

EMBO Member's Review

The complex transcription regulatory landscape of our genome: control in three dimensions

Erik Splinter and Wouter de Laat*

Hubrecht Institute-KNAW & University Medical Center Utrecht, Utrecht, The Netherlands

The non-coding part of our genome contains sequence motifs that can control gene transcription over distance. Here, we discuss functional genomics studies that uncover and characterize these sequences across the mammalian genome. The picture emerging is of a genome being a complex regulatory landscape. We explore the principles that underlie the wiring of regulatory DNA sequences and genes. We argue transcriptional control over distance can be understood when considering action in the context of the folded genome. Genome topology is expected to differ between individual cells, and this may cause variegated expression. High-resolution three-dimensional genome topology maps, ultimately of single cells, are required to understand the *cis*-regulatory networks that underlie cellular transcriptomes.

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Introduction: gene regulation by remote DNA elements

Over 200 cell types exist within the human body, each being different in morphology and function, yet all containing the same genome. These differences are driven by cell-specific gene regulatory programs. Their proper execution not only relies on the protein-coding parts of genes, but also on that of non-coding sequences within and surrounding the genes. This was first realized when a deletion outside the β -globin gene was found to cause aberrant expression of the otherwise intact gene in a thalassaemia patient (Van der Ploeg *et al*, 1980). It is now well recognized that sequence alterations in the non-coding part of our genome, previously known as 'junk DNA', frequently drive the deregulation of critical genes to cause congenital and somatically acquired diseases (Kleinjan and van Heyningen, 2005). These alterations can locate at large distances from the relevant genes. One extreme

example is where point mutations in the DNA located ~1 Mb away from the *Sonic Hedgehog* (*SHH*) gene interfere with its regulation. This has been linked to preaxial polydactyly, a condition where patients suffer from limb malformations (Lettec *et al*, 2003). Chromosomal rearrangements may remove, mutate or separate distant regulatory sequences from genes, but may also lead to so-called 'position effects', where genes are placed adjacent to new regulatory sequences that drive their upregulation or downregulation. This is seen, for example, in B-cell lymphomas and T-cell leukaemias, when translocations juxtapose strong regulatory sequences of antigen receptor loci to proto-oncogenes. How frequent diseases are caused by genetic changes outside gene bodies is unknown, because most large-scale screening efforts only focus on exome integrity. Based on an examination of the database of genome-wide association studies (Hindorff *et al*, 2009), mutations in non-coding regions were estimated to contribute to a staggering 40% of disease cases (Visel *et al*, 2009b). No matter the exact frequency in disease, studies like these clearly underscore the importance of *cis*-linked regions in regulating gene expression and controlling normal development. Current research efforts in functional genomics, therefore, focus on uncovering the full regulatory potential of our genome.

Here, we will review studies that aim to identify and assign function to the regulatory DNA sequences of the mammalian genome and discuss how regulatory DNA elements and genes are wired to properly execute cell-specific transcription regulatory programs.

Identifying and classifying regulatory DNA sites in the genome

Regulatory DNA sequences in the genome can be identified through various methods. Perhaps, the most thorough assay is to screen for DNase I hypersensitive sites (HSs; Crawford *et al*, 2004; Dorschner *et al*, 2004). HSs typically are sites where the nucleosome fibre is locally disrupted, presumably through the action of DNA-binding proteins and associated factors. Any given human cell type appears to have ~100 000 or more HSs (Boyle *et al*, 2008). This includes promoter sequences of active genes, but the majority is located away from transcriptional start sites in non-coding DNA.

To understand their function, we can test and categorize their activity. This is traditionally done using property defining assays, often *in vitro*, in which the isolated sequence element is placed in plasmids carrying a reporter gene. When transfected into cells, they may then activate or repress transcription, or neutralize transcriptional activation when placed between an activator and gene promoter. Accordingly, they are classified as an enhancer, silencer or insulator.

*Corresponding author. Hubrecht Institute-KNAW & University Medical Center Utrecht, Uppsalalaan 8, Utrecht 3584 CT, The Netherlands.
Tel.: +31 030 212 1800; Fax: +31 030 251 6464;
E-mail: w.delaat@hubrecht.eu

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A more laborious but often more revealing assay is to stably integrate an isolated site with a reporter gene in the genome, and measure transcriptional activity. By doing this in transgenic animals, one can also determine an element's tissue-specific activity and define other properties not appreciable in plasmid-based assays. Boundary elements, for example, are defined based on their property to protect against position effects when placed around an integrated transgene (Recillas-Targa *et al*, 2002), an ability not well appreciated using a plasmid-based assay. Similarly, locus control regions (LCRs), which often behave as enhancers in plasmid-based assays, have the additional capacity to confer tissue-specific, position-independent and copy number-dependent expression on linked reporter genes when stably integrated in transgenic animals (Grosveld *et al*, 1987). This defining property is not shared by classic enhancers and can only be appreciated when tested in transgenics.

While the categorization of DNA elements is useful, an activity picked up for a DNA motif in a reporter assay may not be relevant or detectable at its natural chromosomal context (Dillon and Sabbattini, 2000). This has been demonstrated for insulators, enhancers and LCRs (Epner *et al*, 1998; Bender *et al*, 2006; Splinter *et al*, 2006; Ahituv *et al*, 2007; Table 1). Thus, DNA sequences may intrinsically harbour specific activities, and hence be classified accordingly, but the linear and, as we will argue below, three-dimensional chromosomal context often determines whether they exert this activity or not.

With 100 000 or more HSs per cell type, mammalian genomes are emerging as highly complex regulatory landscapes. Alternative strategies for the exposure and classification of regulatory sites confirm this idea. Genome-wide chromatin immunoprecipitation approaches (ChIP-chip and ChIP-seq) have been developed to identify specific classes of regulatory sites based on their unique chromatin signature. For example, enhancers were shown to have high H3K4me1 and promoters high H3K4me3 levels (Heintzman *et al*, 2007). Based on their H3K4me1 mark in two human cell types, ~55 000 potential enhancer elements were uncovered (Heintzman *et al*, 2009). Nearly 80% of the enhancers were unique for the one or the other cell type, despite the two sharing 85% of their active genes. This underscores the idea that enhancers are tissue-specific elements acting on tissue-specific genes. At the same time, it raises the question whether all these sites are actively involved in gene regulation. A further subclassification of H3K4me1 enhancers is now made based on the shared presence of p300 protein or

acetylated H3K27. Both signatures appear to separate the active from the poised pool of enhancers. In the case of p300, a co-activator protein that can acetylate H3K27, several thousand (instead of tens of thousands) active enhancers were identified in various primary mouse tissues (Visel *et al*, 2009a). Similar numbers of active enhancers were found based on the H3K27Ac profile (Creyghton *et al*, 2010; Rada-Iglesias *et al*, 2011). Collectively, these studies show that a given mammalian cell type contains thousands or more regulatory sites. With 200 different cell types, this confirms that our genome harbours a complex regulatory landscape (Figure 1).

The mammalian genome: a complex regulatory landscape

The term 'regulatory landscape' was first coined to describe the complex organization of regulatory sequences around the Hox loci (Spitz *et al*, 2003). A recent study provided further insight into the complexity of mammalian gene regulation (Ruf *et al*, 2011). In this study, hundreds of transgenic mice were generated, each carrying a transposable reporter cassette containing a *LacZ* reporter gene driven by a minimal promoter sequence (50 bp of the human β -globin gene) inserted at a random location in the genome. Each was then analysed for *LacZ* expression in E11.5 embryos, and categorized according to tissue specificity of expression. The minimal promoter by itself was insufficient to drive reporter gene expression, yet nearly 60% of the transgenics showed reporter activity, demonstrating that the majority of genomic locations harbour activating potential. Among the activated transgenics, only a very small percentage showed ubiquitous expression, while the great majority (>95%) demonstrated restricted, tissue-specific expression (Figure 2). Often, but not always, reporter expression followed that of the nearest endogenous gene. However, tissue-specific expression was also found for integration sites near genes with widespread expression patterns. This argues that also the expression of so-called housekeeping genes is modulated in a tissue-specific manner. The flanking transposon sites further enabled the investigators to locally hop around the reporter cassette and assess the regulatory impact at multiple locations within one chromosomal domain. Essentially, all possible outcomes were found. Sometimes, transposition over only a few kilobases resulted in clearly distinct expression patterns, whereas in other examples integration sites separated by hundreds of kilobases gave essentially the same expression profile

Table 1 Property defining activities measured for DNA sequences in reporter assays may not be detectable at their natural chromosomal context

Genomic site	Definition	Property defining reporter assay	Effect of genomic site deletion
β -Globin: HSs upstream of genes	LCR (Grosveld <i>et al</i> , 1987)	Confers position-independent, copy number-dependent transgene expression in mice	No heterochromatinization, basal non-activated gene expression (Epner <i>et al</i> , 1998) ^a
CTCF sites flanking β -globin locus	Insulators (Farrell <i>et al</i> , 2002)	Block enhancer activity and shield reporter genes in plasmid-based assays	No heterochromatinization, no transcription changes measurable (Bender <i>et al</i> , 2006; Splinter <i>et al</i> , 2006)
Ultra-conserved elements close to <i>Dmrt3</i> , <i>Rcn1</i> , <i>Pola1</i> and <i>Sox3</i>	Enhancers (Ahituv <i>et al</i> , 2007)	Tissue-specific reporter gene activation in transgenic mice	No transcription changes measurable (Ahituv <i>et al</i> , 2007)

^aNote that the β -globin LCR is not necessary for maintenance of open chromatin in mice, but does appear necessary for this in humans (Forrester *et al*, 1990).

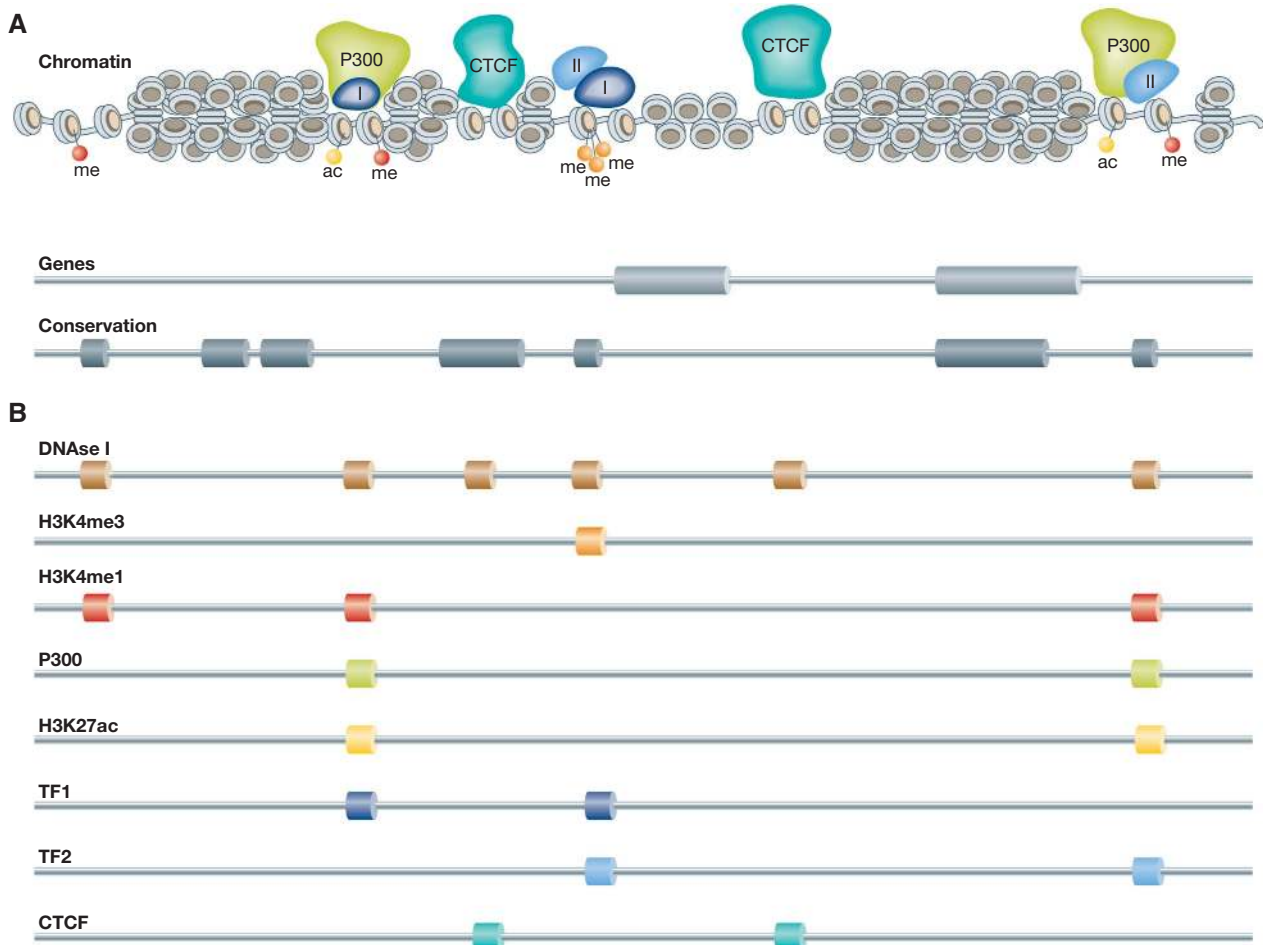


Figure 1 The complex regulatory landscape of the genome. (A) DNA packaged into chromatin with regulatory proteins P300, transcription factors I and II, CTCF and histone modifications present. Underneath the chromatin fibre the position of genes and conserved elements, representing information that can be found in databases (e.g., UCSC, Ensembl). (B) The identification of accessible chromatin (DNase I profile) and various chromatin marks (ChIP-seq) that are associated with regulatory elements yields a picture of a complex regulatory landscape.

(Ruf *et al*, 2011). This led the authors to propose that the genome harbours a ‘regulatory jungle’: chromosomal regions contain many regulatory sites that can activate gene expression over large distances and others that counteract this activity.

How are all these linearly organized activities orchestrated such that genes are expressed at the right time and place? Genetic studies that manipulated the non-coding part of the genome to understand transcriptional control have delineated some primary rules of promoter–enhancer engagement that must be considered when addressing this question. So far, most of these studies focused on gene clusters such as the Hox and globin loci, aiming to understand how transcription of their individual genes is coordinated in time and space.

Rules of engagement in a complex regulatory landscape: (1) linear proximity

It is often assumed that enhancers act on the nearest genes in *cis*, and in many cases this is correct. Proximity on the linear DNA template, or genomic order, is a major determinant of selectivity: first-come, first-served (Figure 3, rule I). This was first demonstrated in plasmid-based competition assays, which showed that proximal genes have an advantage over

distal genes to be activated by a shared enhancer (de Villiers *et al*, 1983; Wasylyk *et al*, 1983). The same principle was then shown to also apply to transcription regulation in the chromosomal context (Hanscombe *et al*, 1991; Dillon *et al*, 1997). Interestingly, order is no longer important when two competing genes are positioned close together at a large distance from a shared enhancer (Heuchel *et al*, 1989; Dillon *et al*, 1997). While linear proximity to a regulatory site is often a good predictor of target genes, many examples exist where enhancers ignore the nearest genes and specifically act on genes further away (de Laat and Grosveld, 2003). The previously mentioned limb bud-specific enhancer of the *SHH* gene is one such example, present in an intron of the *Lmbr* gene, but acting on the *SHH* gene 1 Mb away. Why do enhancers not always stick to the ‘first-come, first-served’ rule, but sometimes act instead on more distal genes?

Rules of engagement in a complex regulatory landscape: (2) promoter specificity

Enhancer reporter assays in cell lines (*in vitro*) and mice (*in vivo*) usually analyse the capacity of test sequences to

activate one and the same minimal or general promoter (Banerji *et al*, 1981; Visel *et al*, 2008; Ruf *et al*, 2011). The assumption is that enhancers and promoters show little specificity and will always act on each other. While this may be true for artificial constructs where the enhancer and minimal promoter are close together, it appears more com-

plex in the context of the genome where regulatory sites do show target specificity. There are numerous examples of enhancers interacting with just a subset of equally nearby target promoters, and there are different possible explanations for this. Sometimes, an enhancer is thought to ignore a gene because its promoter is not accessible in the tissue where the enhancer is active. In the β -globin locus, for example, the LCR exclusively acts on the β -globin genes and totally ignores the nearby olfactory receptor genes, even when potentially interfering insulator sites are disrupted (Splinter *et al*, 2006). The LCR also ignores the nearby fetal globin genes to exclusively act on more distal adult β -globin genes at later stages of development. Inactivity, or promoter inaccessibility, may therefore be a reason for regulatory sites to skip nearby genes (Figure 3, rule II).

Selective gene activation can also be explained by promoter competition, whereby the activation of one promoter precludes the activation of another equidistant promoter. This was shown clearly in *Drosophila* transgenic embryo assays, where different enhancers were demonstrated to prefer distinct classes of promoters, depending on the presence of certain core promoter elements (Ohtsuki *et al*, 1998; Butler and Kadonaga, 2001).

Promoter competition also occurs between mammalian genes. It manifests itself when the deletion of one or more genes impacts on the expression of remaining neighbouring genes, or when the deletion of a regulator causes down-regulation of multiple genes. These phenomena have been described at the *Hox* (Spitz *et al*, 2003; Tschopp *et al*, 2009) and *globin* gene clusters (Forrester *et al*, 1990; Hanscombe *et al*, 1991; Epner *et al*, 1998; Sabatino *et al*, 1998; Lower *et al*, 2009). The implication of gene competition is two-fold: the first is that regulatory sites exist in the genome that can act on multiple endogenous genes. Evidence exist that the number of genes controlled by a given regulatory site probably depends on its chromosomal context. At its natural location, the β -globin LCR activates maximally two

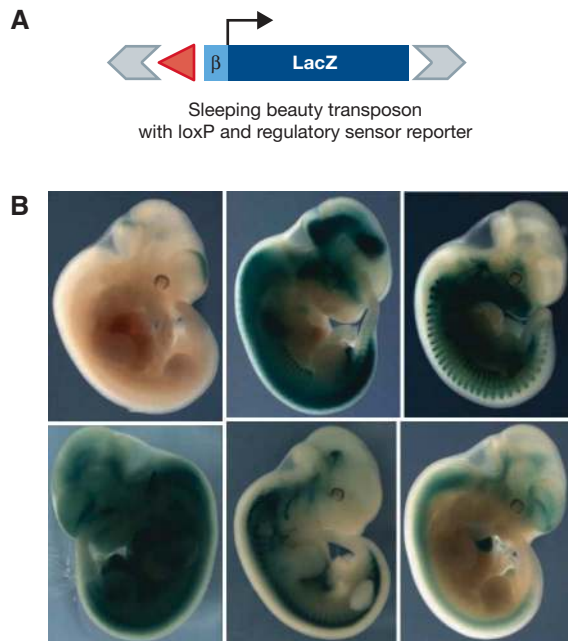


Figure 2 Random integration of a reporter cassette reveals the regulatory potential of the mouse genome. (A) Schematic representation of the randomly integrated reporter cassette consisting of the *LacZ* gene driven by the β -globin minimal promoter. (B) Examples of *LacZ* expression patterns found in the different transgenic lines which, depending on the integration site, range from global to a highly restricted expression pattern. (Reproduced with permission from Ruf *et al*, 2011.)

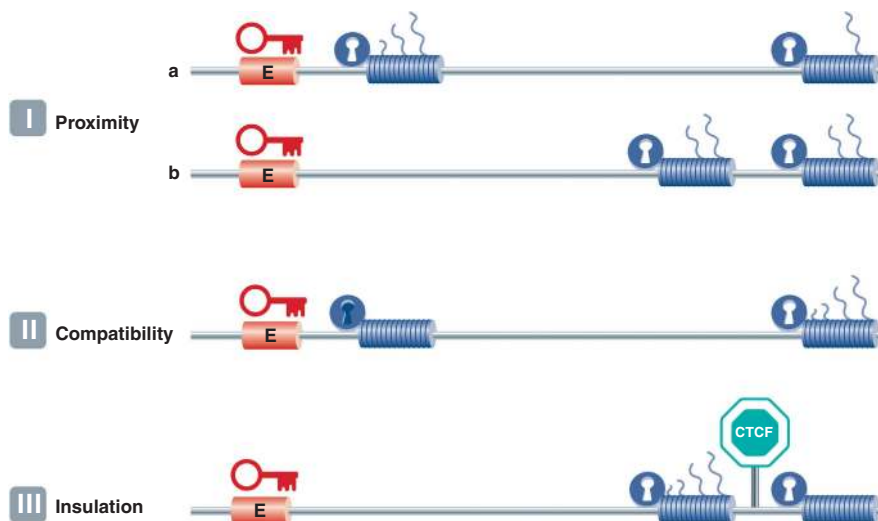


Figure 3 The three rules of engagement that dictate enhancer–promoter interactions. **I: Proximity.** (a) When multiple genes (cylinders) are compatible with (open lock) and relatively close to a shared enhancer (E), the most proximal gene is preferentially activated over the distal gene (represented by the number of transcripts originating from the gene). (b) This competitive advantage disappears when both genes are located far away from the shared enhancer. **II: Compatibility.** Enhancers ignore the ‘first-come, first-served’ rule when the proximal promoter is incompatible (closed lock) with the enhancer. Result: activation of the distal gene. **III: Insulation.** The presence of CTCF can block enhancer function across its binding site and prevent a compatible gene from being activated by the enhancer.

or three β -globin genes at any given developmental stage. However, when tested without globin genes at a defined new location in the genome it was found to activate 6–7 genes up to 150 kb away in *cis* (Noordermeer *et al.*, 2008) and two genes in *trans* (see below) (Noordermeer *et al.*, 2011). A second implication of gene competition is that enhancer–promoter interactions are, at least for some time, mutually exclusive. Convincing evidence for this was obtained in single-cell experiments that measured the ongoing transcriptional activity of LCR-competing β -globin genes in cells with traceable transcriptional history. The LCR was demonstrated to activate only a single gene at the time, but over time to dynamically flip-flop between competing globin genes (Wijgerde *et al.*, 1995). This work provided insight into the mechanism behind competition between clustered genes for shared regulators.

In a genome described as a ‘regulatory jungle’ (Ruf *et al.*, 2011), one might expect that regulators sometimes also ‘fortuitously’ activate more than their presumed target gene. Indeed, bystander activation has been observed in several cases. The B cell-specific human immunoglobulin-beta ($Ig\beta$) gene (or CD79b) is highly expressed, but presumably not functional, in pituitary due to its linear proximity to the LCR that is acting on the more distal growth hormone (hGH) gene in this tissue (Cajiao *et al.*, 2004). A similar phenomenon was recently found at the human α -globin locus that is located in a gene-dense chromosomal region with many housekeeping genes. When a 500-kb region around the locus was analysed for gene expression levels, a gene called *NME4*, 300 kb apart, was found to be upregulated specifically in red blood cells where the α -globin genes are active. Subsequent analysis showed that the α -globin regulatory sequences were responsible for this, and that *NME4* competes with the α -globin genes for these enhancers (Lower *et al.*, 2009). Collectively, these data show that tissue-specific enhancers not always exclusively activate transcription of their real target genes but sometimes also that of unrelated genes nearby in *cis*. Based on arguments explained below, we predict this bystander activation will be seen even more often when transcriptome analysis is performed at the single-cell level rather than the cell population level.

Rules of engagement in a complex regulatory landscape: (3) insulators can block enhancer–promoter interactions

The original idea that led to the discovery of insulator elements was that the genome may be partitioned in physically separate chromatin domains that each has their own independent regulatory activities. If true, the assumption was that boundaries must exist that prevent regulatory cross talk between these domains. To test this hypothesis, two types of assays were developed. One investigated the ability of sequence elements flanking a reporter gene to overcome gene repression when integrated into heterochromatin (Kellum and Schedl, 1991). Another analysed whether an element can block enhancer activity when positioned in between the enhancer and a gene promoter (Kellum and Schedl, 1992). With the discovery of more and more regulatory sites in the mammalian genome that ignore nearby genes to act specifically on much more distal genes, the idea that regulatory activities are strictly separated along the linear chromosome

template had to be adjusted (Dillon and Sabbattini, 2000; de Laat and Grosveld, 2003). Nevertheless, the assays were proven to be very useful to identify an intriguing new class of regulatory sites known as ‘insulators’. In mammals, one protein in particular is associated with insulator activity: CTCF (Chung *et al.*, 1993; Bell *et al.*, 1999). In *in vitro* reporter assays, CTCF bound to DNA often acts as an enhancer blocker (Figure 3, rule III). *In vivo*, CTCF binding sites are found next to genes that are active in an otherwise repressive chromatin surrounding, such as the human and mouse β -globin genes (Farrell *et al.*, 2002) and near genes on the silenced X chromosome that escape X inactivation (Filippova *et al.*, 2005). CTCF also acts as an allele-specific enhancer blocker to mediate imprinted gene expression at the H19-Igf2 locus (Bell and Felsenfeld, 2000; Hark *et al.*, 2000). Interestingly, a single CTCF site can function as an insulator, but the introduction of a second CTCF site in between an enhancer and promoter often alleviates the enhancer blocking effect (Cai and Shen, 2001; Muravyova *et al.*, 2001). ChIP-Seq experiments were carried out to obtain a genome-wide picture of CTCF binding sites. An estimated 20 000–87 000 CTCF binding sites exist in the human genome (Barski *et al.*, 2007; Kunarso *et al.*, 2010), meaning that on average a CTCF binding site is present every 35–155 kb. Most of these sites (50–90%) appear conserved between different cell types (Barski *et al.*, 2007; Chen *et al.*, 2008; Cuddapah *et al.*, 2009; Kunarso *et al.*, 2010). They are enriched at boundaries between repressive (H3K27me3-rich) and active (H3K27me3-poor) chromatin (Cuddapah *et al.*, 2009), and at the borders between so-called lamin-associated domains (LADs) and non-LADs, being chromosomal regions that preferentially locate to the periphery or the interior of the cell nucleus (Guelen *et al.*, 2008). Furthermore, genes separated by a CTCF site show a markedly reduced correlation in gene expression (Xie *et al.*, 2007). Collectively, these studies demonstrate that, while not all CTCF sites will act as insulators, clearly their location, and that of possible other insulators, must be taken into account when considering the wiring of regulatory DNA networks in the genome. Interestingly, substantial overlap exists between the genomic binding sites of CTCF and cohesin (Parelho *et al.*, 2008; Wendt *et al.*, 2008), suggesting that cohesin, a protein complex that can hold two DNA helices together may assist CTCF in its function to separate regulatory activities.

In summary, genetic experiments have uncovered three rules of enhancer–promoter engagement: linear proximity matters, enhancer and promoter need to be compatible, and some sequences exist that can block enhancer activity. To understand the molecular mechanisms behind these rules, we need to know how regulatory sites exert activities over distance.

Chromatin looping and spatial interactions between regulatory sites

The idea that DNA topology can play an important role in long-range gene activation was originally based on observations on bacterial and phage repressor proteins, like the Gal, AraC and λ repressor proteins. They were found to only function when homo-multimerized and bound to separated operator sequences and this was shown by electron microscopy to result in looping out of the intervening DNA fibre (Ptashne, 1986). The first direct evidence in eukaryotes for spatial interactions between regulatory sites and their target genes was provided by two independent studies on the mouse

β -globin locus. One study involved the use of RNA-TRAP to demonstrate a chromatin loop between an active β -globin gene and HS2 of the LCR (Carter *et al*, 2002). The other study applied 3C technology and showed that not only HS2 but also other β -globin regulatory sites participate in the interactions with the genes (Tolhuis *et al*, 2002). The spatial chromatin entity they formed was called an Active Chromatin Hub (ACH; Figure 4). 3C (chromosome conformation capture) technology turned out to be the method of choice for unraveling the three-dimensional regulatory circuitries at gene loci. The technique relies on crosslinking and ligation of spatially proximal DNA sequences, which are then identified and quantified with PCR strategies (Dekker *et al*, 2002). In subsequent studies on the β -globin locus, it was demonstrated that during development the genes dynamically switch their physical interactions with the LCR in relation to their change in gene expression (Palstra *et al*, 2003) and that transcription factors mediate these long-range DNA interactions (Drissen *et al*, 2004; Vakoc *et al*, 2005). 3C also provided evidence for chromatin loops between distal enhancers and target genes at other loci, including the interleukin (Spilianakis and Flavell, 2004), α -globin (Vernimmen *et al*, 2007) and immunoglobulin loci (Liu and Garrard, 2005), and showed that chromatin loops can also be involved in gene repression (Horike *et al*, 2005; Comet *et al*, 2006, 2011; Tiwari *et al*, 2008; Bantignies *et al*, 2011). In a recent study, both microscopy and 3C data showed that the distal limb bud enhancer of *SHH* loops to the gene (Amano *et al*, 2009).

Collectively, these and other studies firmly establish that regulatory sites act on genes via chromatin looping. This knowledge argues that we must know the topological constraints of chromatin in order to understand how transcription is controlled in the regulatory jungle of the genome. Question therefore is how do separated genomic sites find each other?

Rules of engagement in three dimensions: proximity matters

When we ignore all biological activity exerted by DNA-binding proteins and associated factors, a chromatin-packed

chromosome fibre is expected to fold and behave essentially as a polymer with a given flexibility. This implies that random collisions will take place between pairs of sites present on a chromosome, with contact probabilities that exponentially decrease with increasing site separation on the linear template (Rippe *et al*, 1995). This is exactly what is measured *in vivo* by Hi-C technology (Lieberman-Aiden *et al*, 2009; Duan *et al*, 2010; Tanizawa *et al*, 2010; Figure 5A). Hi-C is a high-throughput genomic variant of 3C that analyses interactions between all genomic sites. A smooth, continuous and exponential decline in contact probability is seen with increased site separation when Hi-C measurements for all pairs of sites are plotted in relation to their genomic distance. Beyond certain distances the curves plateau indicating that contact probabilities then no longer depend on the amount of intervening DNA. For human chromosomes, this seems to happen only beyond 90 Mb of DNA or more. Of relevance, the data also show that two given sites on one chromosome, no matter their linear site separation, are much more likely to contact each other than to contact a given site on a different chromosome (Lieberman-Aiden *et al*, 2009).

Thus, Hi-C data confirm what was predicted from polymer physics: any given site in the genome has the ability to contact neighbouring sequences, the chance of which decreases exponentially with increasing site separation on the linear template. This very basic concept of chromosome flexibility can be assumed to underlie the first rule of engagement: linear proximity matters. Without activities interfering with local chromatin flexibility, any regulatory site is much more likely to contact a gene nearby than a gene far away on the chromosome. The genetic observation that linear order no longer matters when two similar genes are close to each other but far apart from a shared enhancer (Dillon *et al*, 1997) is also in line with a polymer-like behaviour of chromatin: both will have a roughly equal chance of colliding into the enhancer.

Rules of engagement in three dimensions: affinity matters

While polymer physics dictates, and Hi-C data shows, that collisions between linearly proximal sequences will be fre-

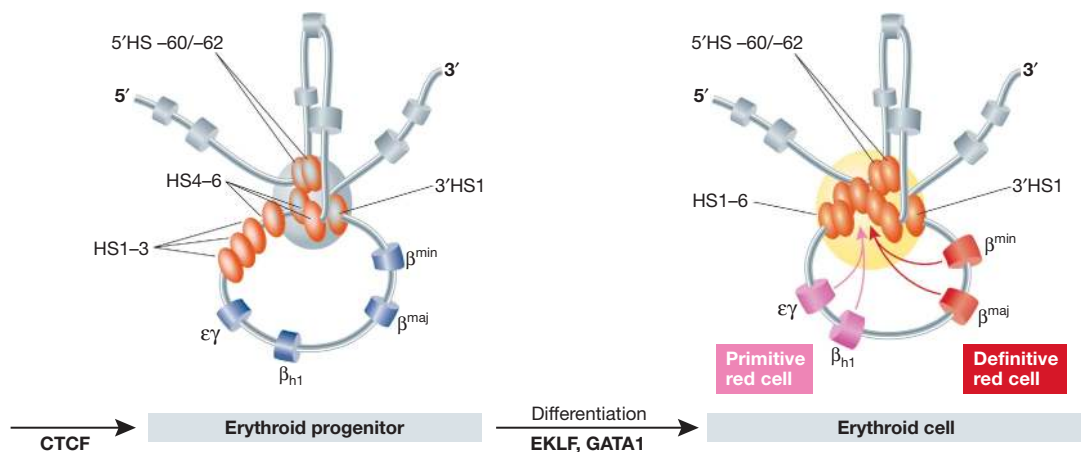


Figure 4 A schematic representation of the three-dimensional structure of the mouse β -globin locus during differentiation. In erythroid progenitors, a 'Chromatin Hub' (CH) is formed by the clustering of the CTCF sites that surround the β -globin locus. Upon differentiation, the remaining hypersensitive sites of the LCR and the *globin* gene that is activated participate in this clustering to form an 'Active Chromatin Hub' (ACH). Hypersensitive sites are represented by the ovals and genes by the cylinders. In grey, the olfactory receptor genes that surround the locus are depicted. A developmental switch in gene usage occurs between primitive and definitive red cells.

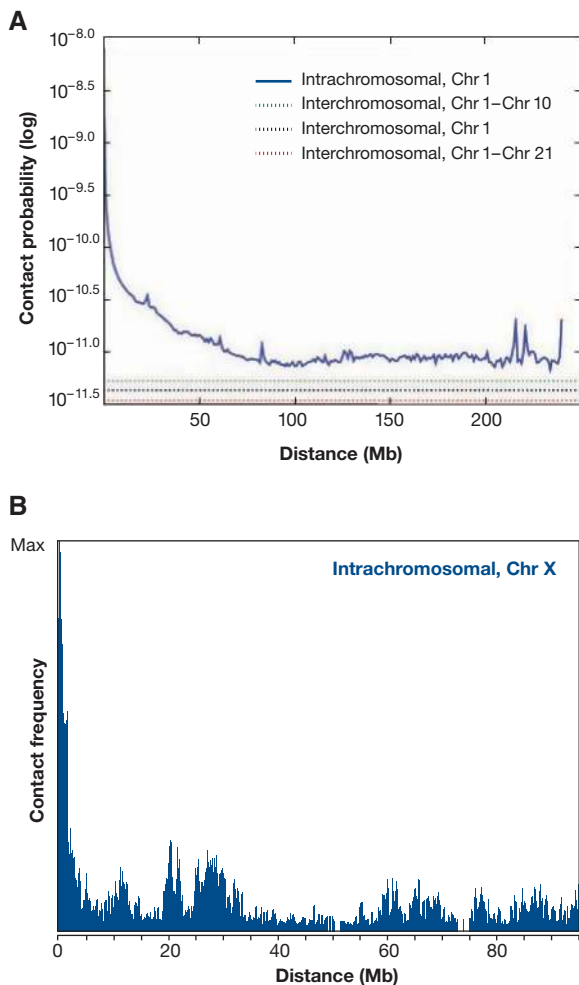


Figure 5 The relationship between contact frequencies (spatial distance) and the position of sequences on the DNA template. (A) Hi-C experiments showing the average contact probabilities between all pairs of sequences (within and between chromosomes). The average profile shows that with an increasing linear distance the interaction frequencies drop exponentially. (Reproduced with permission from Lieberman-Aiden *et al.*, 2009.) (B) 4C experiment that measures interaction frequencies for an individual locus ('viewpoint') versus all other genomic sequences. The same global anti-correlation between distance and contact frequency is seen, but on top specific interactions (peaks) are observed at sequences that are preferentially contacted by the viewpoint.

quent, they will be aspecific and equally transient for all pairs of sites unless two sites have increased affinity. This can be mediated, for example, via the proteins associated with them. Upon collision of two such sites, a stabilization of the contact will occur, which will be measurable as a chromatin loop. This is what is seen by 4C technology (Figure 5B). 4C technology is a different high-throughput version of 3C technology that produces high-resolution DNA contact maps for individual genomic sites. A 4C profile typically shows the same anti-correlation between contact probability and genomic distance as seen by Hi-C, but the curves are no longer smooth: peaks and valleys of contacts are imposed on it (Simonis *et al.*, 2006, 2007). A peak in a 4C contact profile identifies a preferred interaction site and reveals a chromatin loop between this site and the selected target sequence ('viewpoint'). Since 3C-based methods provide average topology impressions of populations of cells, such a loop must

have been present in a relevant proportion of the cells the moment they were fixed. In several instances, it was demonstrated that the stability of such chromatin loops indeed relies on the associated proteins (Drissen *et al.*, 2004; Vakoc *et al.*, 2005; Splinter *et al.*, 2006).

One can speculate that the formation and stabilization of a given chromatin loop has two important consequences: one is that for the duration of the interaction the two sites involved may not be available for direct interactions with other genomic sites. The second is that this structure imposes constraints on the flexibility of the intervening and surrounding genomic sites. The latter is expected to be relevant for insulator function, as will be discussed below. The first would clearly be relevant for promoter competition: as long as an enhancer is stably engaged in an interaction with one gene, it cannot interact with another gene (Wijgerde *et al.*, 1995). Thus, the genetically deduced rule of engagement stating that enhancer–promoter compatibility is essential may well be dependent on the affinities between enhancer- and promoter-bound proteins and their ability to stably form a chromatin loop. The outcome of promoter competition, that is, the number of genes activated and their eventual transcript levels, will therefore depend on their order on the linear template, their relative distance to and their affinity for the enhancer (Figure 6).

Rules of engagement in three dimensions: insulators and DNA flexibility

If chromatin looping between enhancers and promoters is critical for gene activation, would insulators exert their blocking activity also by acting on DNA topology? An increasing body of evidence suggests they do. A role for insulators in organizing genome topology was first appreciated from microscopy observation in *Drosophila*, showing that insulator sequences separated in the genome come together in the nuclear space in so-called insulator bodies (Gerasimova *et al.*, 2000). Direct looping between neighbouring insulator sites was first demonstrated by 3C technology for CTCF sites at the H19-Igf2 locus and the β -globin locus (Kurukuti *et al.*, 2006; Splinter *et al.*, 2006). Binding of CTCF to an internal site of the imprinted H19-Igf2 locus was shown to create a loop encompassing the *Igf2* gene that presumably isolated the gene from enhancers outside the loop (Kurukuti *et al.*, 2006). At the β -globin locus, flanking CTCF sites were demonstrated to form a large chromatin loop containing both enhancers and genes that was further folded later during differentiation into smaller loops to bring stage-specific genes in closer proximity to their enhancers (Splinter *et al.*, 2006). Insulators not only block the activating effects of enhancers, but they can also interfere with the spreading of repression mediated by polycomb group proteins (Sigrist and Pirrotta, 1997; Mallin *et al.*, 1998). It was noticed that chromatin coating by polycomb proteins will stop at an insulator site, but may continue into more downstream regions beyond a second insulator site (Comet *et al.*, 2006). The abrupt block at the first site suggests that insulators act as a physical barrier. The continued spreading beyond the second site suggests these downstream regions are brought into spatial proximity of the upstream source of polycomb protein, which indeed was shown to happen as a consequence of loop formation between the two intervening insulator sites (Comet *et al.*,

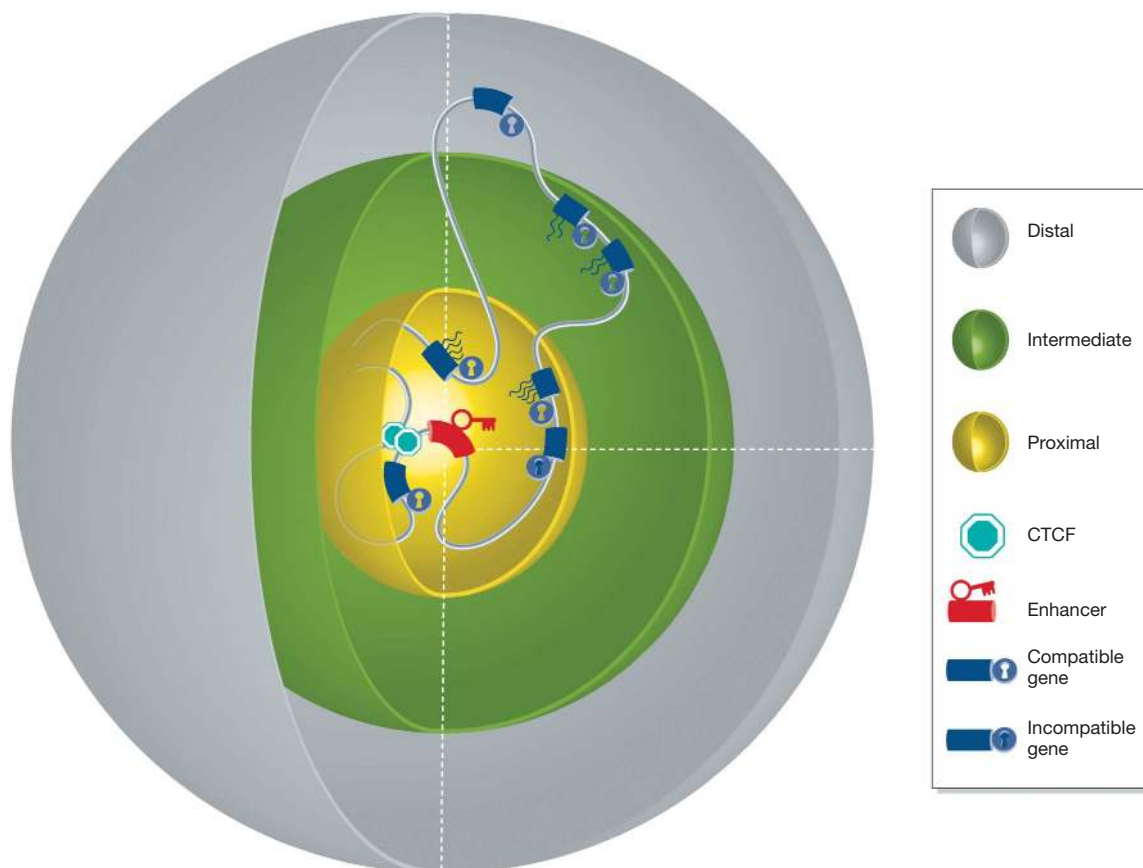


Figure 6 Spatial distance, enhancer–promoter compatibility and sites of insulation are the main determinants of enhancer-mediated gene expression. This figure represents a three-dimensional model of chromatin ‘in action’, explaining all three rules of engagement by considering regulatory action in three dimensions. Genes proximal to the enhancer in 3D space (in the yellow sphere) have a high probability to be contacted, but activation depends on compatibility and whether or not a gene is isolated from the enhancer (CTCF sites). Compatible genes further away in 3D (in the green sphere) have a decreased probability to be contacted and activated, while compatible genes that too far (grey sphere) will not be activated.

2011). These and other detailed transgenic studies (e.g., Maksimenko *et al*, 2008), together with genomic evidence that CTCF sites often locate to borders of spatially separated chromatin domains (Guelen *et al*, 2008), have established that insulator sequences strongly influence chromosome topology. They induce chromatin loops that will affect the flexibility of neighbouring and intervening chromatin sites. The impact hereof on gene regulation can be positive, negative or neutral, depending on the regulatory sites they spatially bring together or separate. Further evidence for this was recently provided in a study that performed large-scale mapping of chromatin loops between CTCF sites (Handoko *et al*, 2011). We expect that within chromosomal segments at any given time enhancer–promoter combination will compete with interspersed CTCF sites for chromatin loop formation, the outcome of which again will depend on linear proximity and affinity between interacting sites.

DNA interactions and gene expression in single cells

For genes that are crucial for cellular identity correct expression must be controllable in all relevant cells. Transcription occurs in bursts, as was shown in live cell imaging studies (Chubb *et al*, 2006). Chromatin looping is thought to bring

additional DNA-binding sites for relevant transcription factors in close proximity to gene promoters; this will increase the local concentration of these factors and consequently, transcription efficiency will increase (Droge and Muller-Hill, 2001; de Laat and Grosveld, 2003). Whether enhancers increase the frequency or amplitude of transcription bursts is not yet known, but it is relevant to ask what the maximum amount of intervening DNA is that can be bridged by an enhancer to contact and activate a gene in every single cell. This question is pertinent also because overall DNA topology is thought to be relatively stable during interphase, both at the level of the genome (Chubb *et al*, 2002; Gerlich *et al*, 2003) and at that of individual chromosomes (Muller *et al*, 2010).

The previously mentioned study that analysed ectopically integrated LCRs in the mouse genome aimed to get insight into the capacity of regulatory sites to reach and activate genes over ultra-long distances in individual cells. By 4C technology, it was shown that the LCR had little impact on overall genome topology, as the many long-range genomic contacts made by the integration site were similar with and without the integrated LCR (Noordermeer *et al*, 2011). Transcriptome analysis then demonstrated that none of the contacted genes benefited from the presence of the new LCR, with the exception of two endogenous mouse β -globin genes

located on another chromosome. They were upregulated not in every single cell but exclusively in so-called ‘jackpot’ cells that showed the interchromosomal interaction. The work uncovered a number of principles behind long-range gene activation. First, it showed that the ability of regulatory sites to search the nuclear interior for preferred target genes is severely limited by their chromosomal context. This is likely to be true for all genomic positions, although the degree of constraint may vary between sites. Second, the data showed that promoter–enhancer compatibility is essential to transform spurious contacts between enhancers and promoters into productive interactions that drive gene activation; of all contacted genes, only two natural target genes of the LCR increased their transcription. Third, the data demonstrated that relatively stable cell-specific genome conformations can induce variegated gene expression. Cells that have their genome folded such that it brings together a regulatory site with a responsive gene can have different transcript levels of this gene than otherwise identical cells (Noordermeer *et al*, 2011). The phenomenon was referred to as ‘Spatial Effect Variegation’ (SEV). SEV may happen in *trans*, as shown in this artificial situation, but may also work in *cis*. Possibly, previous work already provided one example for SEV in *cis*. The interaction over 1 Mb between the limb bud enhancer and *SHH* was shown to occur in the expressing limb bud cells in a manner not dependent on the enhancer *per se*: its deletion abrogated expression without changing the DNA configuration (Amano *et al*, 2009).

We envision that indeed beyond a certain chromosomal distance regulatory sites will not be able to independently find a target gene, but for contact instead depend on the topological constraints imposed by the remainder sequences of the chromosome. The overall genome topology may or may not bring these sites in relative proximity in single cells. Depending on the nature of the interacting regions, transcription may be activated or repressed in these cells, causing variegated expression across the cell population. It is tempting to speculate that such SEV, when acting on key developmental regulators, may provide cells with a mechanism

to make autonomous cell fate decisions, without the need for external signalling.

Future prospects

Functional genomics strives to assign function to all the relevant sites of the genome. Over the last decade, large-scale efforts have produced chromosome maps with the linear distribution of nucleosomes, transcription factor binding sites and chromatin modifications. Collectively, these studies demonstrated that what was previously known as junk DNA in fact appears a regulatory jungle. In order to understand the laws of the jungle, linear information must now be converted into spatial relationships. For this, highly detailed 3D topology maps need to be generated for all regulatory sites individually. They are expected to reveal the function of regulatory sites in gene deserts, to uncover the *cis*-regulatory networks of individual genes and to distinguish the functionally active from inactive regulatory sites. Detailed DNA interaction maps should also uncover the 3D chromosome scaffolds created by insulator sequences, and how the one regulatory site is hampered and the other facilitated in its action by the 3D configuration. Finally, this eventually needs to be done at the single-cell level, as we predict an unknown portion of the genome will only reveal its regulatory potential at the level of the individual cell.

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Conflict of interest

The authors declare that they have no conflict of interest.

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