kinomics chip profiling
Right lungs were snap frozen in liquid nitrogen, after which they were homogenized in three volumes of lysis buffer (MPER (Pierce Rockville, WI, USA) enriched with 1 mM MgCl₂, 1 mM -glycerophosphate, 1 mM Na₃VO₄, 1 mM NaF, 1 mM phenylmethylsulphonyl fluoride). Homogenates were centrifuged at 14,000 RPM for 5 minutes and pellets were discarded. As a control, right lungs were harvested from 3 mice administered with sterile isotonic saline 3 hours earlier and treated as described above. For the kinomics chip kinome profile assay samples were pooled and diluted to a protein concentration of 1 mg/ml. Of these lysates, 80 μl was added to 12 μl of Activation mix (70 mM MgCl₂, 70 mM MnCl₂, 400 μg/ml PEG 8000 and 880 kBq [33P]-ATP) and this mixture was applied to a kinomics chip (Pepscan Presto, Lelystad, The Netherlands) per pool. The chips were incubated at 37°C for 2 hours. The arrays were washed twice in 2 M NaCl (1% TWEEN 20), once in PBS (1% SDS) and rinsed twice in demineralised H₂O. Subsequently the chips were air-dried and exposed to a phosphor imager plate for 72 hours. Analysis

Cytokine and chemokine assays
For cytokine and chemokine measurements, left lungs were excised, weighted and homogenized in saline four volumes of saline. Homogenates were diluted 1:2 in lysis buffer (300 mM NaCl, 30 mM Tris, 2 mM MgCl₂, 2 mM CaCl₂, 2% Triton X-100, AEBSF (4-[2-aminoethyl]benzenesulfonyl fluoride, EDTA-Na₂, 8 μg/ml pepstatin and leupeptin, pH 7.4) and incubated on ice for 30 minutes. Homogenates were centrifuged at 3600 rpm at 4°C for 10 minutes and stored at -20°C. IL-1β, IL-6, TNF-α, KC and MIP-2 were measured in lung homogenates using ELISAs (R&D Systems, Minneapolis, MN, USA) according to the manufacturer’s instructions. Detection limits were: TNF-α: 62.5 pg/ml, MIP-2 and KC: 15 pg/ml and 31.25 pg/ml for IL-1β, IL-6.

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Author Contributions
Conceived and designed the experiments: TvdP MPP CWW. Performed the experiments: AJH SHD. Analyzed the data: AJH MPP CWW. Contributed reagents/materials/analysis tools: TvdP MPP CWW. Wrote the paper: AJH TvdP MPP CWW.

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