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Transcription factor binding predicts histone modifications in human cell lines

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Gene expression in higher organisms is thought to be regulated by a complex network of transcription factor binding and chromatin modifications, yet the relative importance of these two factors remains a matter of debate. Here, we show that a computational approach allows surprisingly accurate prediction of histone modifications solely from knowledge of transcription factor binding both at promoters and at potential distal regulatory elements. This accuracy significantly and substantially exceeds what could be achieved by using DNA sequence as an input feature. Remarkably, we show that transcription factor binding enables strikingly accurate predictions across different cell lines. Analysis of the relative importance of specific transcription factors as predictors of specific histone marks recapitulated known interactions between transcription factors and histone modifiers. Our results demonstrate that reported associations between histone marks and gene expression may be indirect effects caused by interactions between transcription factors and histone-modifying complexes.

epigenetics | gene regulation

The regulation of gene expression is fundamental to biology and is classically predicated on binding of transcription factor proteins to DNA. This view is challenged by large-scale studies correlating gene expression with posttranslational modifications of the histone proteins with which DNA is complexed in cells. Here, we show through a large-scale computational study that histone modifications can be predicted with remarkable accuracy from transcription factor-binding profiles, recapitulating known interactions between transcription factors and chromatin-modifying enzymes. Our results demonstrate that associations between gene expression and histone modifications do not necessarily imply a direct regulatory role for these modifications, but can be explained equally well as an indirect effect of interactions between transcription factors and chromatin-modifying enzymes.

Significance

The regulation of gene expression is fundamental to biology and is classically predicated on binding of transcription factor proteins to DNA. This view is challenged by large-scale studies correlating gene expression with posttranslational modifications of the histone proteins with which DNA is complexed in cells. Here, we show through a large-scale computational study that histone modifications can be predicted with remarkable accuracy from transcription factor-binding profiles, recapitulating known interactions between transcription factors and chromatin-modifying enzymes. Our results demonstrate that histone modifications can be predicted significantly more accurately from TF-binding patterns than from DNA sequence. We also show that the predictive power of TF-binding data extends to predict histone modifications genome-wide on a large dataset of putative functional loci. Furthermore, TF-based predictors trained on data from one cell line accurately predict histone modifications in a different cell line. Our use of statistical modeling affords insights into the relative predictive power of each TF, recapitulating known interactions between TFs and histone-modifying enzymes. Our results show that the correlative evidence for a regulatory role of chromatin is equally well

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The authors declare no conflict of interest.

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BACKGROUND

TECHNICAL

RESULTS

CONCLUSION


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explained as an indirect effect of TF binding and suggest that interactions between TFs and histone-modifying enzymes might be important in driving the deposition of histone modifications.

**Results**

To computationally explore the mechanisms responsible for the deposition of histone marks in mammalian genomes, we made use of the recently released ENCODE datasets (14). To focus on a biologically homogenous sample population of genomic elements, we initially examined which factors might determine histone modification patterns at gene promoters. Briefly, we defined 29,828 unique protein-coding transcription start sites (TSSs) from the ENSEMBL database and assigned histone modifications to each of these based on ChIP-Seq data for the three ENCODE tier 1 cell lines (H1 ES cells, K562 erythroleukemia cells, and GM12878 lymphoblastoid cells). Each TSS was assigned a positive label for a given histone mark if a ChIP-Seq peak was detected within 100 bp; if not, it was assigned a negative label. The size of the window was chosen to capture promoter proximal histone marks, which are most likely to interact with transcription. We tested promoter-associated marks that could be assigned to ≥5% of TSSs in at least one cell line. Out of the 10 histone marks assayed in all tier 1 ENCODE cell lines, this resulted in the following set of marks: H3K4me3, H3K4me2, H3K4me1, H3K9ac, H3K27ac, and H3K27me3. H3K4me1 was present above threshold only in the K562 cell line (61% of TSSs). We then further discarded H3K4me2 as it is primarily found flanking H3K4me3 at promoters (4) (Table S1). We used logistic regression (LR) to investigate which factors might determine histone modification patterns at these promoters by testing their ability to predict the presence of each histone modification independently.

**DNA Sequence Predicts Presence of Histone Marks.** Initially, we examined whether histone modifications might be predictable from DNA sequence alone. We therefore extracted sequence features (k-mers) from genomic regions of ±2 kb from the TSS by counting the frequency of all possible k letter words in the A, C, G, T alphabet and merging reverse complement pairs to prevent strand biases; we used $k = 6$ in our analysis as in ref. 15.

We then trained LR classifiers on these 6-mer counts using a random subset of 70% of the TSSs for each histone modification and cell line. Each classifier was then tested on its ability to predict the status of the remaining 30% of TSSs and assessed by examination of receiver operator characteristic (ROC) curves, which plot the true-positive rate vs. the false-positive rate. To test the stability of these predictions, we repeated this procedure 10 times for each mark and cell line, computing the mean and SE in the area under the curve (AUC) for these 10 iterations. The AUC scores for predictions of all histone marks were very high in H1 cells, ranging from 0.806 for H3K27me3 to 0.918 for H3K4me3 (Fig. 1 and Table 1). Sequence-based predictions of histone marks in the other two cell lines also gave high AUCs (Fig. S1 and Table S2).

The ability of DNA sequence to predict histone marks was independent of the window size used to define TSSs as marked by a particular modification, as high AUCs were observed at multiple window sizes (Table S3). We obtained similar levels of accuracy for a selection of marks in H1 cells using a 6-mer support vector machine in place of LR (Fig. S2), suggesting that the predictability of histone modification patterns from genomic sequence is robust and independent of the method used.

**TF ChIP-Seq Significantly Improves Prediction of Histone Marks over DNA Sequence.** A plausible explanation for the predictability of histone modifications from sequence is that this may be a by-product of histone modifications being predictable from sequence-specific TFs. To test this, we constructed histone modification classifiers based upon data from TF ChIP-Seq experiments. TF ChIP-Seq data were downloaded for the three cell lines and filtered to remove proteins that lacked sequence-specific DNA-binding TF activity or that possessed histone-modifying activity (SI Materials and Methods). This resulted in data on 30 TFs assayed in H1 cells, 45 in K562, and 51 in GM12878. Of these, 17 TFs were assayed in all three cell lines. A complete list of all TFs used is given in Dataset S1. We tested the ability of TF-binding locations to predict the histone modification status of promoters by calculating input-normalized read count values for a window ±2 kb from each TSS. These read counts were then used as input features to train LR classifiers on 10 samples of 70% of the TSSs and tested on the remaining 30% of TSSs as above.

These TF-based classifiers predicted the histone modification status of TSSs with a high degree of accuracy, irrespective of the window size chosen for defining positive regions (Fig. 24, Fig. S3, Table 1, and Tables S3 and S4). A quantitative comparison of sequence and TF-based predictions demonstrated that TF LR always significantly outperformed sequence-based LR models (Fig. 2B, $P < 10^{-5}$ rank-sum test). All points fall significantly

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*Fig. 1.* Histone modifications can be predicted from DNA sequence. (A) Representative ROC curves of the performance of k-mer LR-based classifiers for histone modifications at gene promoters in H1 cells. The AUC for each task is indicated in the legend. The ROC curves shown are for a single iteration of a 70–30 split of the data. (B) H3K4me3 profile at test set promoters in H1 cells. Shown on the Left is the mean H3K4me3 profile at promoters predicted to be positive (green) and negative (red) for H3K4me3 in a single iteration of the analysis. The cutoff used was $P = 0.5$. The panel on the Right shows the profile at all of the promoters in the test set ordered by their predicted probability of being marked by H3K4me3 (white, low; red, high).
above the diagonal line (equal predictive power), indicating that TFs are considerably more predictive of histone modifications than sequence. (Notice that prediction of H3K27me3 was carried out only in H1 cells, as this mark was not present at a sufficiently high number of TSSs in the other cell lines to meet our inclusion criteria.) TF-based models also resulted in a greater separation between the observed histone modification profiles at predicted positive and negative TSSs when compared to sequence-based models (Fig. 2C). Our results, therefore, demonstrate that the binding patterns of TFs accurately predict the histone modification status of mammalian gene promoters.

**TF ChIP-Seq Enables Predictions Across Different Cell Lines.** Histone modifications exhibit dynamic and cell-specific patterns that clearly cannot be explained on the basis of DNA sequence content. TFs do exhibit cell type specificity and, given the excellent performance of TF-based classifiers in single-cell lines, we tested to what extent the TF-based classifiers trained on data from one cell line (e.g., H1) can predict histone markings on another cell line (e.g., K562).

We therefore generated LR-based classifiers on the data for the 17 TFs that were assayed in all three cell lines. These classifiers were each able to accurately predict the histone modification status of gene promoters in the cell type they were trained upon; however, in each case, this was to a lower degree than classifiers trained on the full set of TFs available for that cell line (Fig. 3, diagonal figures). Therefore, the inclusion of more complete information on TF-binding patterns in predictive models improves the performance of these models, as would be expected if TF-binding patterns were important in determining the histone modification status of promoters.

The classifiers based upon the common TFs were then tested for the ability to predict the histone modification status across cell types. Although the cross-cell predictions produced reduced performance, we observed striking accuracy in the prediction of histone marks based on classifiers trained in a separate cell type (Fig. 3 for H3K4me3 and Fig. S4 for other marks). The reduced performance of cross-cell predictors might suggest that cell type-specific TFs play a strong role in determining histone modification profiles. This fact may be particularly prominent in the prediction of GM12878 marks from K562-trained classifiers where the greatest drop in performance was noted. We were unable to perform this analysis for H3K27me3, a repressive mark associated with Polycomb complexes, as it occupies large diffuse chromatin domains in nonstem cells (16); this resulted in too few peaks being called in either GM12878 or K562 to meet our inclusion criteria.

Overall, the results of our cross-cell analysis support our hypothesis by demonstrating the ability of data on TF-binding profiles to predict the histone modification status of mammalian gene promoters.

**TFs Predictive Power Recapitulates Known TF–Histone Interactions.** LR modeling produces a vector of weights determining the sensitivity of the histone mark prediction to changes in the TF input. Analysis of these weights revealed several features that corroborated reported interactions between TFs and histone-modifying enzymes (Fig. 4 and Fig. S5). In H1 ES cells, SP4 was the highest weighted predictor of H3K4me3 marking and the presence of its paralogue specificity protein 1 (SP1) was also positively predictive of H3K4me3. These TFs were also positively predictive of the other two active marks analyzed (H3K9ac and H3K27ac), and SP1 received positive weights in predicting all three active marks in K562 and GM12878 cells (Fig. S5). SP1 binding on human chromosomes 21 and 22 has previously been associated with CpG island promoters (17), which are generally enriched for H3K4me3 (18). The top predictive TF for H3K27me3 in H1 cells, transcription factor 12 (TCF12), has

**Table 1. Predictions of histone modification presence in H1 cells (mean AUC ± SE)**

<table>
<thead>
<tr>
<th>Mark</th>
<th>Sequence promoters</th>
<th>TF promoters</th>
<th>TF DNase loci</th>
<th>TF Enhancers</th>
</tr>
</thead>
<tbody>
<tr>
<td>H3K4me1</td>
<td>N.D.</td>
<td>0.918 ± 0.001</td>
<td>0.950 ± 0.001</td>
<td>0.854 ± 0.001</td>
</tr>
<tr>
<td>H3K4me3</td>
<td>0.857 ± 0.002</td>
<td>0.890 ± 0.001</td>
<td>0.976 ± 0.001</td>
<td>0.974 ± 0.001</td>
</tr>
<tr>
<td>H3K27ac</td>
<td>0.828 ± 0.002</td>
<td>0.921 ± 0.001</td>
<td>0.976 ± 0.001</td>
<td>0.968 ± 0.001</td>
</tr>
<tr>
<td>H3K27me3</td>
<td>0.808 ± 0.002</td>
<td>0.877 ± 0.002</td>
<td>0.916 ± 0.001</td>
<td>0.916 ± 0.001</td>
</tr>
</tbody>
</table>

**Fig. 2.** Histone modifications can be predicted from TF-binding data. (A) Representative ROC curves of the performance of TF ChIP-Seq LR-based classifiers for histone modifications at gene promoters in H1 cells. The AUC for each task is indicated in the legend. The ROC curves shown are for a single iteration of a 70–30 split of the data. (B) TF-binding prediction outperforms DNA sequence. Shown is a scatter plot comparing the AUCs achieved from TF-binding LR classifiers (y axis) and DNA sequence LR classifiers (x axis). Each point represents the mean of 10 computational experiments for one histone mark in one cell line. (C) H3K9ac profile at test set promoters. Shown on the Left is the mean H3K9ac profile at test set promoters predicted to be positive (green) and negative (red) for H3K9ac. Both predictions were performed on the same set of promoters. The dashed lines are predictions from sequence, and the solid lines are predictions from TFs. Notice the higher average of TF predicted positive marks. On the Right are heat maps of H3K9ac levels (white, low; red, high) at the individual promoters ordered by predicted positive probability (increasing along the y axis) as provided by sequence LR (Center) and by TF LR (Right).
recently been reported as a repressor of E-cadherin in association with the H3K27me3 methylase enhancer of zeste homologue 2 (EZH2) (19).

Interestingly, the core pluripotency factor NANOG was predictive of the activation-associated marks in H1 cells and POU5F1 (OCT4) was predictive of H3K9ac and H3K27ac, consistent with their roles in specifying ES cell identity (3). In K562 cells, the oncogene CMYC was the second strongest predictor of activation-associated histone marks consistent with this cancer cell line being derived from an erythroleukemia (20).

Two lymphocyte-specific TFs, nuclear factor of activated T-cells, calcineurin-dependent 1 (NFATC1) and interferon regulatory factor 4 (IRF4), were the strongest predictors of activation-associated marked promoters in GM12878 lymphoblastoid cells. IRF4 in particular has been shown to be critical for the development of B cells from which lymphoblastoid cell lines are derived (21). Although NFAT1 is generally regarded as a T-cell–specific factor, its ablation in B cells affects both their proliferation and differentiation (22). We also note that these key predictors of histone modifications in GM12878 cells were not assayed in K562 cells, potentially explaining the drop in cross-cell predictive performance of classifiers trained in K562 cells and tested on GM12878 cells (Fig. 3). Taken together, these results suggest that cell type–specific TFs are strong predictors of histone modifications in the analyzed cell lines, consistent with the cell type–specific distribution of histone marks observed in epigenomic profiling studies.

**Discussion**

The regulation of transcription is fundamental to the control of the genetic information encoded in cellular DNA. Recent attention has focused on a potential direct role for histone modifications in regulating gene expression based on their correlation with active or inactive promoters. By demonstrating that histone modifications can be predicted from the binding patterns of TFs, our results suggest that such correlations might be equally well explained as indirect effects of interactions between TFs and chromatin-modifying enzymes.

Descriptive analyses of ENCODE data have revealed significant overlaps between TF-binding loci and histone marks (14). However, to our knowledge, a quantification of the power of TFs as predictors of histone modifications was not attempted. The difference between descriptive and predictive analyses is important: for example, it would be impossible to assess whether cross-cell line predictions are possible within the limits of a descriptive analysis. Predictive analyses were performed as part of ENCODE and other studies but have focused on predicting TF binding (15) or gene expression levels (7, 8) from histone modification data. Although these predictive analyses are valuable, such models do not provide mechanistic explanations for the specificity of gene expression, in the way that TF-based regulatory mechanisms do (1). Intriguingly, one analysis of the ENCODE data suggested that the addition of histone modification data resulted in only minor improvements to the prediction of gene expression levels based on TF-binding data (25). Furthermore, a recent study demonstrated that depletion of the canonical activating mark H3K4me3 has only a modest effect on transcription,
weakening the case for the causative role of this mark in transcription (26). It is therefore important to establish whether alternative explanatory variables may underlie the association between gene expression and histone modification. Our results provide such an alternative explanation by demonstrating that histone modifications can themselves be predicted with high accuracy from TF binding genome-wide. We also note that DNA sequence variants are also frequently reported to interact with the H3K27me3 methyltransferase EZH2 (19), and the computational study (36) has also associated EZF with the SET1 methyltransferase subunit CFP1. A striking recent example of TF–histone interaction is the finding that insertion of the RE1-silencing transcription factor (REST) binding motif was capable of inducing ectopically H3K27me3 in mouse ES cells (37). In our analysis, we find REST is positively predictive of H3K27me3 localization, albeit weakly. Instead, we find that binding of TCF12, a TF that has recently been reported to interact with the H3K27me3 methyltransferase EZH2 (19), is the most predictive of H3K27me3 deposition, potentially reflecting differences between human and mouse ES cells. It is remarkable that our model was able to recapitulate such knowledge directly from binding data.

Family- and population-level genetic analyses have described the association of DNA sequence variants with altered histone modification patterns (38–40), suggesting a causal role of sequence-specific factors in determining chromatin state. The genetic inheritance of DNA sequence variants has also been suggested to be the primary cause of allele-specific variations in levels of DNA methylation (41). These analyses implicate the alteration in sequence-specific TF binding by DNA sequence variants as the primary cause of allele-specific variation in epigenetic state in mammalian genomes. An analysis of a handful of mouse promoters in ES cells has also demonstrated that DNA methylation state is primarily determined by the presence of binding sites for sequence-specific TFs (42). Taken together, these reports provide further support for the simplest interpretation of our work, that interactions between TFs and the epigenetic machinery, whether direct or indirect, play central roles in determining epigenetic state in mammalian genomes.

In summary, our results demonstrate a remarkable level of prediction of epigenetic marks from TF-binding profiles. Although such analyses do not demonstrate a causative role of TFs in determining epigenetic state in the genome, they show that previously reported associations between chromatin state and expression may be indirect effects. Our results confirm the need for caution in the mechanistic interpretation of genome-wide analyses (13), and provide useful pointers toward the complex biochemical pathways regulating gene expression.

Materials and Methods

Datasets Used. Datasets were downloaded from the Encyclopedia of DNA Elements UCSC repository at https://genome.ucsc.edu/ENCODE. A complete list of all of the identifiers of the datasets used, as well as scripts to recreate our analysis, are available upon request. TSSs were retrieved from ENSEMBL using the human reference genome hg19. A detailed description of the pipeline used is given in SI Materials and Methods.

Statistical Methods. Throughout the paper, we used logistic regression as the classifier of choice due to its simplicity and interpretability. Logistic regression assigns the label 1 to an output with probability given by the logistic function of the input $x$ as follows:

$$p(y=1|x, w) = \frac{1}{1 + \exp(-w \cdot x)}$$

where $w$ is a vector of weights of the same dimensionality of the input data. The weights were learnt by maximum likelihood on a training set; throughout the paper, we used random splits of the data into 70% training and 30% testing, and reported only results on test data.

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