Network Modeling Reveals Steps in Angiotensin Peptide Processing

John H. Schwacke, John Christian G. Spainhour, Jessalyn L. Ierardi, Jose M. Chaves, John M. Arthur, Michael G. Janech, Juan Carlos Q. Velez

Abstract—New insights into the intrarenal renin–angiotensin (Ang) system have modified our traditional view of the system. However, many finer details of this network of peptides and associated peptidases remain unclear. We hypothesized that a computational systems biology approach, applied to peptidomic data, could help to unravel the network of enzymatic conversions. We built and refined a Bayesian network model and a dynamic systems model starting from a skeleton created with established elements of the renin–Ang system and further developed it with archived matrix-assisted laser desorption ionization-time of flight mass spectra from experiments conducted in mouse podocytes exposed to exogenous Ang substrates. The model-building process suggested previously unrecognized steps, 3 of which were confirmed in vitro, including the conversion of Ang(2–10) to Ang(2–7) by neprilysin, Ang(1–9) to Ang(2–9), and Ang(1–7) to Ang(2–7) by aminopeptidase A. These data suggest a wider role of neprilysin and aminopeptidase A in glomerular formation of bioactive Ang peptides and shunting their formation. Other steps were also suggested by the model, and supporting evidence for those steps was evaluated using model-comparison methods. Our results demonstrate that systems biology methods applied to peptidomic data are effective in identifying novel steps in the Ang peptide processing network, and these findings improve our understanding of the glomerular renin–Ang system.

Key Words: mass spectrometry ■ proteomics ■ renin-angiotensin system ■ systems biology

The renin–angiotensin system (RAS) is one of the most important and well-studied regulatory hormonal systems in medicine and plays a role in blood pressure regulation, fluid and electrolyte balance, and development.1 The decapetide angiotensin (Ang) I, (Ang[1–10]), is cleaved from the N terminus of angiotensinogen by renin, and further cleavage by Ang-converting enzyme (ACE), chymase, neprilysin (NEP), aminopeptidase (AP) A, AP N, ACE2, and other RAS-associated peptidases produce a cocktail of bioactive fragments which act through various cell surface receptors (Ang II type 1 [AT₁], AT₂, AT₃, and AT₄). Distinct receptor activation can lead to opposing biological effects (eg, vasoconstriction versus vasodilatation), and our understanding of how these effects associate with the signaling flux across this cocktail of peptides is limited. Pharmacological blockade of the RAS is a therapeutic modality extensively used in clinical practice and specifically aimed to antagonize the generation or actions of Ang II (Ang[1–8]) to treat essential hypertension, heart failure, and chronic kidney disease.7–11 Although the introduction of RAS antagonists, that is ACE inhibitors, Ang AT₁ receptor blockers, and direct renin inhibitors into clinical practice have significantly improved treatment options, there are certain scenarios where the lack of a complete understanding of the intricacies of the local RAS may be limiting the potential for designing therapeutically valuable manipulations of the system.12–15 To date, study of the RAS has focused primarily on Ang II. Nonetheless, pharmacological alterations of the RAS result in simultaneous changes in abundance of various Ang peptides, as well as in compensatory changes in expression and activity of the participating RAS enzymes. The final stimulatory signal at a given cell reflects the combined concentrations of a cocktail of Ang peptides and their corresponding receptors present locally. In addition to Ang II, other peptide fragments (Ang[1–7], Ang[1–9], Ang[2–10], Ang III [Ang[2–8]], Ang IV [Ang[3–8]], Ang[2–7], Ang[3–7], and Ang[3–4]) have been identified as potentially bioactive, with actions in concert or in opposition.16–22 Local RAS systems have been identified in the kidney, heart, lung, liver, vasculature, and nervous system, and are, presumably, part of nearly every organ system.23 Of note, the RAS localized in the kidney is characterized by the highest tissue concentration of Ang II.24,25 We are only now beginning to understand the complexity of the network of peptidases that produce this profile and how that network differs across localities.

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Methods from the field of proteomics have significantly improved our ability to identify, classify, characterize, and quantify proteins and peptides in complex mixtures. Mass spectrometry (MS), coupled with stable, isotopically labeled peptide references and applied using the Absolute Quantification (AQUA) strategy, provides an effective tool for targeted quantification of peptides and proteins. In our applications, a cocktail of labeled Ang peptides of known concentrations is mixed with cell media and spotted on a matrix-assisted laser desorption ionization (MALDI) plate from which a spectrum is collected. Peak areas from isotopic clusters associated with native and AQUA peptides are calculated and native peptide quantities estimated from the cluster area ratios and known AQUA peptide concentrations. This method has proven effective in our laboratory and has resulted in an extensive archive of MALDI spectra from cell culture experiments. A recent reexamination of the archive indicated that many of the Ang peptides with masses >600 Da were clearly detectable and suggested that the normalized peak areas associated with these peptides might be informative as to the underlying peptide processing network. We therefore sought to determine whether a data mining and network modeling effort, applied to these data, might lead to the identification of novel steps in this important pathway.

The field of computational systems biology provides methods for integrating large data sets in support of efforts to identify, model, and understand the networks central to biological systems. One modeling approach, the Bayesian Network, has proven useful in identifying novel signaling biological systems. Another method, dynamic systems modeling, goes further, attempting to develop a mathematical model of the dynamic behavior of the system. Often, dynamic systems models are constructed using sets of ordinary differential or stochastic differential equations and the associated kinetic parameters. These models capture temporal relationships among the constituents of the network (eg, molecules of the signal transduction system) from observations of the network under various conditions of stimulation and inhibition. The resulting conditional dependencies give insight into potential interactions among the signaling system components and lead to novel discoveries in cell signaling systems. Another method, dynamic systems modeling, goes further, attempting to develop a mathematical model of the dynamic behavior of the system. Often, dynamic systems models are constructed using sets of ordinary differential or stochastic differential equations and the associated kinetic parameters. These models capture temporal relationships not easily represented in Bayesian networks but present a more challenging network identification and parameter estimation task.

Here we report on efforts to identify and confirm novel steps in the Ang peptide processing network using a database of spectra from previously conducted experiments. The study was executed in 2 phases. During the first phase, Ang peptide peak areas were extracted from an archive of spectra and used to build a Bayesian network representation of Ang peptide processing. Predictions from that network focused further experimental efforts that confirmed new steps suggested by the model. In the second phase, spectra from these additional experiments were added to the archive and the network model rebuilt. Steps suggested in the second model were then assessed in the context of a dynamic systems model. The study considered all Ang peptides identifiable in our archive without consideration for bioactivity, as we attempted to identify paths that bypass bioactive molecules as well as those that lead to bioactive molecules. We used computational methods from systems biology to build and refine the Bayesian networks and then to build a dynamic systems model from which the strength of evidence for novel edges can be assessed. Finally, we present confirmatory experimental evidence for 3 of the edges predicted through these methods; thus expanding our understanding of the Ang network and demonstrating the potential for mining archives of proteomic data using methods from systems biology.

### Materials and Methods

#### Mouse Podocyte Cell Culture

Immortalized mouse podocytes (generously provided by Dr Peter Mundel [Massachusetts General Hospital, Boston, MA] and Dr Jeffrey Kopp [National Institutes of Health, Bethesda, MD]) were grown under standard conditions as previously published. Cells were exposed to Ang substrates as previously described. See details in online-only Data Supplement.

#### MALDI-Time of Flight MS

Samples obtained at various time points were assayed by MALDI-time of flight (TOF) MS, as previously described, with minor modifications. See details in online-only Data Supplement.

#### Recombinant RAS Enzyme Activity

For an in vitro AP A activity assay, 100 ng of human recombinant AP A (R&D Systems, Minneapolis, MN) in assay buffer (25 mmol/L Tris, 50 mmol/L CaCl₂, 0.2 mol/L NaCl, pH 8.0) were preincubated in the presence or absence of 100 μmol/L amastatin (AP A inhibitor, Sigma-Aldrich, St. Louis, MO) for 20 minutes at room temperature and subsequently exposed to 1 μmol/L Ang(1–7) for 30 to 120 minutes. Reactions were quenched with 1% trifluoroacetic acid acidification. Cleavage of Ang peptide was analyzed by MALDI-TOF MS and isothe-labeled peptide quantification as described above. For an in vitro NEP activity assay, 100 ng of human recombinant NEP (R&D Systems) in assay buffer (50 mmol/L Tris, pH 7.4) were preincubated in the presence or absence of 1 μmol/L SCH33970 (NEP inhibitor) or 50 to 100 nmol/L thiorphan (Sigma–Aldrich) for 20 minutes at room temperature and subsequently exposed to 1 μmol/L Ang(2–10) for 15 to 60 minutes. Reactions were quenched with 1% trifluoroacetic acid acidification. Cleavage of Ang peptide was analyzed by MALDI-TOF MS and isothe-labeled peptide quantification as described above. All experiments were run in triplicate.

#### Mass Spectra Data Processing

Quantification in AQUA experiments and other peak area calculations were performed using a custom-developed software package developed in the R statistical computing language, version 2.11. Briefly, the elemental composition of each peptide (and its AQUA reference) was determined from the amino acid sequence and isotopic spectra were convoluted to compute the relative abundance of each isotopic peak. A search algorithm was used to find the peak width (resolution), mass error, baseline, and isotopic cluster area. The algorithm searches the space of mass errors and peak widths in a ~1 Da to +7 Da region about the monoisotopic mass and a linear fit to the observed intensity is computed giving the cluster area. The isotopic cluster area for the mass error and peak width giving the lowest R² value is taken as the area estimate. To account for overlap in isotopic clusters from nearby native peptides (eg, Ang[1–9], m/z 1183.6 and Ang[2–10], m/z 1181.7) and their associated AQUA peptides, groups of overlapping peptides were fit simultaneously, sharing a common baseline and peak width. Doing so facilitated decomposition of the overlapping isotopic clusters.
Estimated Peak Area Quality Assessment

Because we are not able to confirm the identity of each peak from the archived MALDI spectra, we must consider the possibility that some non-Ang peptide or source of noise might yield fits comparable to that of the peptides of interest. To assess the quality of the fitted isotopic clusters, we compared the distribution of $R^2$ for the Ang peptide fits with that obtained by fitting random peptide sequences of similar length. We also found that the $R^2$ distribution for fits to Ang peptides had a bathtub shape, indicative of a mixture of fits to noise (similar to the null case) and fits to peptides of interest. The minima of the bathtub occurred at $R^2 = 0.65$. This value was used as a threshold for accepting a peak area estimate in our modeling effort. The data set was then filtered, replacing peak areas having $R^2$ values below this threshold with a small value.

Bayesian Network Inference

Bayesian network inference was performed using the bnlearn package, version 2.4, executed within the R statistical computing environment, version 2.11. Network nodes included all Ang peptides with length >5 amino acids (see online-only Data Supplement, Table S1), all added substrates, all inhibitors, and time since substrate addition. We treat the data as continuous and use Gaussian Bayesian Networks where the global distribution is taken to be multivariate normal and local distributions are normal and linked by linear constraints associated with edges. Peptide areas from spectra were normalized to total Ang ion current and log transformed. Times were also log transformed. All edges are assumed excluded unless either (1) the edge extends from a peptide to a shorter peptide that can be obtained through a single site cleavage, or (2) the edge extends from a stimulus to its associated peptide, or (3) the edge extends from an inhibitor to any peptide, or (4) the edge extends from the time node to any peptide. An edge inclusion list was constructed and included edges associated with processing steps that are part of the processing pathway established in the literature. The network was constructed using the bnlearn tabu function using the Bayesian Information Criterion as score. Network edge strength assessment was performed using the bnlearn arc.strength function.

Dynamic Systems Model Inference and Comparison

Although the Bayesian network model used here proved useful in identifying novel steps in the Ang pathway, its ability to capture the transient response is limited by the available data. Dynamic model parameter inference and time course calculations were performed using a custom-developed software package implemented in the R statistical computing language, version 2.11. The model is expressed as a system of linear differential equations. In each reaction, the rate is assumed proportional to the available substrate. In experimental cases where inhibition is applied, the rate constant is set to 0 for all reactions associated with the inhibited peptidase. The time course for this model can be solved in closed form, eliminating the need for numeric integration. We assume the observed area is log transformed. All edges are assumed excluded unless either (1) the edge extends from a peptide to a shorter peptide that can be obtained through a single site cleavage, or (2) the edge extends from a stimulus to its associated peptide, or (3) the edge extends from an inhibitor to any peptide, or (4) the edge extends from the time node to any peptide. An edge inclusion list was constructed and included edges associated with processing steps that are part of the processing pathway established in the literature. The network was constructed using the bnlearn tabu function using the Bayesian Information Criterion as score. Network edge strength assessment was performed using the bnlearn arc.strength function.

Gaussian Bayesian Network Inference

The set of edges exceeding the strength threshold suggested several processing steps not found in the baseline network. Extending from Ang(1–9), the set included edges from Ang(1–9) to Ang(2–9), Ang(2–9) to Ang(3–9), and Ang(3–9) to Ang(4–9). Also included was a step from Ang(1–7) to Ang(2–7) as well as steps from Ang(1–10) to Ang(5–10), Ang(2–10) to Ang(2–9), and Ang(1–10) to Ang(3–10) (see Table S2).

Confirmation of Ang(1–9) to Ang(2–9) via AP A

Using Ang(1–9) as the substrate, we found evidence of Ang(2–9) production and significant inhibition of Ang(2–9) production in the presence of 100 μmol/L amastatin (AP A inhibition) (Figure 1). These data suggest that Ang(1–9) is cleaved to Ang(2–9) by AP A in mouse podocytes and, therefore, support the existence of the Ang(1–9) to Ang(2–9) step indicated in our network model. This finding is not surprising given the established Ang(1–10) to Ang(2–10) and Ang(1–8) to Ang(2–8) conversions catalyzed by AP A. This step might be important.
as an alternative path for degradation of Ang(1–9), away from Ang(1–7).

Path From Ang(2–10) to Ang(5–10) Established

Experiments involving addition of Ang(2–10) produced evidence of Ang(3–10), Ang(4–10), and Ang(5–10), indicating that Ang(5–10) is reachable from Ang(2–10) (Figure 2). This is consistent with the Bayesian network’s indication of a weak Ang(5–10) dependency on Ang(4–10) (strength of 59%), but an associated processing step cannot be confirmed from this experiment because possible indirect paths might exist. More interesting in these data was evidence of Ang(2–7) production. Although a step from Ang(2–10) to Ang(2–7) was not suggested by the Bayesian network, an initial bottom-up modeling effort performed by our group (unpublished) had identified the need for an Ang(2–10) to Ang(2–7) step, catalyzed by NEP, to explain a large increase in Ang(2–10) under NEP inhibition after Ang I addition. We also note that in the Bayesian network, Ang(2–10) was found to depend on NEP inhibition (appeared in 89% of the bootstrapped networks) and had a positive coefficient [Ang(2–10) increases in the presence of NEP inhibition] which would be consistent with our earlier observation.
Confirmation of Ang(2–10) to Ang(2–7) Conversion by NEP

To confirm the proposed conversion of Ang(2–10) to Ang(2–7), additional experiments were performed. Ang(2–10) was exposed to human recombinant NEP untreated or after pretreatment with 1 μmol/L SCH39370 (NEP inhibitor) or 70 nmol/L thiorphan (NEP inhibitor) for 15 minutes and subjected to MALDI MS (Figure 3). For the conditions where inhibitor was omitted, the Ang(2–7) peak was 2.9±0.16-fold that of the Ang(2–10) area, at 15 minutes. Under SCH39370 treatment, none of the spectra contained Ang(2–7) peaks with $R^2$ above our quality threshold indicating nearly complete inhibition (0.009±0.002-fold, relative to Ang(2–10) peak area). Treatment with thiorphan yielded a similar result with a relative Ang(2–7) peak area of 0.037±0.007. Together, these findings support NEP as the enzyme responsible for Ang(2–10) conversion to Ang(2–7). Of note, the conversion Ang(2–7) peak was 2.9±0.16-fold that of the Ang(2–10) area, at 15 minutes. Under SCH39370 treatment, none of the spectra contained Ang(2–7) peaks with $R^2$ above our quality threshold indicating nearly complete inhibition (0.009±0.002-fold, relative to Ang(2–10) peak area). Treatment with thiorphan yielded a similar result with a relative Ang(2–7) peak area of 0.037±0.007. Together, these findings support NEP as the enzyme responsible for Ang(2–10) conversion to Ang(2–7). Of note, the conversion
of Ang(2–10) to Ang(5–10) via NEP was also evident when inhibitor was omitted, but the magnitude of the Ang(5–10) peak area was significantly smaller. These data support the possibility of a direct Ang(2–10) to Ang(5–10) conversion by NEP, in addition to the Ang(2–10) to Ang(2–7) conversion. We performed additional experiments adding the substrate Ang(2–10) with or without amastatin (100 μmol/L) or SCH39370 (10 μmol/L) pretreatment. Samples were collected immediately after the addition of substrate and hours postaddition. The peptides Ang(2–10), Ang(2–7), and Ang(3–10) were quantified using AQUA peptides, and Ang(4–10) and Ang(5–10) were normalized to the sum of the included AQUA peptide signals (Figure 4). These experiments indicated a significant decrease in Ang(2–7) production after pretreatment with SCH39370, thus providing additional evidence of the NEP-catalyzed Ang(2–10) to Ang(2–7) conversion. We additionally note that a significant decrease in net Ang(3–10) conversion after treatment with amastatin is accompanied by a significant increase (at 4 hours) in Ang(2–7). Also, Ang(2–10) levels at 2 and 4 hours in the presence of amastatin were significantly higher than control. Because amastatin was exposed to human recombinant AP A untreated or after pretreatment with 10 μmol/L amastatin for 60 or 90 minutes, subjected to MALDI MS (Figure 5B), and quantified using Ang(2–7) and Ang(1–7) AQUA peptides. Most of Ang(1–7) was converted to Ang(2–7) after 90 minutes (725±64 nmol/L, 66%) and Ang(2–7) production was blocked after treatment with amastatin (12.8±2.5 nmol/L, 1.2%). These data support findings regarding Ang(1–9), it appears that AP A may play a role in converting Ang I, Ang II, Ang(1–9), and Ang(1–7) to Ang(2–7) conversion by AP A in mouse podocytes as indicated by our network model. Together with our findings regarding Ang(1–9), it appears that AP A may play a role in converting Ang I, Ang II, Ang(1–9), and Ang(1–7) to Ang(2–10), Ang III, Ang(2–9), and Ang(2–7), respectively.

Confirmation of Ang(1–7) to Ang(2–7) Conversion via AP A

From the cell culture experiments using Ang(1–7) as the substrate, we found evidence of Ang(2–7) production (Figure 5). The Ang(2–7) signal reached 28% of the total Ang ion current at 2 hours and was well above baseline (19%–28% of Ang ion current) at 1, 2, and 4 hours. Inhibition with thiorphan (NEP inhibitor) had no significant effect on the Ang(2–7) response. To confirm the proposed conversion of Ang(1–7) to Ang(2–7), additional experiments were performed. Ang(1–7) was exposed to human recombinant AP A untreated or after pretreatment with 10 μmol/L amastatin for 60 or 90 minutes, subjected to MALDI MS (Figure 5B), and quantified using Ang(2–7) and Ang(1–7) AQUA peptides. Most of Ang(1–7) was converted to Ang(2–7) after 90 minutes (725±64 nmol/L, 66%) and Ang(2–7) production was blocked after treatment with amastatin (12.8±2.5 nmol/L, 1.2%). These data support findings regarding Ang(1–9), it appears that AP A may play a role in converting Ang I, Ang II, Ang(1–9), and Ang(1–7) to Ang(2–10), Ang III, Ang(2–9), and Ang(2–7), respectively.

Network Revision and New Discoveries

After confirmation of predictions from our initial Bayesian network model, we revised the model using data collected subsequent to the initial analysis. Repeating the procedure described above, we incorporated experimental data from the Ang(1–9), Ang(1–7), and Ang(2–10) substrate addition experiments. Additionally, we performed a short time series experiment in mouse podocyte cultures. In these experiments, cells were incubated with 1 μmol/L Ang I and sampled immediately after substrate addition and at 5, 10, 15, 30, and 60 minutes postaddition. Samples were analyzed by MALDI-TOF MS and normalized areas extracted as before. The complete data set included 665 spectra, of which 465 were used in this analysis.
The Bayesian network inference process was repeated using this subset. In addition to the steps suggested in the initial version of the Bayesian network, the revised version included Ang(2–10) to Ang(3–10), Ang(4–10) to Ang(5–10), Ang(2–10) to Ang(4–10), and Ang(2–9) to Ang(4–9) (see Table S2).

System Model Inference and Reaction Set

Of the combinations of additional steps analyzed using the dynamic systems model, we found that inclusion of Ang(2–10) to Ang(3–10), Ang(4–10) to Ang(5–10), Ang(2–10) to Ang(4–10), and Ang(2–9) to Ang(4–9) as a group provided the lowest deviance information criterion of the networks tested. Surprisingly, the edge from Ang(2–10) to Ang(2–9), which had a strength of 95% in the revised version of the Bayesian network, did not appear to improve the fit in the dynamic systems model. Inclusion of steps from either Ang(1–10) to Ang(3–10) or Ang(2–9) to Ang(3–9) also failed to significantly improve the fit. A final model, built from the baseline and our confirmed steps, augmented with steps from Ang(4–10) to Ang(5–10), Ang(1–10) to Ang(5–10), Ang(2–10) to Ang(4–10), and Ang(2–9) to Ang(4–9), was examined further to better understand the remaining uncertainty, and the 95% credible intervals for each of those trajectories were computed and are plotted, along with the observed data, in Figure 6.

Discussion

Our findings demonstrate that computational systems biology methods can be successfully used to model the multilayered Ang peptide processing network contained in mammalian cells. In addition to designing a model system that performed satisfactorily in reproducing biological experiments, using this approach, we identified enzymatic cleavages not previously described in the literature and with potential biological significance. Conversion of Ang(2–10) to Ang(2–7) by NEP, Ang(1–9) to Ang(2–9) by AP A, and Ang(1–7) to Ang(2–7) by AP A, constitute paths within the network that expand on the well-recognized robust degrading capacity of
Ang(2–7) peptides down to length 5 including bioactive peptides (red), undetected peptides (yellow), and all other peptides (blue). Edges in black were supported in the literature and summarized in Velez.2 Edges in red were predicted in the first phase of our effort and confirmed by experiments reported here. Edges in blue were predicted in the revised model and found to significantly improve model fit (based on deviance information criterion [DIC]) in the dynamic systems model. The histogram of the incoming peptide profile (left) is based on measured reported plasma values of Ang peptides. The response profile is included for illustration purposes only. ACEi indicates Ang-converting enzyme inhibitor; APA, aminopeptidase A; DP?, an unidentified dipeptidyl aminopeptidase; and NEPi, nephrilysin inhibitor.

An illustration of the proposed network, based on the analysis described here, is given in Figure 7. We depart from the more standard representation of the RAS network and adopt the layout shown in the figure to emphasize (1) that placing the bioactive peptides in context with all other Ang peptides makes routes to and around this subset are extensive, and most of these steps have the potential for influencing flux to the bioactive components. Additionally, possible regulatory feedback paths, such as inhibition of APA by Ang IV,48 suggest that downstream peptides might act indirectly to modulate network peptidases and, thus, flux to bioactive peptides, influencing cellular responses without receptor interaction. Whereas our efforts did indicate the presence of nearly all peptide fragments, we failed to find sufficient evidence in our existing data set to include paths from Ang(2–9) to Ang(3–9) or Ang(2–8), or from Ang(2–7) to Ang(3–7). It is likely that with additional effort these steps will emerge and may result in paths back into the subset of bioactive components [back to Ang III, Ang IV, or Ang(3–7)]. At present, therapeutic modulation of this pathway has focused primarily on the steps from angiotensinogen to Ang I (direct renin inhibitors), conversion of Ang I to Ang II (ACE inhibitors), and Ang II action through the Ang AT1 receptor blockers. New approaches are emerging, such as enhancement of ACE2 activity55 and modulation of the prorenin receptor.56 Our increasing realization of the complexity of this pathway and the activity of its components calls into question a strictly Ang II–centric treatment approach and systems-based studies, as used here, will likely be necessary to design more directed targeting of therapeutics.

We find that in the application of omics techniques, we often collect much more data than are analyzed attributable in part to the act that experiments were designed to address a specific hypothesis. In this effort, we found that the totality of
these data, when considered using a systems-based approach has value in network discovery efforts. Although the current model is insufficient to capture the regulatory feedback mechanisms that must eventually be considered, we see it as an essential first step toward that goal. Key to the discovery process is this unifying model that links observations across time and experimental conditions (stimulus and inhibition), and inference methods that provide a disciplined approach to assess the weight of evidence for structural variations within the model.

In this study, cell culture experiments, inhibitor-based perturbations of the system response, and use of data collected over 6 years of evolving experimental procedures presents challenges, limitations, and benefits. A key challenge was the development of complete and consistent characterizations of each of the spectra from the archive. Whereas the spectra were readily recovered from data files recorded by the instrument, identifying the covariates from the associated experiment was somewhat more difficult. Generally, spectra used in earlier publications were well documented but many of the spectra from our archive came from experiments that might have been performed as a precursor to the published work. In our model-based approach, a critical underlying assumption is that the selected perturbations to the system are peptidase specific and essentially complete. We recognize that some level of nonspecific or incomplete inhibition is likely to occur, thus, contributing additional unexplained variation in our observations. We find that, even with these additional sources of error and variation, enzymatic steps suggested by the approach were readily confirmed in follow-up experiments, thus, suggesting that the approach has utility.

Conversions to tetrapeptides or smaller fragments were not included because matrix ions would often coexist in the same m/z window as the peptide. Because our archived samples mainly reflect ectoenzymatic activity, our analysis does not account for intracellular cleavage of Ang peptides, although we cannot completely exclude a minor contribution of intracellular peptide processing to the detected spectra. Although other RAS enzymes, such as chymase, prolylendopeptidase, prolylcarboxypeptidase, thimet oligopeptidase, dipeptidyl AP, etc, were not included in our model because of their low activity in podocytes, they may be important in other kidney cells or disease states. It is conceivable that the podocyte RAS likely includes peptidases not considered in our analysis. In addition, we did not incorporate the potential enzymatic inhibitory actions of some Ang peptides. Notably, Ang IV has been reported to inhibit AP A, whereas ACE can be inhibited by Ang 1–7. Moreover, biologically active Ang peptides generated through enzymatic decarboxylation have also been reported to be detectable in human plasma. Altogether, these unaccounted aspects of the RAS further emphasize its complexity.

**Perspectives**

In summary, the Ang peptide processing network can be successfully modeled using computational tools and data mining. Although our effort was based on an artificial system, we were able to elucidate intermediate pathways within the network that were not previously recognized. Because in vivo maneuvers to alter the system involve inhibition or inactivation of RAS enzymes, we speculate that our methods may help predicting and better understanding systemic or local effects of those manipulations and guide future research. Further exploration of the Ang peptide processing network by refined computational systems biology methods could improve our understanding of the intricacies of the RAS with potential impact in medical therapies.

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**Disclosures**

None.

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treatment: does it exist and does it affect the hypertensive response?


Novelty and Significance

What Is New?
• Our study is the first to apply computational tools to model a cell-based network of angiotensin (Ang) peptides and peptidases and, through the process, reveal novel steps within that network.

What Is Relevant?
• We demonstrated that conversion of Ang(2–10) to Ang(2–7) by neprilysin, Ang(1–9) to Ang(2–9) by aminopeptidase A, and Ang(1–7) to Ang(2–7) by aminopeptidase A constitutes elements of the cascade of fragmentation of Ang substrates in mouse podocytes.

Summary
The Ang peptide processing network can be successfully modeled using Bayesian network inference and dynamic systems modeling coupled with peptidomic data mining. Our tools proved effective in revealing steps of the network that lead to either transient generation of bioactive peptides or shunting of their formation.
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Network Modeling Reveals Steps in Angiotensin Peptide Processing

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Author Contributions
J.H.S., M. G. J. and J.C.Q.V.: conception and design of research; J.H.S., J.C.G.S., J.L.I., J.M.C. and J.C.Q.V.: performed experiments; J.H.S., J.C.G.S., M. G. J. and J.C.Q.V analyzed data; J.H.S., M. G. J., J.M.A. and J.C.Q.V interpreted results of experiments; J.H.S. prepared figures and drafted manuscript; M. G. J. and J.C.Q.V edited and revised manuscript.

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EXPANDED MATERIALS AND METHODS

Mouse Podocyte Cell Culture. Immortalized mouse podocytes [generously provided by Dr. Peter Mundel (Massachusetts General Hospital, Boston, MA) and Dr. Jeffrey Kopp (National Institutes of Health, Bethesda, MD)] were grown under standard conditions as previously published. Cells were exposed to angiotensin (Ang) substrates as previously described. Following overnight starvation, differentiated cells were incubated in serum-free medium and exposed to 1 µmol/L Ang(1-10) (also called Ang I), Ang(2-10), Ang(1-9), Ang(1-8) (also called Ang II) or Ang(1-7) for 15 minutes - 8 hours, in the presence or absence of RAS enzyme inhibitors added 20 minutes prior to exposure to the Ang substrate, as previously described. The concentrations of the inhibitors were selected based on the manufacturer’s recommendation or IC50/Ki of the compound, and confirmed by dose/concentration response curves: 100 µmol/L captopril (Ang-converting enzyme inhibitor), 100 µmol/L chymostatin (chymase inhibitor), 1 µmol/L thiorphan (neprilysin inhibitor), 10 µmol/L SCH39370 (NEP inhibitor), 100 µmol/L amastatin (aminopeptidase A inhibitor) and 1 µmol/L DX600 (ACE2 inhibitor). All inhibitors were obtained from Sigma-Aldrich (St Louis, MO), except DX600 (Phoenix Pharmaceuticals, Burlingame, CA) and SCH39370 (gift from Dr. Mark Chappell, Wake Forest University, Winston-Salem, NC). Conditioned cell culture media were collected at various time points and stored at -20ºC until assayed.

MALDI-TOF Mass Spectrometry. Samples obtained at various time points were assayed by matrix-assisted laser desorption ionization (MALDI) time of flight (TOF) mass spectrometry (MS), as previously described, with minor modifications. Briefly, peptides were purified using C18 Zip-Tip columns (Milipore, Billerica, MA). Columns were equilibrated with 100% acetonitrile (ACN), washed with 0.1% -trifluoroacetic acid (TFA), loaded with 20 µl of sample, washed with 10 µl of 0.1%-trifluoroacetic acid, and eluted with a low-pH MALDI matrix compound (10 g/L α-cyano-4-hydroxycinnamic acid in a 1:1 mixture of 50% ACN and 0.1% TFA). Prior to column loading, samples were acidified with 1% TFA. Biological samples were analyzed in triplicate. Eluted matrix (1.5 µl) from each sample was applied to the surface of a target plate in duplicate. The plate was air-dried prior to collecting spectra. Spectra were collected in reflectron mode using a MALDI-TOF mass spectrometer (Waters Corp., Milford, MA). Results were analyzed using MassLynx 2.0 software (Waters). Peptide identities were confirmed by MS/MS de novo sequencing from ion series generated by MALDI-TOF-TOF (ABI 4800 Series, AB Sciex, Framingham, MA) and Triple Time of Flight MS (ABSCIEX 5600, Framingham, MA). Quantifications of observed peaks were performed using customized isotopic Absolute Quantification (AQUA) peptides (Sigma-Aldrich), as previously described. AQUA peptides are 6 Da larger than the native peptide as a result of [13C.15N]-valine incorporation into the amino-acid sequence. A cocktail of AQUA peptides was mixed with each sample of conditioned buffer prior to MALDI-TOF MS analysis. The final concentration of each AQUA peptide in the mix was set between 10 and 500 nmol/L (0.25 – 12.5 pmols), depending on the qualitative appearance of the peptide peaks on the mass spectra. In the absence of cells, all Ang peptide levels were found to be stable over up to 8 hours of incubation.
Peptide Peak Intensity Normalization. While many of the spectra from our archive contained AQUA reference peptides, this was not universally so, and, when present, quantitative measures were available for only 1 to 4 peptides. To overcome this limitation we sought options for normalizing the data so that peak areas could be compared across spectra. We chose to normalize spectra to their total angiotensin peptide ion current (the sum of the isotopic cluster areas for all angiotensin peptides) following elimination of poor quality fits. To assess the suitability of the selected normalization procedure, we selected a subset of spectra in which an AQUA peptide with known amount was present. The AQUA peptide area was found to correlate well with the total angiotensin peptide current in these data ($r = 0.87$). While the selected normalization method is not ideal, it provides a consistent approach that could be applied to all spectra from the archive. The angiotensin peak area estimates were normalized using this approach.

Gaussian Bayesian Network Inference. In order to learn the network structure, we employed Bayesian network inference. Nodes in this network represent angiotensin peptide abundances as well as factors that influence abundance (stimulation and inhibition) and edges represent conditional dependencies between nodes. Network nodes included all Ang peptides with length greater than 5 amino acids (Table S1), all added substrates, inhibitors, and time since substrate addition. We treat the data as continuous and employ Gaussian Bayesian Networks where the global distribution is taken to be multivariate normal and local distributions are normal and linked by linear constraints associated with edges. Peptide areas are log-transformed prior to application of the inference process. In the most general case, network structure identification considers the space of directed acyclic graphs linking the network variables. In our case, however, we can significantly reduce this space and simultaneously constrain allowable networks to directed acyclic graphs by banning edges that do not adhere to the constraints of the peptide cleavage process. We only allow edges for steps that involve cleavage at a single site and thus result in shorter peptides. We therefore constrain the search space by constructing a list of edges that violate these constraints and ban the inference process from considering their inclusion in the network. The decapeptide Ang I, for example, could only be cleaved at 9 different sites, each cleavage yielding 2 peptide fragments. For 8 of the 9 sites, one or the other of the fragments would be below the lower mass limit of our data (smaller than 5 amino acids) and so a maximum of 10 edges from Ang I to each of the larger fragments would be allowed for consideration in the graph. Similar logic is applied to all angiotensin peptide fragments to identify allowable edges. Nodes representing each of the stimuli were also included and edges were allowed between each stimulus and its associated angiotensin peptide. Inhibitors were treated similarly but were allowed to influence all peptides. In these experiments, inhibitors lack specificity and, due to alternative paths to a given node, do not completely determine node states. We therefore include inhibitors as orphaned nodes with state determined by experimental conditions and allow edges from these nodes to nodes representing angiotensin peptide abundances. Known steps in the pathway representing our baseline network were added to a list that forced their inclusion in the network. All spectra taken from the archive were collected from experiments evoking a transient response through substrate addition. The time points at which the samples were collected were coarse (several hours) and collection times
varied from experiment to experiment. As such, the data was considered insufficient for model development using a Dynamic Bayesian Network modeling framework. To allow for some temporal effect, the time after substrate addition was included as a node in the model with edges allowed to all peptides. The network model was constructed using the tabu search algorithm. This method leads to a point solution. To assess the strength of each network edge, we employed bootstrapping where networks were built from edge sets formed by sampling from the constructed network. The frequency with which each edge remained in the network resulting from the bootstrapped set was taken as a measure of the strength of that edge and we focused further effort on those edges that appeared in more than 80% of the networks associated with the bootstrapped edge sets.

**Ang Peptide Flyability.** The observed peak areas from the mass spectra vary not only according to the amount of analyte present but also the physical properties of the analyte and its propensity for ionization. In this analysis, we include a scaling parameter for each peptide that relates the normalized isotopic cluster area to the underlying amount of analyte in the sample \( A_p = F_p X_p \). Under this model, relative peptide areas are assumed proportional to relative peptide amounts, related by \( F_p \). These flyability parameters are taken to be unique to each peptide and constant across all experiments and conditions. To test this approach, we constructed known mixtures of Ang I, Ang(1-9), Ang(2-10), Ang II, and Ang(1-7) with individual peptide concentrations at 0.1, 0.25, 0.5, 0.75, or 1 µM, collected MALDI mass spectra from the mixtures, and compared the peptide peak areas, normalized to total angiotensin current, to the known relative concentrations. The normalized area to relative concentration ratios were found to have a strong linear correlation \( r = 0.95 \), thus supporting our use of the proposed scaling approach. These flyability parameters were estimated in the Markov Chain Monte Carlo process along with the rate constants, and priors for these parameters were based on the flyability estimates derived from our mixture tests.

**System Model Inference and Reaction Set.** A series of models were constructed, starting from a baseline, with additional reaction steps included if they provided an improvement in the model's ability to explain the observed data. Steps suggested by the Bayesian network were sorted into groups along a particular branch of the pathway [Ang(2-10), Ang(1-9), etc.] extending down from the stimulation points used in our experiments. The baseline model was established based on a proposed network augmented with the three steps confirmed in our experiments, and an initial model was fit using that structure. Model comparison was accomplished using the Deviance Information Criterion (DIC) in an approach similar to that proposed elsewhere. For all models we computed the mean of the deviance, taken from samples of the posterior parameter distribution (following burn-in and thinning), and the deviance of the mean of the posterior to compute the DIC. Repeated executions of the inference process in independent Markov Chains were used to provide an estimate of the variance in the DIC and model comparisons were then based on DIC differences and their variance estimates.
Supplemental references


9. Spiegelhalter DJ, Best NG, Carlin BP. Bayesian Deviance, the Effective Number of Parameters, and the Comparison of Arbitrarily Complex Models: Division of Biostatistics, University of Minnesota;1998.

Table S1. Angiotensin Peptides (Nodes) included in the Bayesian Network Model

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Table S2. Bayesian Network Edge Strengths for Models Built from Archive (Phase 1) and Archive Augmented by Subsequent Experiments (Phase 2)

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