

Aberration in NF κ B–I κ B binding may cause two states of NF κ B activity

Raghvendra Singh*

Department of Chemical Engineering, Indian Institute of Technology, Kanpur 208 016, India

NF κ B activation is involved in cell survival and aberration of NF κ B signalling is found in cancer. I κ B is an inhibitor that sequesters NF κ B in the cytoplasm. By mathematical modelling, we predict that under an aberrant condition in which I κ B does not bind to NF κ B, there exist two states of NF κ B activity: a constitutive activity state for any positive value of the stimulus and a zero activity state for no stimulus. Further, under the assumption that NIK can be activated by TAB1–pTAK1, we predict that TAB1 has a role in the basal activity of NF κ B. Thus, we predict the importance of TAB1 and I κ B in NF κ B activation. Our prediction may have implication for cell survival and cancer.

Keywords: Basal activity, cancer, cell survival, constitutive activation, protein complex.

PREVIOUSLY, others and the present author¹ have described the network that causes p38 activation in response to IL1. A similar network², which shares many proteins with the IL1/p38 network, can also cause the nuclear accumulation of NF κ B in response to IL1. Starting with the IL1 receptor till the activation of TAK1, the two networks share most of the proteins and diverge at TAK1. There are two mechanisms of TAK1 activation by IL1. The first mechanism involves TAB2 and the ubiquitin ligase TRAF6 (ref. 3), while the second involves TAB1. The first mechanism is the ubiquitination-dependent activation of TAK1, while the second mechanism may be a phosphorylation-dependent activation of TAK1 (refs 4, 5). It is not clear whether both mechanisms can cause NF κ B accumulation in the nucleus. TAK1 makes a complex, called TRAF6-regulated IKK activator (TRIKA2), with TAB1 and TAB2 (ref. 6). Although the TRIKA2 complex activated IKK in the presence of ubiquitin-conjugating enzymes Ubc13 and Uev1A and the ubiquitin ligase TRAF6, the role of TAB1 in this complex is not clear⁷. TAK1 phosphorylates NIK, which activates IKK². Since role of TAB1 in TAK1 and NIK activation is not clear, we have considered both cases: (i) NIK can associate with pTAK1 activated by TAB2–TRAF6, but not with pTAK1 activated by TAB1 and (ii) NIK can associate with both pTAK1 phosphorylated by TAB2–TRAF6 and by TAB1. Active IKK phosphorylates I κ B, leading to its proteasomal degradation, which causes accumulation of NF κ B in the nucleus.

I κ B is a cellular inhibitor of NF κ B⁸. I κ B sequesters NF κ B in the cytoplasm and prevents NF κ B-induced gene transcription. Aberration in I κ B production, degradation and phosphorylation has been implicated in many diseases⁹. For this reason, we considered NF κ B accumulation in the nucleus also in the absence of NF κ B–I κ B binding reaction.

Taking into account the reactions of IL1/p38 and IL1/NF κ B networks, we constructed a mathematical model of NF κ B activation by IL1. The model shows that under normal conditions, NF κ B is activated transiently over several hours and finally achieves a steady state. Under the aberrant condition, in which I κ B does not bind to NF κ B, we found that the cells have two states. The first state is the zero NF κ B activity state which occurs under zero concentration of IL-1. On the other hand, in the second state, a constitutive activation of NF κ B is achieved for any positive stimulation. Further, we found that under the assumption in which NIK can associate and be activated by TAB1-activated TAK1, the basal activity of NIK and NF κ B is affected, which is similar to our earlier prediction that TAB1 affects the basal activity of p38 (ref. 1).

The method used in the mathematical modelling of IL1-induced NF κ B signalling network has been described in detail in the earlier work¹. Briefly, in the IL1-induced p38 signalling network¹, we have added a module to model activation of NF κ B (Figure 1). Reactions of this module have been modelled using the law of mass action. All reactions of IL1-induced NF κ B signalling network

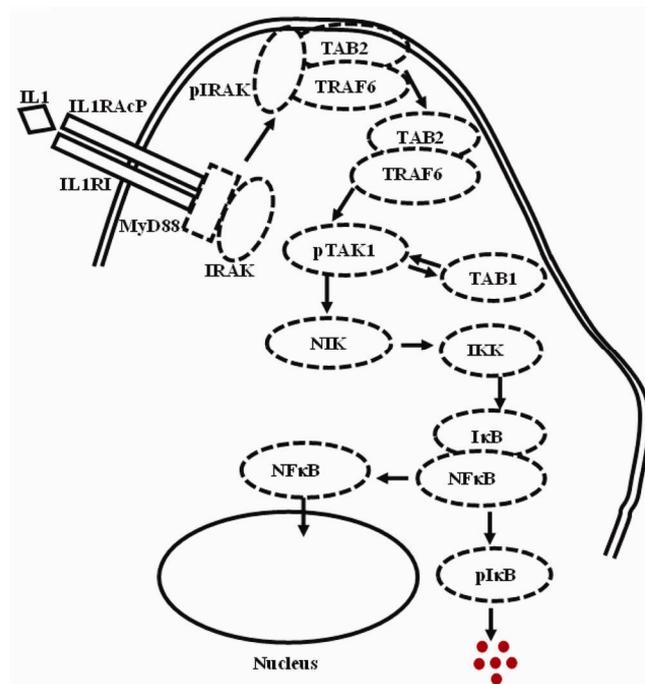


Figure 1. IL1/NF κ B activation network. IL1-induced degradation of I κ B and nuclear translocation of NF κ B are shown.

*e-mail: raghvend@iitk.ac.in

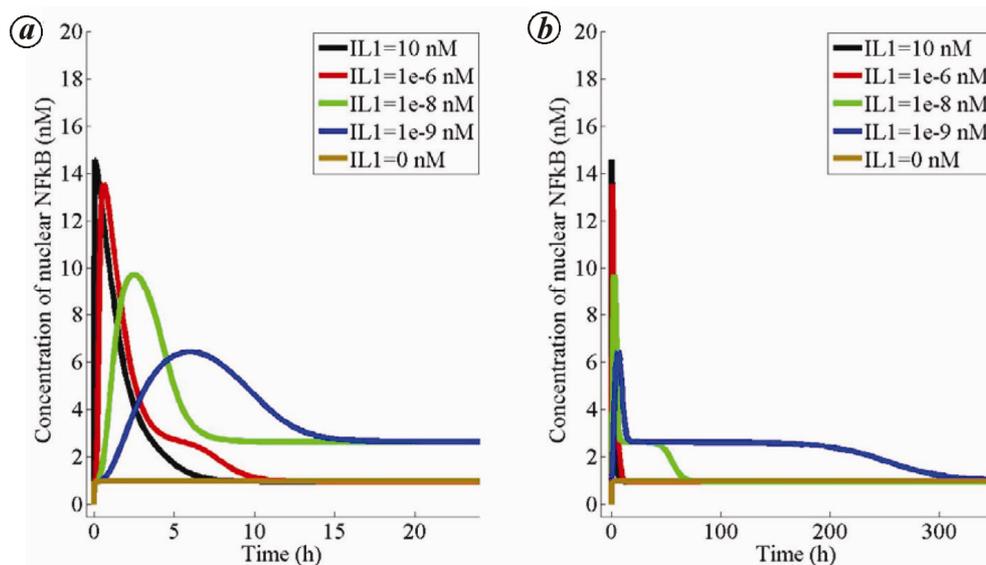


Figure 2. IL1 causes transient accumulation of NF κ B in the nucleus. It has been assumed that TAK1, activated by TAB1, cannot activate NIK.

and the rate constants are given in the ‘Supporting Information’. A cell has been modelled as a batch reactor using the batch reactor design equation

$$\frac{dC_i}{dt} = \sum_j r_{ij},$$

where C_i is the concentration of a protein/protein complex in the IL1/NF κ B signalling network and r_{ij} is the rate of formation of the species i in the j th reaction. The resulting set of ordinary differential equations has been solved using the ode solver ODE15s of MATLAB R2010b (Math Works, MA, USA) with initial conditions, which are given in the Supporting Information.

First, we investigated nuclear accumulation of NF κ B over a 24 h period and found that the NF κ B response consists of a transient phase of 5–10 h duration followed by a steady state (Figure 2 *a* and *b*). The steady state is independent of IL1 concentration (Figure 2 *b*). As IL1 concentration decreases, the peak of NF κ B transient phase becomes lower and gets delayed. This response is similar to that of p38 in the presence of IL-1, although p38 activation happens within an hour¹ and is thus more rapid.

Since I κ B is required for the sequestration of NF κ B in the cytoplasm, we explored the dynamics of NF κ B nuclear accumulation when NF κ B–I κ B binding reaction is disrupted. We found that every concentration of IL1 causes constitutive accumulation of NF κ B in the nucleus (Figure 3 *a*). As the concentration of IL1 decreases, the response gets delayed although the steady state remains the same (Figure 3 *b* and *c*). In the absence of IL1, NF κ B nuclear accumulation is zero. Thus even a small perturbation of cells, in the form of IL1 stimulus, causes constitu-

tive nuclear accumulation of NF κ B. This binary response can be seen as cells having two steady states: one in the presence of the stimulus and the other in its absence. This all-or-none response resembles ON/OFF states of an enzyme. In the absence of I κ B binding to NF κ B, the latter is primed to translocate to the nucleus. Any small perturbation in the form of IL1 stimulus can cause this to happen.

TAK1 can be activated by TAB2-TRAF6 in an IL1-dependent manner or by TAB1 in an IL1-independent manner⁴. It is not clear whether TAK1 activated by both mechanisms can cause nuclear accumulation of NF κ B. Thus, we investigated NF κ B nuclear response in the presence and absence of NIK activation by TAB1. We first considered TAK1 activation by IL1 in the presence and absence of NIK activation by TAB1 and found that like p38 (ref. 1) and NF κ B nuclear responses, TAK1 activation consists of a transient phase and a basal activity and is independent of whether or not NIK is activated by TAB1 (Figure 4 *a–d*). TAK1 activation is also independent of whether or not NF κ B–I κ B binding reaction has been disrupted (Figure 4 *a* and *c*), which is expected since TAK1 activation is upstream of NF κ B–I κ B binding reaction.

Next, we studied NIK activation by IL1 in the presence or absence of such activation by TAB1 and in the presence or absence of NF κ B–I κ B binding reaction. Similar to pTAK1, NIK activation also consists of a transient phase and a steady state (Figure 5 *a–d*). Regarding the effect of TAB1, we found that it affects only the basal activity of NIK (Figure 5 *b* and *d*). Further, we did not find any effect of NF κ B–I κ B binding reaction on NIK activation (Figure 5 *a–d*), which is expected since NIK activation is upstream of NF κ B–I κ B binding reaction.

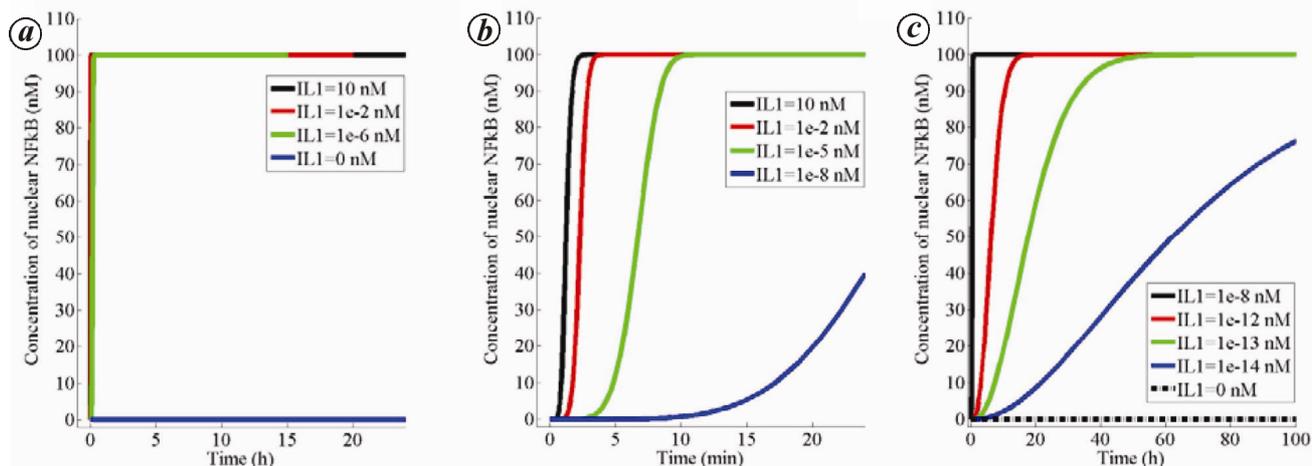


Figure 3. Absence of $I\kappa B$ binding with $NF\kappa B$ causes constitutive accumulation of $NF\kappa B$ in the nucleus. It has been assumed that TAK1, activated by TAB1, cannot activate NIK. Further, it has been assumed that due to aberration $I\kappa B$ cannot bind with $NF\kappa B$.

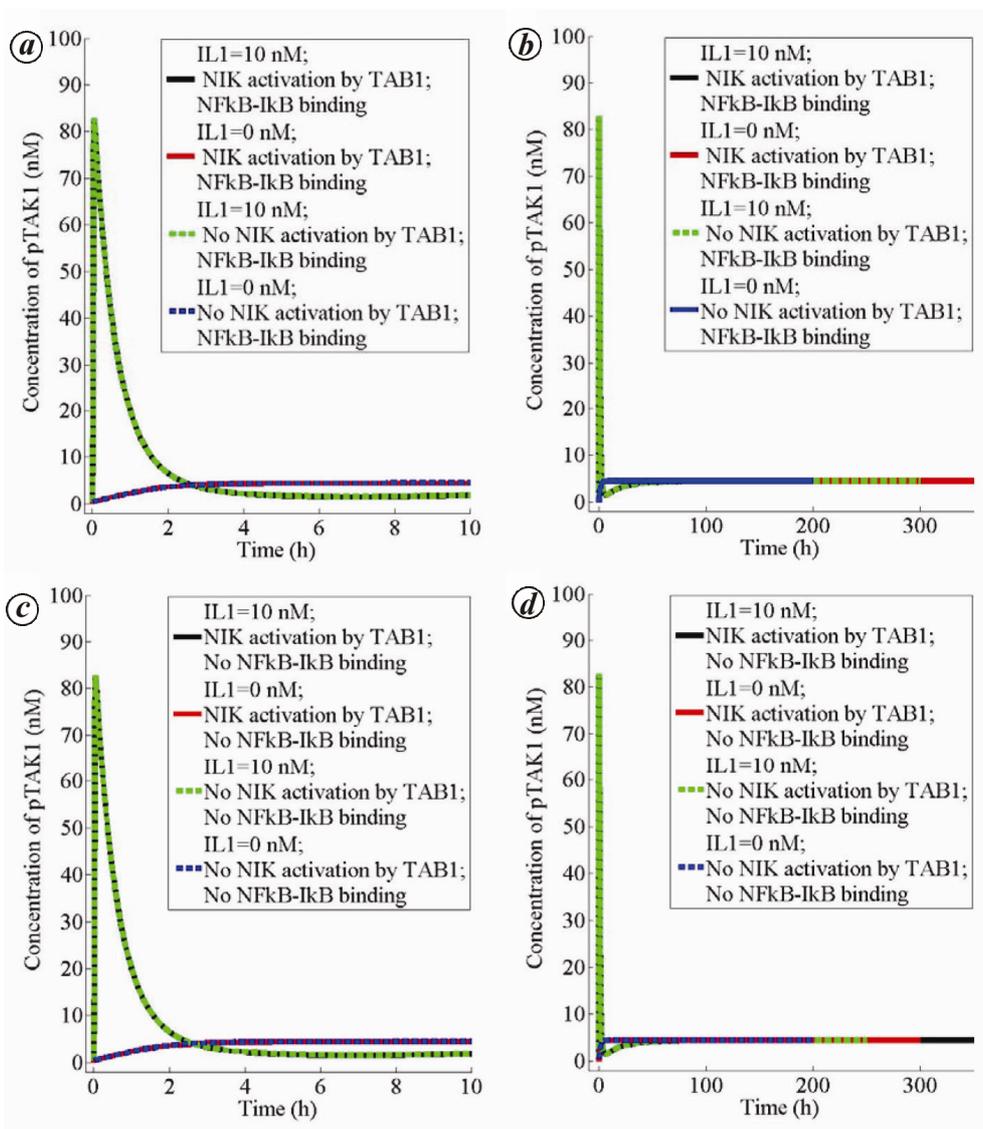


Figure 4. TAK1 activation is not affected by TAB1–pTAK1–NIK interaction and $NF\kappa B$ – $I\kappa B$ binding reaction.

We studied the role of TAB1 in nuclear accumulation of NF κ B, both in the presence and absence of the NF κ B–I κ B binding reaction and found that NIK activation by TAB1 affects only the basal accumulation of NF κ B in the nucleus in the presence of the binding reaction (Figure 6 *c* and *d*). On the other hand, in the absence of NF κ B–I κ B interaction and presence of NIK activation by TAB1–pTAK1, all of the NF κ B is found in the nucleus (Figure 6 *a*), suggesting that under this aberrant condition NF κ B can accumulate in the nucleus even in the absence of the stimulus. Further, in the absence of both the NIK activation by TAB1–pTAK1 and the NF κ B–I κ B interaction, NF κ B is not activated in the absence of the stimulus (Figure 6 *b*), suggesting that the stimulus-independent activation of NF κ B occurs only in the aberrant condition in which NF κ B–I κ B interaction is abolished and NIK can be activated by TAB1–pTAK1. In the absence of the NF κ B–I κ B binding reaction, NIK (thus TAB1) is not connected to the NF κ B nuclear import (Figure 1). Thus, under the aberrant condition, NIK and TAB1 have no role in the nuclear accumulation of NF κ B, and NF κ B accumulates maximally in the nucleus.

We investigated the effect of TAB1 on the dynamics of nuclear NF κ B, which shows that increasing TAB1 level has no effect on the dynamics of NF κ B (Figure 7 *a* and *b*), if TAB1 does not activate NIK. On the other hand, if TAB1 can activate NIK through pTAK1, TAB1 increases the basal level of nuclear NF κ B (Figure 7 *c* and *d*), suggesting a role of TAB1 in the basal activity of NF κ B.

Previously, we modelled and predicted the time course of nuclear activation of p38 in response to IL-1, and showed that p38 activation peaks at around 2 min and reaches a basal level within an hour. Nuclear accumulation of NF κ B also includes a transient phase followed by a steady state. However, NF κ B translocation to the nucleus is slower and reaches a basal level within 5 h. Like p38, the peak of NF κ B accumulation in the nucleus is delayed as the IL-1 concentration is decreased and the dynamics is robust to changes in IL-1 concentration. However, dynamics of nuclear NF κ B is much more robust to changes in the IL-1 concentration, since reduction of IL-1 over seven orders of magnitude has only minor effect on the dynamics of NF κ B. For a concentration of 10 nM, the peak of NF κ B activity is attained at around 3 min while for a concentration of 10^{-6} nM, the peak is attained at around 35 min. Thus, in the physiological concentration range 1–10 pg/ml or $57e-6$ – $57e-5$ nM, the peak is attained within 35 min (ref. 10). A concentration of 10^{-8} nM may cause around ten-fold activation (relative to the basal activity) of NF κ B. However, at this concentration of IL-1, the peak is attained at around 2.5 h and attainment of basal activity may take up to 70 h of treatment with IL-1. Thus relative to p38 activation, NF κ B activation is more sustained. In support of our prediction, Rasmussen *et al.*¹¹ studied the time course of NF κ B activation due to IL-1 in HepG2 cells. They showed that

there is a basal level of nuclear NF κ B. Further, they showed that NF κ B peaks within 15 min of addition of IL-1 and activation continues for more than 24 h in the presence of IL-1. Similarly, Moynagh *et al.*¹² studied the dynamics of NF κ B activation by IL-1 in C6 glioma cells, and found that it is activated within 20 min and activation continues up to 24 h. However, we do not see a clear variation of NF κ B activity at different time points in the study of Moynagh *et al.*¹². It is possible that in their case, the NF κ B detection assay might have been saturated.

Since in some cancer cell lines NF κ B has been found to be constitutively active^{13,14}, we explored the dynamics of NF κ B in the absence of binding of its inhibitor I κ B. The binding of NF κ B–I κ B may be abolished due to the aberrant transcription or mutations in the I κ B gene. Our model predicts that under this condition the cells have two states: (1) a zero nuclear NF κ B activity under no stimulation condition, and (2) a constitutive nuclear NF κ B activity under any non-zero stimulation condition. Thus, stimulation may be considered as a perturbation to the cells, and a cell maintains any of the two states.

Previously, we have shown that TAB1 regulates the basal activity in p38 activation. In the p38 activation we assumed that TAK1 activated both by TAB2–TRAF6 and TAB1, can activate p38. However, due to possible involvement of ubiquitin, it is not clear whether TAK1 activated by TAB1 can also activate NIK. Therefore, we chose two conditions: (i) NIK is activated by pTAK1 activated by TAB2–TRAF6, but not by TAB1, and (ii) NIK is activated by pTAK1 phosphorylated both by TAB2–TRAF6 and TAB1. By analysing these two conditions, we predict that TAB1 may regulate the basal activity of both NIK and NF κ B. In support of our prediction, Neil *et al.*¹⁵ reported a truncated TAB1 in 4T1 cells, which decreased both the basal and TGF- β -induced activity of NF κ B. Similarly, Lu *et al.*¹⁶ studied NF κ B activation in the absence of a stimulus and found that X-linked inhibitor of apoptosis (XIAP) induces NF κ B activity through interaction with TAB1, implicating TAB1 in the basal activity of NF κ B.

We investigated the condition under which NF κ B will be constitutively active. Two conditions resulted. In the first condition, in which NF κ B–I κ B binding reaction has been abolished and pTAK1 activated by TAB1 can activate NIK, NF κ B is constitutively active. In the second condition, in which NF κ B–I κ B binding reaction has been abolished but pTAK1 activated by TAB1 cannot activate NIK, NF κ B is active for all positive stimulation while NF κ B activity is zero for no stimulation condition. Experimentally, both conditions will result in constitutive activation of NF κ B, since a positive stimulation in terms of a perturbation will be always present in the microenvironment of a cell. Thus, disruption of NF κ B–I κ B binding reaction may be the aberrant condition that may occur in some cancers.

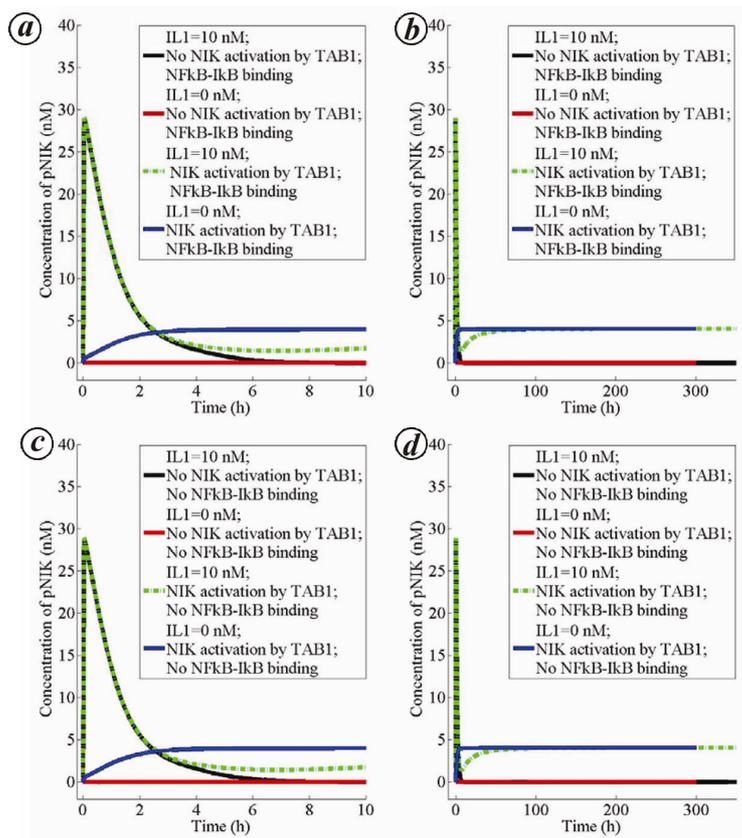


Figure 5. Basal activity of NIK is affected by TAB1.

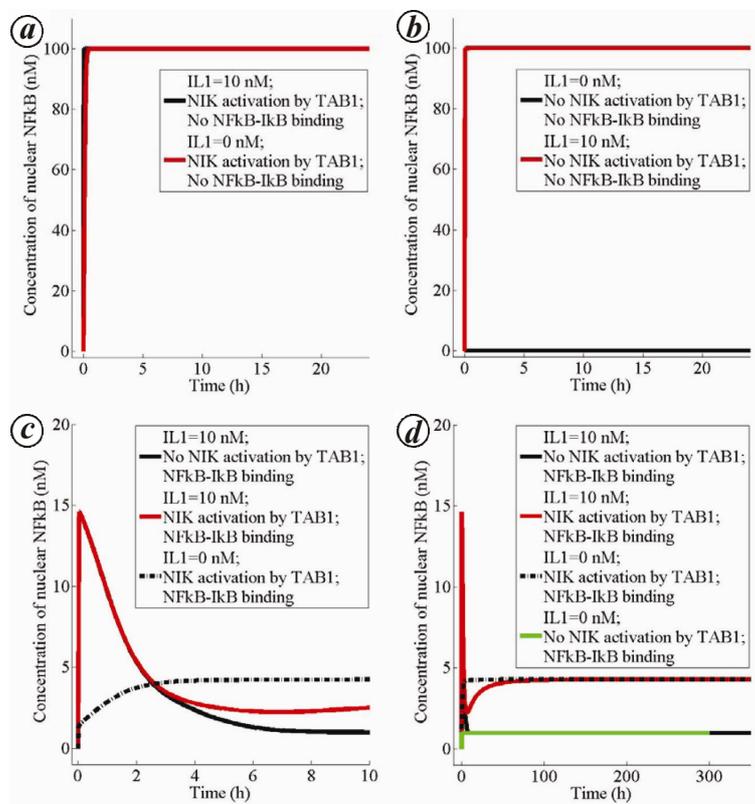


Figure 6. NIK activation by TAB1-pTAK1 causes constitutive activation of NFκB in absence of NFκB-IκB interaction.

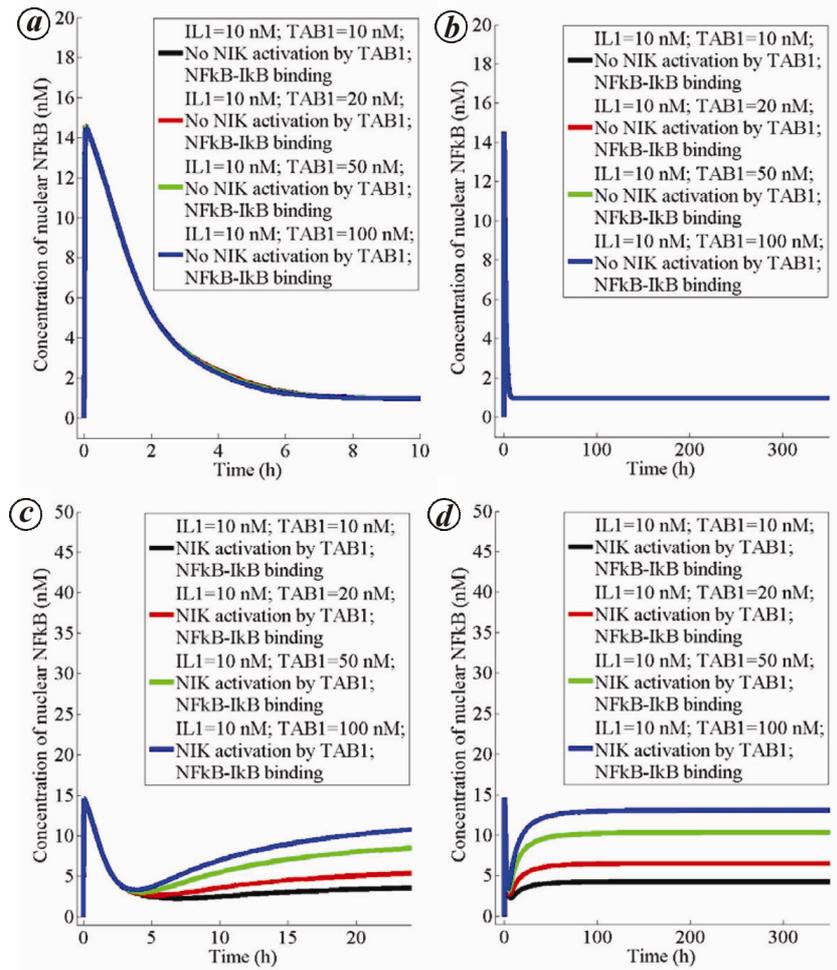


Figure 7. TAB1 affects the basal activity of NFκB.

NFκB has roles in many diseases including inflammatory and metabolic diseases^{17,18}, autoimmune diseases¹⁹, cancer²⁰ and HIV latency²¹. In HIV latency, IκBα has been found to inhibit HIV replication by inhibiting HIV-Rev transactivation inside the infected cells²¹. In cancer, several mutations in proteins in the NFκB signalling network have been identified²⁰. Besides, NFκB activation has been found in the underlying inflammation leading to cancers²⁰. Similarly, among the autoimmune diseases, NFκB has been found to affect type-I diabetes²². Thus, our study has implications for several diseases, including cancer.

In summary, TAB1 may regulate the basal activity of NFκB. Further, in the absence of NFκB-IκB binding as well as NIK activation by TAB1-pTAK1, NFκB may have two states – an all or none kind of activation. All of NFκB will be in the nucleus for any stimulation and none will be present in the nucleus for zero stimulation. On the other hand, in the absence of NFκB-IκB binding and in the presence of NIK activation by TAB1-pTAK1, NFκB is constitutively active.

Conflict of interest. The author declares that he has no conflict of interest.

1. Singh, R., Model predicts that MKP1 and TAB1 regulate p38 alpha nuclear pulse and its basal activity through positive and negative feedback loops in response to IL-1. *PLoS ONE*, 2016, **11**, e0157572; doi:10.1371/journal.pone.0157572.
2. Ninomiya-Tsuji, J. *et al.*, The kinase TAK1 can activate the NIK-I kappaB as well as the MAP kinase cascade in the IL-1 signalling pathway. *Nature*, 1999, **398**, 252–256; doi:10.1038/18465.
3. Takaesu, G. *et al.*, TAB2, a novel adaptor protein, mediates activation of TAK1 MAPKKK by linking TAK1 to TRAF6 in the IL-1 signal transduction pathway. *Mol. Cell*, 2000, **5**, 649–658.
4. Sakurai, H., Miyoshi, H., Mizukami, J. and Sugita, T., Phosphorylation-dependent activation of TAK1 mitogen-activated protein kinase kinase kinase by TAB1. *FEBS Lett.*, 2000, **474**, 141–145; doi:10.1016/S0014-5793(00)01588-X.
5. Shibuya, H. *et al.*, TAB1: an activator of the TAK1 MAPKKK in TGF-beta signal transduction. *Science*, 1996, **272**, 1179–1182.
6. Wang, C. *et al.*, TAK1 is a ubiquitin-dependent kinase of MKK and IKK. *Nature*, 2001, **412**, 346–351; doi:10.1038/35085597.
7. Shim, J. H. *et al.*, TAK1, but not TAB1 or TAB2, plays an essential role in multiple signaling pathways *in vivo*. *Genes Dev.*, 2005, **19**, 2668–2681; doi:10.1101/gad.1360605.

8. Karin, M., How NF-kappaB is activated: the role of the IkappaB kinase (IKK) complex. *Oncogene*, 1999, **18**, 6867–6874; doi: 10.1038/sj.onc.1203219.
9. Rayet, B. and Gelinas, C., Aberrant *rel/nfkb* genes and activity in human cancer. *Oncogene*, 1999, **18**, 6938–6947; doi:10.1038/sj.onc.1203221.
10. Barakat, A. F., Elson, C. J. and Westacott, C. I., Susceptibility to physiological concentrations of IL-1beta varies in cartilage at different anatomical locations on human osteoarthritic knee joints. *Osteoarthritis Cartilage*, 2002, **10**, 264–269; doi:10.1053/joca.2002.0515.
11. Rasmussen, M. K. *et al.*, IL-8 and p53 are inversely regulated through JNK, p38 and NF-kappaB p65 in HepG2 cells during an inflammatory response. *Inflamm. Research: Off. J. Eur. Histamine Res. Soc.*, 2008, **57**, 329–339; doi:10.1007/s00011-007-7220-1.
12. Moynagh, P. N., Williams, D. C. and O'Neill, L. A., Interleukin-1 activates transcription factor NF kappa B in glial cells. *Biochem. J.*, 1993, **294**(Pt 2), 343–347.
13. Li, W., Tan, D., Zenali, M. J. and Brown, R. E., Constitutive activation of nuclear factor-kappa B (NF-kB) signaling pathway in fibrolamellar hepatocellular carcinoma. *Int. J. Clin. Exp. Pathol.*, 2009, **3**, 238–243.
14. Nagel, D., Vincendeau, M., Eitelhuber, A. C. and Krappmann, D., Mechanisms and consequences of constitutive NF-kappaB activation in B-cell lymphoid malignancies. *Oncogene*, 2014, **33**, 5655–5665; doi:10.1038/ncr.2013.565.
15. Neil, J. R. and Schiemann, W. P., Altered TAB1 : I kappaB kinase interaction promotes transforming growth factor beta-mediated nuclear factor-kappaB activation during breast cancer progression. *Cancer Res.*, 2008, **68**, 1462–1470; doi:10.1158/0008-5472.CAN-07-3094.
16. Lu, M. *et al.*, XIAP induces NF-kappaB activation via the BIR1/TAB1 interaction and BIR1 dimerization. *Mol. Cell*, 2007, **26**, 689–702; doi:10.1016/j.molcel.2007.05.006.
17. Tak, P. P. and Firestein, G. S., NF-kappaB: a key role in inflammatory diseases. *J. Clin. Invest.*, 2001, **107**, 7–11; doi:10.1172/JCI11830.
18. Baker, R. G., Hayden, M. S. and Ghosh, S., NF-kappaB, inflammation, and metabolic disease. *Cell Metab.*, 2011, **13**, 11–22; doi:10.1016/j.cmet.2010.12.008.
19. O'Sullivan, B., Thompson, A. and Thomas, R., NF-kappa B as a therapeutic target in autoimmune disease. *Expert Opin. Therap. Targets*, 2007, **11**, 111–122; doi:10.1517/14728222.11.2.111.
20. Karin, M., NF-kappaB as a critical link between inflammation and cancer. *Cold Spring Harbor Perspect. Biol.*, 2009, **1**, a000141; doi:10.1101/cshperspect.a000141.
21. Wu, B. Y., Woffendin, C., Duckett, C. S., Ohno, T. and Nabel, G. J., Regulation of human retroviral latency by the NF-kappa B/I kappa B family: inhibition of human immunodeficiency virus replication by I kappa B through a Rev-dependent mechanism. *Proc. Natl. Acad. Sci. USA*, 1995, **92**, 1480–1484.
22. Zhao, Y., Krishnamurthy, B., Mollah, Z. U., Kay, T. W. and Thomas, H. E., NF-kappaB in type 1 diabetes. *Inflamm. Allergy Drug Targets*, 2011, **10**, 208–217.

ACKNOWLEDGEMENT. This work was supported by the Indian Institute of Technology Kanpur grant IITK/CHE/20090282 to RS.

Received 26 December 2016; revised accepted 7 July 2017

doi: 10.18520/cs/v113/i1/2168-2174

Experimental analysis of the ratio of similar materials by similarity model test on raw coal

Fan Zhang^{1,*}, Geng Ma¹⁻³, Xiao Liu¹, Yunqi Tao¹⁻³, Rui Li⁴ and Dan Feng⁵

¹School of Energy Science and Engineering,

Henan Polytechnic University, Jiaozuo, Henan 454003, China

²Research Institute of Henan Energy Resource and Chemical Industry Group Co, Ltd, Zhengzhou, Henan 450046, China

³Henan Engineering Research Center of Simultaneous Extraction of Coal and Gas with Low Permeability and Outburst Coal Seam, Zhengzhou 450046, China

⁴Applied Technical College, China University of Mining and Technology, Xuzhou, Jiangsu 221008, China

⁵State Key Laboratory for Coal Mine Disaster Dynamics and Control, Chongqing University, Chongqing 400044, China

Similarity model test is an effective approach to study the mechanism of hydraulic fracture propagation in coalbed methane reservoirs as well as theoretical analysis and numerical simulation. The efficiency of the similarity model test result is closely related to the selection and ratio of similar materials. Similar material ratio test was conducted to simulate the mechanical parameters of raw coal using orthogonal method and an appropriate similarity model for hydraulic fracturing experiment was developed in this study. Results show that it is suitable to select cement, gypsum as binder and apply pulverized coal as aggregate through the analysis of experimental data. The mechanical parameters of similar materials, including uniaxial compressive strength, elastic modulus, Poisson ratio and firmness coefficient are tested using laboratory tests. The impact of diverse ratios of similar materials on the mechanical parameters is analysed. A proper ratio is selected to make the mechanical parameters of raw coal close to the ones of similar material, in order to meet the demand of the similarity model test based on raw coal. The results can provide theoretical basis and technical support for the selection of similar materials to carry out hydraulic fracturing experiments.

Keywords: Experimental investigation, hydraulic fracturing, raw coal, similar materials, mechanical parameters.

COALBED methane (CBM) reserves are abundant in China, ranking third in the world, but have the characteristics of low permeability, saturation and porosity, which make it difficult to realize commercial development of CBM¹. Hydraulic fracturing technology can effectively improve coal reservoir permeability, and prevent coal and gas outburst²⁻⁵. Hydraulic fractures are the main channel for CBM; the efficiency of hydraulic fracturing depends

*For correspondence. (e-mail: CZzhangfan0210@126.com)