



RESEARCH ARTICLE

UPDATED Global identification of genes and pathways regulated by Akt during activation of T helper cells [v2; ref status: indexed, <http://f1000r.es/14h>]

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Abstract

We previously demonstrated that Akt differentially modulated a subset of NF-κB target genes during T cell activation. In the current study, we further explored the broader effects of Akt inhibition on T cell gene induction. Global microarray analysis was used to characterize T helper cell transcriptional responses following antigen receptor stimulation in the absence or presence of Akt1/2 (an allosteric inhibitor which targets Akt1 and Akt2), to identify novel targets dependent upon Akt and obtain a more comprehensive view of Akt-sensitive genes in Th2 helper T cells. Pathway analysis of microarray data from a CD4⁺ Th2 T cell line revealed effects on gene networks involving ribosomal and T cell receptor signaling pathways associated with Akt1/2 treatment. Using real-time PCR analysis, we validated the differential regulation of several genes in these pathways, including *Ier3*, *Ii13*, *Egr1*, *Ccl1* and *Ccl4*, among others. Additionally, transcription factor target gene (TFactS) analysis revealed that NF-κB and Myc were the most significantly enriched transcription factors among Akt-dependent genes after T cell receptor and CD28 stimulation. Akt activation elicited increases in the enrichment of NF-κB- and Myc-targeted genes. The present study has identified a diverse set of genes, and possible mechanisms for their regulation, that are dependent on Akt during T cell activation.

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UPDATED Changes from Version 1

We thank the reviewers for their thorough and insightful comments on our manuscript, and their overall positive response to it. We have now responded to the comments and concerns that were raised. In brief, we have cited additional references to better put our results into context with previous studies. In addition, we have added further justification for our approach and slightly narrowed the scope of our conclusions. As a result, we feel that the revised manuscript is clearer and more accurately reflects the data and their analysis.

See referee reports

Introduction

Akt/protein kinase B (PKB) is a serine/threonine kinase that is activated downstream of PI-3 kinase. The activation of Akt leads to the phosphorylation and regulation of a wide spectrum of substrates involved in multiple cellular processes, including cell survival, growth, differentiation, cell cycle progression, proliferation and metabolism¹. The expression of a constitutively active form of Akt (myr-Akt) in transgenic mice was reported to influence thymocyte selection, lead to accumulation of CD4⁺ T cells in peripheral lymphoid organs, and to enhance T cell survival in the presence of various apoptosis-inducing stimuli². We have previously studied the role of the Akt kinase in T cells, and most recently showed that a subset of NF- κ B-dependent genes required Akt for optimal upregulation during T cell activation³. Studies of individual transcription factors and their target genes have uncovered numerous aspects of Akt signaling in T cells, including regulation of not only NF- κ B, but also FOXO and NFAT⁴⁻⁹. However, the overall gene expression program controlled by Akt signaling in activated helper T cells has not been elucidated. Mapping global changes in gene expression has proven extremely useful in revealing previously unappreciated connections between groups of expressed genes and biological events, such as development and tumorigenesis. A study from the Cantrell lab¹⁰ concluded that the chief role of Akt in CD8⁺ cytotoxic T cells is to control the transcriptional programs that direct effector versus memory cell fate. Nonetheless, Akt may not have the same role in all T cell subpopulations. For example, constitutively active Akt can stimulate the growth and survival of CD4⁺ T cells but not CD8⁺ T cells^{11,12}.

In the current study, we tested the effects of a selective, allosteric inhibitor of Akt1 and Akt2 (Akti1/2)¹³⁻¹⁶ on activated T cells and further explored potential mechanism of action of Akt, by performing network analysis of gene expression data and validating the expression changes of selected genes by real-time qPCR analysis. Our findings demonstrate that Akt inhibition by Akti1/2 significantly affects ribosomal protein expression and the cytokine-cytokine receptor interaction gene expression axis. Asthma and the antigen receptor signaling pathways were also impaired by Akti1/2 in activated T cells. Moreover, Akt inhibition decreased the enrichment of NF- κ B- and Myc-targeted genes after CD3/CD28 stimulation. These effects may contribute to the functions of dysregulated Akt activation in tumorigenesis, as well as in normal T cell activation and development¹².

The importance of Akt for T cell activation and transformation led us to explore the underlying pathways and mechanisms (or target genes and downstream cellular pathways) by a genome-wide gene expression profiling approach. Therefore the aims of the present study were to (1) identify, at the genome-wide level, the genes that are differentially expressed in activated Th2 helper T cells, with or without Akt inhibition and (2) conduct bioinformatics analyses to identify the pathways and possible mechanisms involved.

Materials and methods

Antibodies and reagents

Biotin-anti-mCD28 (37.51) and biotin-anti-mCD3 ϵ (145-2C11) were obtained from BD-Biosciences (San Jose, CA). Streptavidin was obtained from Invitrogen (Carlsbad, CA) and Akti1/2 was from EMD Biosciences (San Diego, CA). rhIL-2 was obtained through the NIH AIDS Research and Reference Reagent program, Division of AIDS, NIAID, NIH (Cat.#136 from Hoffman-LaRoche, Inc.).

T cells

The D10 T cell line, a fast-growing variant of the D10.G41 murine Th2 T cell clone¹⁷⁻¹⁹ was maintained in RPMI 1640 media (Mediatech, Manassas, VA), supplemented with 10% heat-inactivated bovine growth serum (BGS; Hyclone, Logan, UT), 0.1 mM nonessential amino acids (Lonza, Walkersville, MD), 2 mM L-glutamine, 50 μ M 2-ME, 100 U/ml penicillin, 100 μ g/ml streptomycin (Mediatech, Manassas, VA) and 25 IU/ml rhIL-2.

RNA extraction and microarray gene expression profiling

D10 T cells were left untreated or pretreated with 10 μ M Akti1/2 for 1 h and then stimulated with biotinylated anti-mCD3/CD28 and streptavidin for 0, 2, 6 and 12 hrs. RNA extraction was performed using a commercially available kit (RNeasy, Qiagen, Frederick, MD) according to the manufacturers' recommendations. RNA quality was confirmed based on a RNA integrity number >8 by use of the Agilent 2100 bioanalyzer (Agilent Technologies, Palo Alto, CA). The microarray analysis was performed by Genomics and Proteomics Core Laboratories (GPCL) of the University of Pittsburgh, USA. An Illumina mouse RefSeq8 chip was used. Microarray data have been deposited in the GEO database and are accessible through the GEO series accession number [GSE45221](https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE45221).

Statistical analysis of gene expression microarray data

To compare the molecular characteristics between different time points, Automated Efficiency Analysis was first performed using 7 transformation methods, 9 normalization methods and 5 tests for differentially expressed genes²⁰. A global normalization method and the J5_Quantile95_None method were applied on each time point. The differentially expressed genes were identified using caGEDA with a reasonable threshold of J5 for each time point²¹. To survey the spectrum of biological functions within genes, which were differentially expressed between different groups, functional classification of the genes were performed using Pathway Express (<http://vortex.cs.wayne.edu>; a pathway level Impact Analysis as described by Draghici *et al.*, 2007²²). Pathway Express was designed to provide both statistical and biological significance in the indication of which pathways may be affected by the observed

changes in gene expression. The results are summarized as Impact scores and p-values. Pathway-Express orders the affected pathways in the decreasing order of their expected importance for the given condition.

Real-time PCR analysis

Quantitative real-time PCR was performed using the ABI Step One Plus Real-time PCR system (Applied Biosystems, Foster City, CA) as described previously³. Amplification was performed on a cDNA amount equivalent to 25 ng total RNA with 1×SYBR green universal PCR Master mix (Applied Biosystems) containing deoxyribonucleotide triphosphates, MgCl₂, AmpliTaq Gold DNA polymerase, and forward and reverse primers. Specific primers for each gene were purchased from SABiosciences (Qiagen, Frederick, MD). Experimental samples and no-template controls were all run in duplicate. The PCR cycling parameters were: 95°C for 10 min, and 40 cycles of 94°C for 15s, 60°C for 1 min. The amount of cDNA in each sample was calculated by the comparative threshold (Ct) method and expressed as 2^{exp (Ct)} using 18S RNA as an internal control. Statistical significance was determined using the Student's T test. All statistical tests were performed using GraphPad Prism (GraphPad Prism, San Diego, CA).

Enrichment in transcription factor target gene analysis

TFactS was used to predict the activities of transcription factors in our microarray data²³. The lists of up- and down-regulated genes were compared to a list of curated target gene signatures. The nominal p-value (Pval) represents the risk of a false positive for a single test. Since the list of query genes is systematically compared to each target gene signature, a multi-testing condition is required. The e-value (Eval) represents the expected number of false positives for a given nominal value. It is computed using the formula: Eval=Pval*T, where T is the number of tests.

Results

Identification of genes regulated by Akt signaling in activated CD4⁺ T cells

We previously demonstrated that Akt activity was rapidly inhibited in T cells by addition of the allosteric inhibitor Akti1/2, which inhibited phosphorylation of Akt within one minute, an effect that can last as long as twelve hours³. In the present study, microarray analysis was performed at three different time points after CD3/CD28 stimulation to characterize the effects of Akt inhibition on the T cell gene activation program in helper T cells. Thus, D10 T cells (a murine Th2 T cell line) were pre-incubated with 10 μM Akti1/2 or solvent, then stimulated for 2–12 hours. We chose this concentration of inhibitor for two reasons. First, in our recent study we observed good concordance between results obtained with 10 μM Akti1/2 and those obtained with combined siRNA-mediated knock-down of Akt1 and Akt2³. In addition, although 1–5 μM can substantially inhibit Akt activity in different cell types under acute conditions^{24,25}, at least one study has demonstrated that a higher concentration (10 μM) of Akti1/2 was required for more significant inhibition of Akt substrate phosphorylation over the course of several hours²⁵. This could be related to the fact that full-length Akt is only inhibited approximately 80% by 1 μM (and 90% by 10 μM) Akti1/2 in *in vitro* kinase assays, as shown in a kinase profiling study by Cohen and colleagues²⁶. After stimulation, mRNA was isolated, which was converted into labeled cDNA for hybridization to Illumina chips for microarray analysis (Figure 1A). A rough analysis of the genes modulated in our study after six or twelve hours of CD3/CD28 stimulation (using the default settings with the GEO2R tool at the GEO database) revealed that of the top 30 genes in each case, seven were modulated to a nearly identical degree in the presence or absence of 10 μM Akti1/2. Thus, we were reasonably confident that Akti1/2, with this cell type, and at the concentration used in our study, did not have widespread, off-target, effects on gene transcription or cell viability.

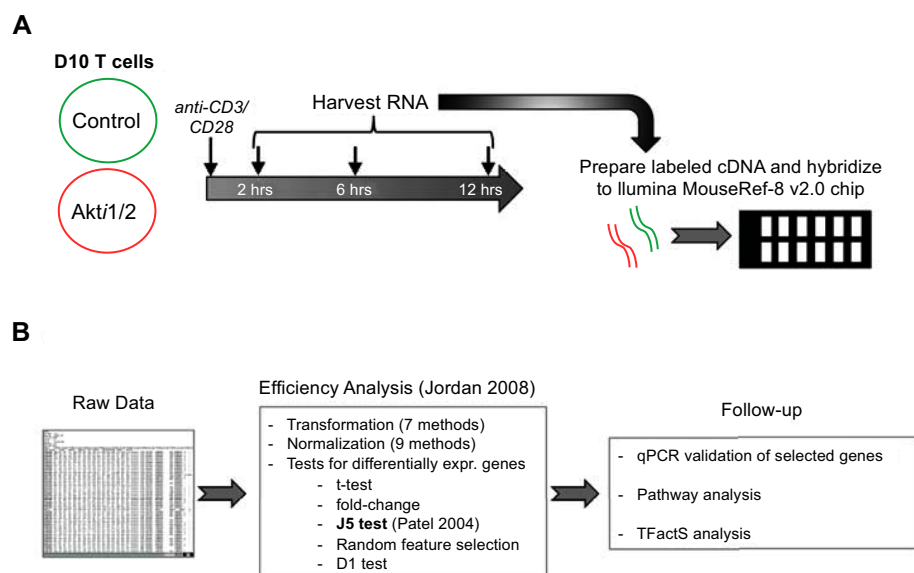


Figure 1. Flowchart of experimental outline (A) and data analysis (B), as described further in the text.

We next determined which genes were differentially modulated after T cell receptor (TCR) stimulation using *caGEDA* with reasonably chosen thresholds for different time points (2 h, 6 h and 12 h). This methodology allows for the capture of a more complete set of differentially modulated genes, which is less dependent on overall expression levels. Further validation and downstream analysis were then performed to confirm some of the differentially expressed genes and to extract functional information from the dataset (Figure 1B). We identified differentially expressed gene sets that were dependent on Akt among the three different time point groups. We compared the gene expression patterns of cells plus or minus addition of Akt1/2. First, we generated two gene lists for each time point. Gene list one represents the genes that were differentially expressed between the unstimulated and CD3/CD28 stimulated group in the absence of Akt1/2. Gene list two represents the genes that were differentially expressed between the unstimulated and CD3/CD28 group in the presence of Akt1/2. When comparing the two gene lists, three different patterns were observed:

1. Genes significantly modulated by CD3/CD28 alone but not modulated in the presence of Akt1/2 (genes in this category showed Akt-dependent expression after T cell activation; column 1, top, in [Data File 1–Data File 3](#) and [Supplementary Figure 1](#)).
2. Genes significantly modulated by CD3/CD28 alone but less strikingly modulated in the presence of Akt1/2 (genes in this category showed some dependence on Akt; columns 1–2, middle, in [Data File 1–Data File 3](#) and [Supplementary Figure 2](#)).
3. Genes not modulated by CD3/CD28 alone but significantly modulated in the presence of Akt1/2 (genes in this category displayed Akt1/2-specific expression; column 2, bottom, in [Data File 1–Data File 3](#) and [Supplementary Figure 3](#)).

Genes with significant modulation at 2 hours of CD3/CD28 stimulation in the presence or absence of Akt1/2

1 Data File

<http://dx.doi.org/10.6084/m9.figshare.678213>

Genes with significant modulation at 6 hours of CD3/CD28 stimulation in the presence or absence of Akt1/2

1 Data File

<http://dx.doi.org/10.6084/m9.figshare.678214>

Genes with significant modulation at 12 hours of CD3/CD28 stimulation in the presence or absence of Akt1/2

1 Data File

<http://dx.doi.org/10.6084/m9.figshare.678215>

By examining multiple time points after stimulation, we were able to obtain a kinetic picture of gene expression \pm Akt inhibition. The 6 h Akt1/2 (+) and Akt1/2 (-) comparison showed the highest number of differentially expressed genes, and there were fewer differentially expressed genes after two or twelve hours of TCR/CD28 stimulation.

Among these, only the genes that expressed the most consistent differences (either increased or decreased expression) were selected for further analysis. Genes with no known function were excluded.

Our previous work identified several NF- κ B target genes that were dependent on Akt after TCR stimulation in T helper cells, including those encoding the cytokines TNF- α , GM-CSF, and IL-10, among others³. Analysis of the microarray data confirmed the dependency of these genes on Akt activation, which inspired confidence in our results. Moreover, expression of the mRNAs encoding many secreted proteins was also decreased by Akt inhibition, including IL-13, IL-5, IL-3 and IL-4 (Figure 2). The protein products of these genes (except IL-3) were examined in our previous paper³, which confirmed similar decreases after Akt inhibition. Our data agrees with Patra *et al's* study⁷, which showed that myr-Akt expression in activated CD4⁺ T cells resulted in increased IL-4 and IL-13 expression. In addition we found that expression of *Ltb* (encoding lymphotoxin β), *Areg* (encoding amphiregulin) and genes encoding the chemokines CCL1, CCL3 and CCL4 were also affected by Akt inhibition (Figure 2).

Of note, several cell-surface proteins, including CD69, CD52 and CD82 were among the Akt-dependent genes after T cell activation (Figure 2). The CD82 molecule is a type III integral membrane protein with four transmembrane domains and is part of the tetra-span-transmembrane (TST) family, which also includes CD9, CD37, CD53, CD63 and CD81/TAPA-1²⁷. Interestingly, proteins of this family are involved in cell activation. For example, engagement of CD82 can deliver a co-stimulatory signal, similar to CD28, for full T cell activation, leading to strong IL-2 production²⁸. CD52 is a small glycopeptide molecule and tethered to the outer surface of the plasma membrane by a glycosylphosphatidylinositol (GPI)-anchor²⁹. CD52 crosslinking can also provide a co-stimulatory signal that causes the activation of normal human T lymphocytes³⁰ and induction of CD4⁺ regulatory cells³¹. Since Akt was reported to mimic CD28 co-stimulation in a T cell line by synergizing with TCR-induced signals to increase transcription of the IL-2 promoter⁵, activation of these other co-stimulatory molecules might also function through this pathway.

Interestingly, inhibition of Akt resulted in impaired up-regulation of the genes encoding many ribosomal proteins (Figure 3). These included: Rps6 (a major substrate of ribosomal protein kinases³²); Rps8, Rps9 (reported to be activated in various tumors, including colon cancer³³); Rps10, Rps15, Rps24 (mutations in these gene result in Diamond-Blackfan anemia³⁴); Rpl7a (which interacts with a subclass of nuclear receptors and inhibits their ability to activate transcription³⁵); Rplp1 (important for elongation during protein synthesis³⁶). All these proteins belong to either small or large subunits of ribosomes; changes in their expression may contribute to an increase in protein synthesis to accommodate numerous cellular processes involved in T cell activation, in addition to the possible connections to cancer. Importantly, the expression of 18S ribosomal genes, which was used for our qPCR housekeeping gene, did not differ between our experimental groups.

Expression validation of selected genes

In order to validate the microarray data and obtain more quantitative data on specific genes, real-time PCR analysis was performed

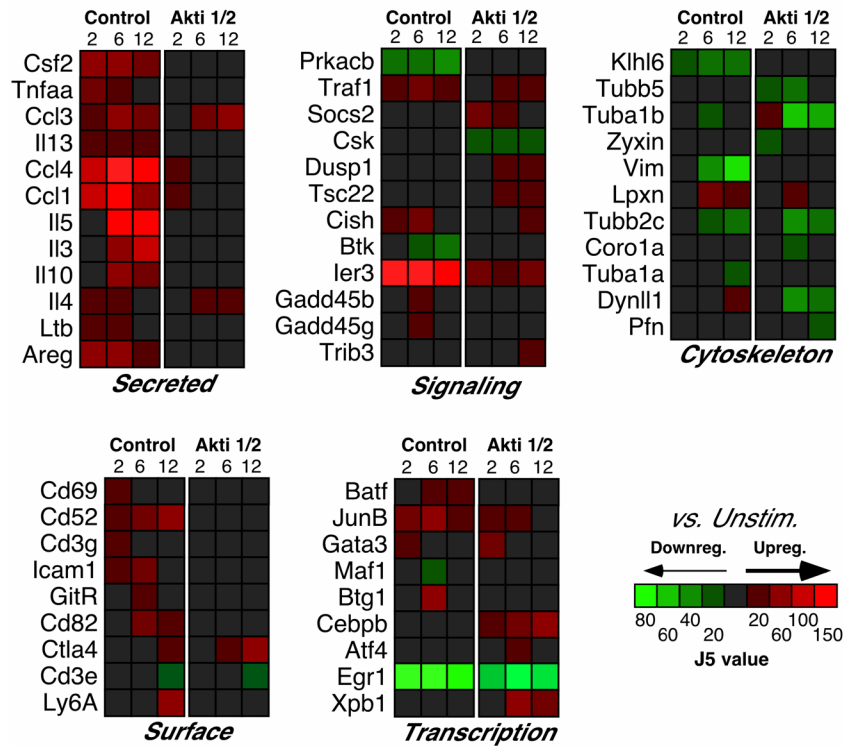


Figure 2. Selected Akt-dependent genes differentially expressed between control (0 h) and 2 h, 6 h and 12 h CD3/CD28 stimulation groups. Relative levels of expression are represented by the J5 score.

at different time points after CD3/CD28 stimulation \pm Akti1/2. *Ier3* (also named IEX-1, immediate early response gene X-1), *Il13*, *Ccl1* and *Ccl4* were selected for real-time PCR validation because their expression was greatly enhanced after CD3/CD28 stimulation and decreased in the presence of the Akt inhibitor. Of note, the gene expression of *Ccl1* and *Il3* was rapidly up-regulated by CD3/CD28 stimulation, while the up-regulation of *Ier3* and *Ccl4* expression by CD3/CD28 stimulation was delayed. *Egr1* was also selected as a control gene, which showed no CD3/CD28 dependent increase in gene expression, but rather a sharp decrease. Thus, Akt inhibition could affect different genes that showed diverse kinetics after CD3/CD28 stimulation. At least for these specific genes, the changes in expression, as assessed by real-time PCR, confirmed the microarray results, giving us confidence in the overall quality of the dataset.

Akt is known to directly phosphorylate FOXO3a (including in T cells) and, once phosphorylated, FOXO3a is excluded from the nucleus and becomes transcriptionally inactive³⁷. One of the best characterized FOXO target genes in T cells is *Klf2*³⁸. For reasons that are unclear, we did not observe modulation of *Klf2* expression after CD3/CD28 stimulation, with or without Akti1/2. Among known or suspected FOXO target genes^{38,39}, several that did display enhanced expression in our microarray experiment in the presence of Akti1/2 were *Ctla4*, *Gadd45*, *Cebpb* and *Klf6*. The latter was recently identified as a FOXO target gene, which was confirmed by chromatin immunoprecipitation^{40,41}. Our own real time PCR analysis confirmed that in Akti1/2-treated samples, there was an

up-regulation of *Klf6*, relative to stimulation with anti-CD3/CD28 alone, which by itself resulted in a sharp decline in the *Klf6* message (Figure 4).

Functional classification of the gene expression signature for Akt inhibition in activated T cells (pathway analysis of Akti1/2-mediated transcriptome changes)

From our previously published array data, we found that at two, six and twelve hours after CD3/CD28 stimulation. Akti1/2 elicited a wide range of effects on expression of numerous genes, including both over- and under-expressed genes. In the present study, genes that showed changes in expression after two, six and twelve hours of stimulation in the presence of Akti1/2 were largely not overlapping and cannot be combined for subsequent analysis. There were 54, 71 and 58 genes dependent on Akt at the two, six and twelve hour time points, respectively, after CD3/CD28 stimulation (Data File 1– Data File 2 and Supplementary Figure 1).

To determine whether our gene expression signature was enriched in specific subsets of genes with known biological functions, bioinformatic functional classification analysis of the genes that were differentially expressed was carried out as described in the Methods. The functional classifications of gene sets are illustrated in Figure 5. We found that genes involved in ribosome, cytokine-cytokine receptor interaction, antigen receptor signaling pathway, hematopoietic cell lineage and asthma were significantly enriched among genes affected by Akt inhibition in the presence of CD3/CD28 stimulation.

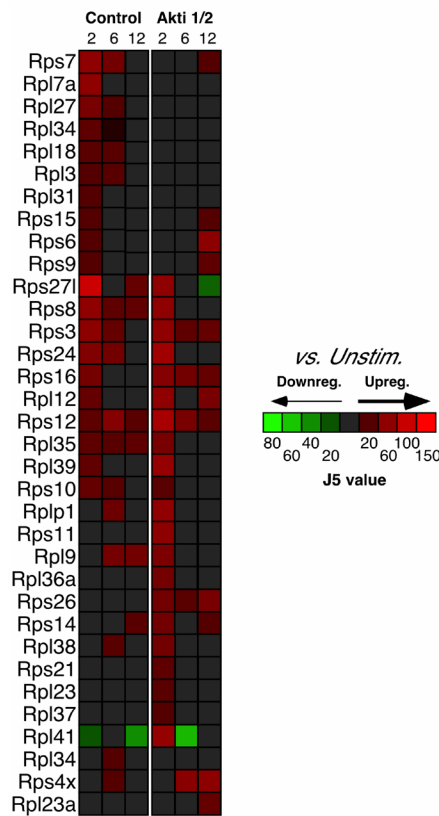


Figure 3. Akt-dependent ribosomal subunit genes differentially expressed between control (0 h) and 2 h, 6 h and 12 h CD3/CD28 stimulation groups. Relative levels of expression are represented by the J5 score.

Enrichment of transcription factors in target genes

Co-expressed genes are often regulated by common transcription factors. Therefore, we separately analyzed the genes that showed altered expression at 2, 6 and 12 h time points after CD3/CD28 stimulation using **TFactS**, an algorithm that used a catalog of well-characterized transcription factor targets to predict the activity of transcription factors based on microarray data³³. Enrichment of transcription factors was found at all the time points tested (Figure 6). These included NF- κ B family members (RelA, Rel, NF- κ B1), Myc, Jun and C/EBP. At the 2 h time point, Myc, NF- κ B family members (Nfkb1, RelA and Rel) and Egr1 were significantly enriched. RelA, Nfkb1 and Rel, along with Myc and Egr1 were also significantly regulated after 6 h of CD3/CD28 stimulation. Moreover, other transcription factors, including Sp1, C/EBPB, Ets1, Jun and Nfam1, were also enriched at the 6 h time point. At 12 h after stimulation, however, fewer transcription factors were regulated, with Myc and NF- κ B1 still significantly regulated. In summary, the most significantly enriched transcription factor binding sites in the regulatory regions of Akt-dependent genes after CD3 and CD28 stimulation were those of NF- κ B family members and Myc.

Discussion

Akt activation impacts the expression of genes responsible for cell proliferation and survival^{42,43}. The majority of previous global gene expression studies have investigated transcriptional programs

under the combined control of both PI3K and Akt^{44,45}. Despite much attention in recent years to the role of Akt-regulated metabolism in T cells⁴⁶, a recent study provided clear evidence that Akt indeed contributes to changes in gene expression after activation of cytotoxic T cells¹⁰. We have also been interested for some time in achieving a greater level of clarity in separating the effects of PI3K and Akt during helper T cell activation⁴⁷. Our recent study identified a subset of NF- κ B-dependent genes that require Akt for optimal upregulation during helper T cell activation by using a targeted gene profiling approach³. In the present study, we performed a broader microarray analysis to characterize the global changes in gene expression resulting from inhibition of Akt in activated CD4⁺ helper T cells. Analysis of the affected genes revealed pathways that are central to the effects of Akt on helper T cell activation. Finally, analysis of the enrichment in transcription factor binding sites in our target genes further confirmed NF- κ B as a regulator of these genes in response to TCR stimulation.

The generation and maintenance of memory T cells is central to the development of protective immunity, as characterized by a rapid and vigorous response after a secondary encounter with a given pathogen or antigen^{48,49}. Recent studies have suggested that proper regulation of Akt activity is essential for the development of memory T cells. Riou *et al.*, found that Akt plays a critical role in the phosphorylation of FOXO3 in CD4⁺ central memory T cells (T_{CM}), thereby promoting T_{CM} survival⁵⁰. Abrogating the Akt survival pathway led to a greater degree of apoptosis in T_{CM} as compared with effector memory T cells (T_{EM}), confirming that T_{CM} are more dependent on these pathways for their survival. Sustained and strong activation of Akt was also shown in CD8⁺ cytotoxic T cells (CTL) to coordinate the TCR and IL-2-induced transcriptional programs that control expression of key cytolytic effector molecules, adhesion molecules, and cytokine and chemokine receptors that distinguish effector from memory and naive T cells¹⁰. It has been suggested⁵¹ that Akt simultaneously induces and represses expression of key genes, leading to the development of effector CTL, with the FOXO transcription factors being at the center of this process. Thus, Kim *et al.*, found that Akt appeared to function as a cellular rheostat, controlling distinct facets of the program that governed differentiation of Ag-activated CD8⁺ T cells into effector cells or memory CD8⁺ T cells⁵¹. Myristoylated Akt transgenic mice were found to accumulate memory phenotype CD4⁺ T cells and to develop both tumors and autoimmunity⁵², effects that could, in principle, be due in part to non-metabolic outcomes of Akt activation, such as NF- κ B activation⁶. In addition, FOXO transcription factors control the development and function of natural regulatory T cells (nTreg)⁵³, and the generation of inducible Treg (iTreg) is also regulated by both Akt and FOXO's^{54,55}.

The enrichment of multiple NF- κ B family members in Akt-dependent genes confirmed our previous study emphasizing the important role of NF- κ B in Akt-dependent biological processes¹. Although FOXO did not appear in the list of the most significantly affected transcription factors in our analysis of Akt-dependent genes, expression of multiple FOXO target genes (including *Klf6*, *Gadd45* and *Ctla4*) was increased in the presence Akt inhibition, relative to stimulation with anti-CD3/CD28 alone. Using RT-PCR, we confirmed that *Klf6* expression was decreased, as expected, by stimulation with

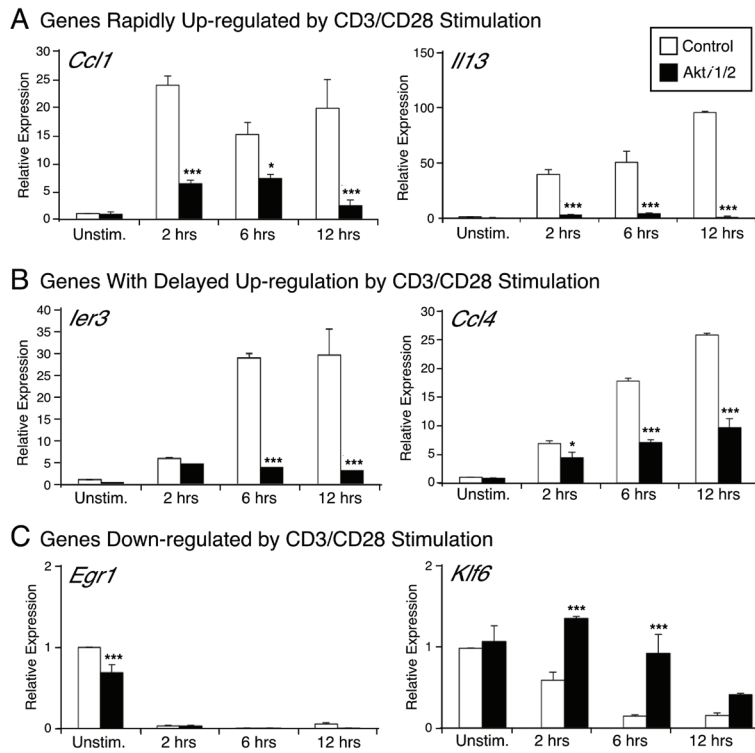


Figure 4. Quantitative real-time PCR (qPCR) confirmation of the stimulation-dependent expression of selected Akt-dependent genes. qPCR was used to validate the gene expression of *Ier3*, *Il13*, *Klf6*, *Egr1*, *Ccl1* and *Ccl4*. The RNA samples were the same as those used for the microarray. Results are presented as relative mRNA expression, compared to the unstimulated control sample, normalized to 18S RNA expression. ***p<0.001, *p<0.05 compared with the control group.

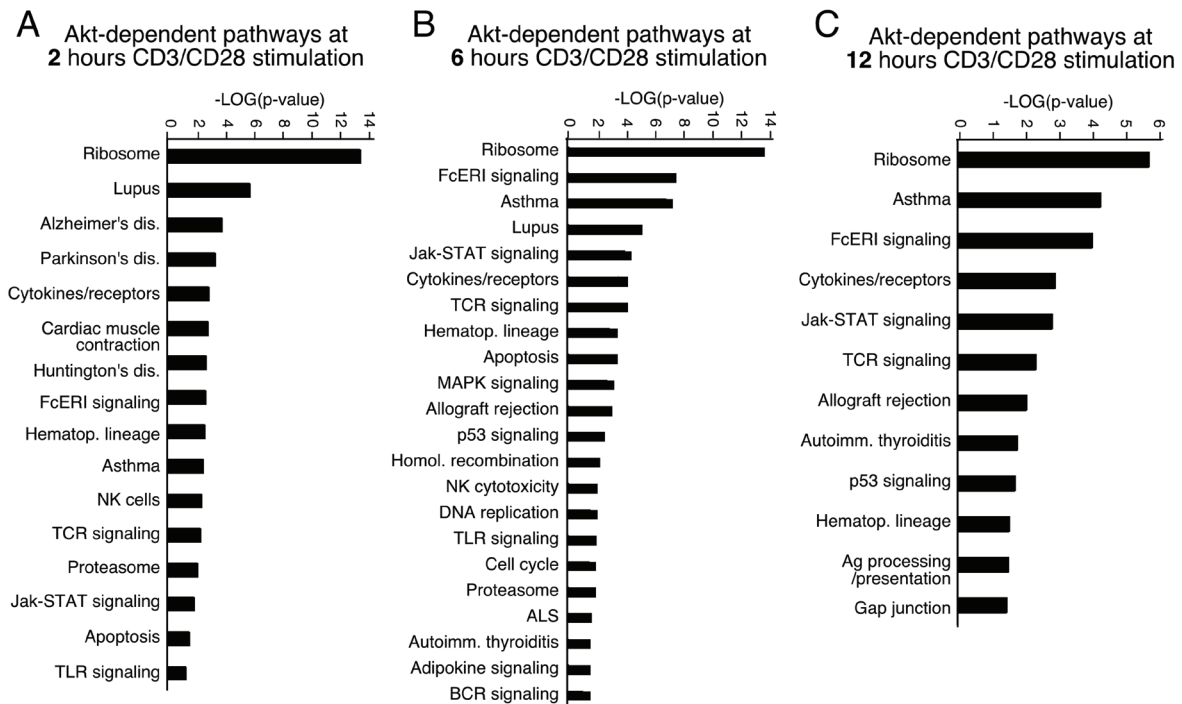


Figure 5. Functional classification of Akt dependent genes. Classification enrichment was determined using Pathway Express. Significance is indicated as -Log (p-value).

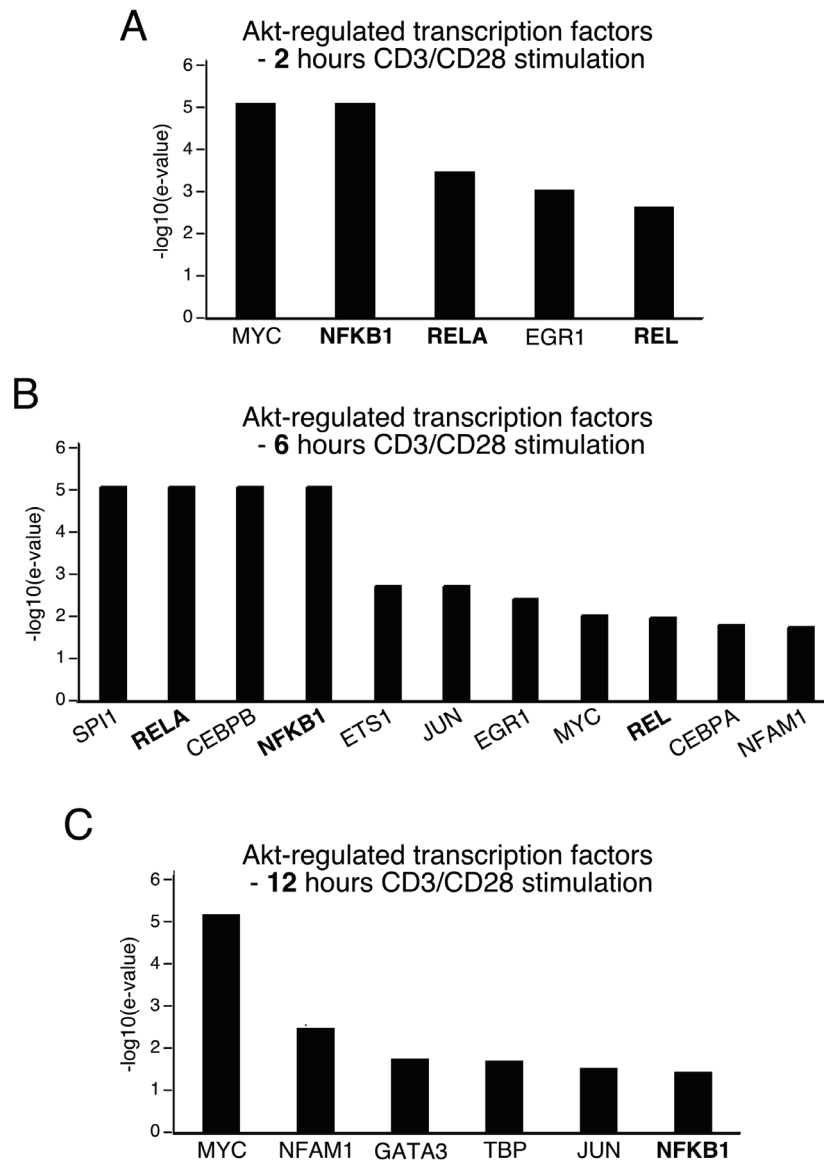


Figure 6. Transcription factor binding sites enriched in Akt-dependent genes, as predicted by TFactS. The list of Akt-dependent genes was submitted to TFactS (sign-less) using default settings. Significance of regulated transcription factors was determined with $-\log_{10}(\text{e-value})$.

anti-CD3/CD28 alone, an effect that was significantly retarded (particularly at earlier time points) in the presence of the Akt inhibitor. Although *Klf6* is not the most commonly discussed FOXO target gene, a recent whole transcriptome analysis of FOXO-deficient liver endothelial cells identified *Klf6* as one of the top two most significantly down-regulated genes with the highest number of conserved FOXO-binding elements⁴⁰. Moreover, a ChIP-based study identified *Klf6* as a direct transcriptional target of FOXO1⁴¹. Further study will be necessary to determine to what extent the global effects of Akt on CD4⁺ T cell biology are due specifically to effects on FOXO vs. NF- κ B.

Of note, Myc target genes were also found enriched in the subset of Akt-dependent genes after T cell activation. It is well known that Myc is associated with cell activation. However, it is now thought that Myc is not an on-off specifier of a particular transcriptional program(s) but is a universal amplifier of gene expression, increasing output at all active promoters⁵⁶. Relevant for our findings, N-Myc was reported to function as a regulator of cell growth by stimulating expression of genes functioning in ribosome biogenesis and protein synthesis⁵⁷. Akt was also reported to cooperate with c-Myc to increase ribosome biogenesis and cell growth, which includes the synthesis of rRNA and ribosomal proteins, processing of 45S rRNA, and assembly of

functional ribosomal subunits⁵². In our present study, we showed that Akt inhibition decreased the expression of many ribosomal proteins, including components of both the small (40S) and large (60S) ribosomal subunits. Putting together these disparate observations, it may be that in activated T helper cells, one of the mechanisms through which Akt broadly regulates ribosomal subunit transcription is by activating Myc.

Akt is also known to enhance ribosomal protein production through the mammalian target of rapamycin (mTOR) pathway. However, it was reported that direct inhibition of Akt only weakly suppressed the phosphorylation of S6 and S6K1 in CTLs¹⁰ and Akt1/2 could only weakly suppress the CD3/CD28 stimulation dependent phosphorylation of S6 in Jurkat T cells and primary helper T cells (unpublished data from our lab). Akt could signal through mTORC1-dependent and independent mechanisms to promote rDNA transcription in mammalian cells⁵². Dissecting out the mTOR-independent mechanism that Akt utilizes to regulate ribosomal biogenesis is crucial to understand the therapeutic response to Akt inhibitors in cancer.

Author contributions

The project was conceived by LPK. Experiments were carried out by JC. Data were analyzed by JC and LPK, in consultation with the University of Pittsburgh Genomics and Proteomics Core Laboratory (GPCL). The paper was written by JC and LPK.

Competing interests

No competing interests were disclosed.

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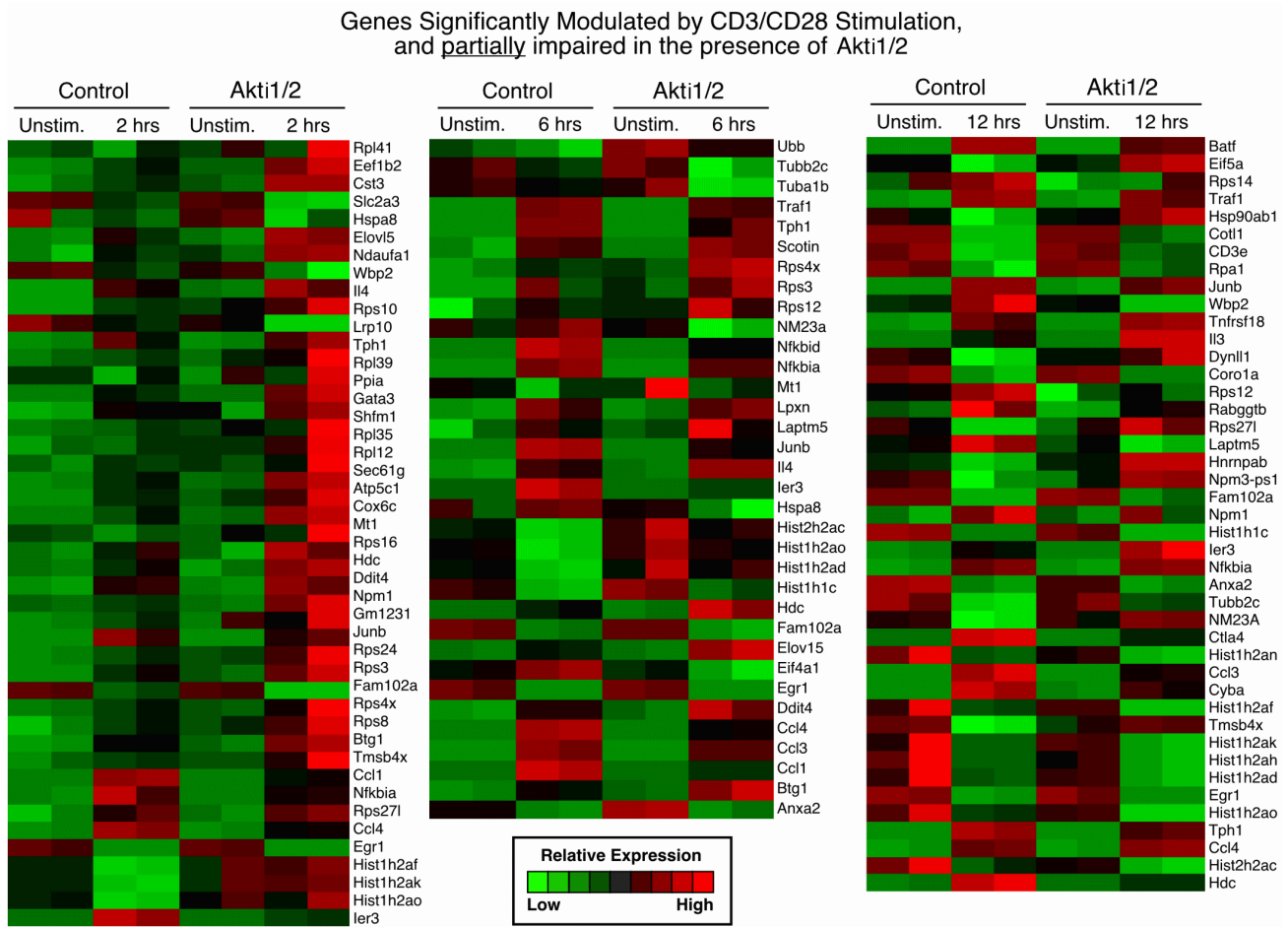
We thank James Lyons-Weiler and Haiwen Shi of the University of Pittsburgh Genomics and Proteomics Core Laboratory (GPCL) for assistance with data analysis.

Supplementary materials

Genes Significantly Modulated by CD3/CD28 Stimulation, but not in the presence of Akti1/2



Supplementary Figure 1. Genes significantly modulated by CD3/CD28 stimulation alone, but not modulated in the presence of Akti1/2. Each row represents a gene and each column shows one of the duplicates from two different groups (from left to right 0 h vs. 2 h, 0 h vs. 6 h, 0 h vs. 12 h). The red and green colors reflect high and low expression levels, respectively.



Supplementary Figure 2. Genes significantly modulated by CD3/CD28 stimulation alone but less modulated in the presence of Akti1/2. Each row represents a gene and each column shows one of the duplicates from two different groups (from left to right 0 h vs. 2 h, 0 h vs. 6 h, 0 h vs. 12 h). The red and green colors reflect high and low expression levels, respectively.

Genes not Modulated by CD3/CD28 alone,
but significantly modulated in the presence of Akti1/2



Supplementary Figure 3. Genes significantly modulated by Akti1/2 alone. Each row represents a gene and each column shows one of the duplicates from two different groups (from left to right 0 h vs. 2 h, 0 h vs. 6 h, 0 h vs. 12 h). The red and green colors reflect high and low expression levels, respectively.

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Current Referee Status:



Version 2

Referee Report 04 March 2014

doi:[10.5256/f1000research.1457.r1602](https://doi.org/10.5256/f1000research.1457.r1602)



David Finlay

School of Biochemistry and Immunology, Trinity College Dublin, Dublin, Ireland

While some of my concerns that I stated in my first report remain, the authors have clarified most of the issues that I highlighted. This article contributes to our knowledge of Akt in CD4 T cells and so I am happy to approve it.

I have read this submission. I believe that I have an appropriate level of expertise to confirm that it is of an acceptable scientific standard.

Competing Interests: No competing interests were disclosed.

Referee Report 22 January 2014

doi:[10.5256/f1000research.1457.r3257](https://doi.org/10.5256/f1000research.1457.r3257)



Ursula Bommhardt

Otto-von-Guericke University Magdeburg, Magdeburg, Germany

I have read the revised and improved version of the manuscript and approve it.

I have read this submission. I believe that I have an appropriate level of expertise to confirm that it is of an acceptable scientific standard.

Competing Interests: No competing interests were disclosed.

Referee Report 21 January 2014

doi:[10.5256/f1000research.1457.r3241](https://doi.org/10.5256/f1000research.1457.r3241)



Michael Gold

Microbiology & Immunology, University of British Columbia, Vancouver, BC, Canada

I have looked through this revised version and approve of this one as well, with some of the same caveats that are indicated in my initial review. Nevertheless, this is a valuable addition to the field and data that will be of use to researchers, so I approve of its publication in its present form.

I have read this submission. I believe that I have an appropriate level of expertise to confirm that it is of an acceptable scientific standard.

Competing Interests: No competing interests were disclosed.

Version 1

Referee Report 20 May 2013

doi:10.5256/f1000research.1303.r957



Michael Gold

Microbiology & Immunology, University of British Columbia, Vancouver, BC, Canada

This article provides useful information for further assessing the role of Akt signaling in the activation of CD4+ T cells. The microarray experiments that assess the effect of an Akt inhibitor compound on gene regulation by TCR/CD28 co-stimulation are well done and the accompanying bioinformatics analyses are quite sophisticated such that identified changes in gene expression needed to have passed multiple statistical tests.

Although a good starting point for further studies, the data presented have several limitations. First, the experiments were carried out entirely with a T cell line. It would have been straightforward, and of significant value, to confirm some of the key gene expression changes in primary T cells stimulated with anti-CD3/anti-CD28 in the presence or absence of the Akt inhibitor. It is of interest that two of the Akt-dependent genes identified in this report are IL-13 and IL-4, suggesting that Akt is critical for the effector functions of Th2 cells. It would be worthwhile to discuss the role of Akt signaling in Th2 polarization versus Th2 function and to refer to, or propose, further studies to address this question.

Second, as for any study employing chemical inhibitors, it would have been useful for the authors to briefly review selectivity of this compound as well as known off-target effects on other kinases. In this regard, confirming some of the key gene expression changes by using other commercially available Akt inhibitors with different off-target effects would help confirm the dependence on Akt.

Similarly, the conclusion that many of the Akt-regulated genes may be co-regulated by NF- κ B or Myc could have been tested in a limited fashion.

Despite these limitations, which will likely be dealt with in follow-up studies by these authors and others, this article provides useful data that will stimulate further work and discussion.

I have read this submission. I believe that I have an appropriate level of expertise to confirm that it is of an acceptable scientific standard.

Competing Interests: No competing interests were disclosed.

Referee Report 03 May 2013

doi:10.5256/f1000research.1303.r925



Ursula Bommhardt

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In this publication, Cheng and Kane mapped the gene expression profile of a Th2 cell line stimulated with cross-linked CD3/CD28 Abs in the presence of Akti1/2 inhibitor using microarray and qRT-PCR analysis. They found gene expression that is not moderately or strongly affected by Akti1/2. Akt-dependent genes included cytokines (like IL-4, IL-5 and IL-13), chemokines (CCL1, CCL3 and CCL4), and a number of genes involved in the biosynthesis and function of ribosomes. Major Akt-dependent transcription factors included members of the NFkappaB family, c-myc and their target genes.

The study provides interesting and novel information on Akt-dependent signalling and Akt target genes which will be very useful for the further understanding of Akt function in T cells. In this line, previous publication by Patra *et al.* on myrAkt expression in activated CD4+ T cells had shown increased expression of Th1 as well as Th2 cytokines, including IL-10, IL-4, IL-13 (Patra *et al.*, [JI, 2004](#)). Thus, the data of the current study support those previous results. The authors should include this publication in their citation list as well as other publication from the groups of P. Ohashi, C. Thompson and others with regard to Akt, NFkappaB and tumorigenesis.

I have read this submission. I believe that I have an appropriate level of expertise to confirm that it is of an acceptable scientific standard.

Competing Interests: No competing interests were disclosed.

Referee Report 24 April 2013

doi:10.5256/f1000research.1303.r910



David Finlay

School of Biochemistry and Immunology, Trinity College Dublin, Dublin, Ireland

This paper aims to determine to what extent Akt regulates the transcriptional landscape in TCR/CD28 activated CD4 T cells. While a considerable amount is known regarding Akt regulation of gene expression in activated CD8 cytotoxic T cells (McIntyre *et al.*, 2011 [Immunity 34\(2\) 224-236](#)) less information exists with respect to CD4 T cells. Indeed it is true, as the authors say, that Akt may have distinct roles in different T cell subsets. Therefore, determining the role of Akt in controlling the transcriptome in CD4 T cell subsets addressed an important and relevant question. However, the data would have been of a much higher value had this study been carried out in primary T cells rather than a CD4 T cell line. There is no reason that using primary CD4 T cells would not have been feasible and I struggle to understand why this was not done. Therefore, this data needs to be viewed with this major caveat in mind.

I have substantial concerns regarding the concentration of Akti1/2 that is used in this study. In CD8 T cells 1µM Akti1/2 is sufficient to completely block all Akt activity. This study uses 10µM, 10 times the dose used in CD8 T cell. When using kinase inhibitors, it is extremely important to use the lowest dose that effectively inhibits the kinase activity, as excessive doses can have increased off target effects. For example it has been shown that Akti1/2 has multiple off target effects at 10µM when screened against a panel of 80 kinases (Bain J, *et al.*, 2007, [Biochem. J. 408, 297-315](#)). Additionally, in CD8 Cytotoxic T cells, 10µM Akti1/2 is toxic and compromises cell viability, a clear demonstration of off target effects

(unpublished data). The authors should demonstrate that they are using the minimum effective dose and consider what aspect of the results that they present in this paper might be due to off target effects of the Akti1/2 compound.

With respect to their data, the authors discuss the role of Foxo transcription factors as Akt substrates and their role in CD4 T cells despite the fact that they have little to no evidence that the activity of Foxo transcription factors are altered in response to Akt inhibition in this model. They state Klf6 as a Foxo target. **The authors must clearly reference the work that describes Klf6 as a Foxo Target.** At best Klf6 is an obscure Foxo target gene. There are numerous well defined Foxo targets in T cells, Klf2 for example, yet the absence of these Foxo target genes in the Akti1/2 regulated gene lists is not discussed at all.

A minor point, in the text it is stated that CREB was one of the transcription factors predicted by TFactS to be altered in activity (bottom of page 5), yet CREB does not appear in the corresponding figure (Figure 6).

I have read this submission. I believe that I have an appropriate level of expertise to confirm that it is of an acceptable scientific standard, however I have significant reservations, as outlined above.

Competing Interests: No competing interests were disclosed.
