Figure 1 | Rambling genes. **a**, Nunez *et al.*³ find that, in the absence of oestrogen, two genes (*TFF1* and *GREB1*) that are activated by this hormone and found on different chromosomes, reside in different locations within the nucleus. **b**, On exposure to oestrogen, these genes make interchromatin contacts, facilitated by the nuclear receptor ERα, transcriptional coactivators (CoAs), actin and molecular motor proteins. **c**, Subsequently, the gene pair interacts with a nuclear speckle in an LSD1-dependent manner, creating a multiprotein complex that might act as a transcriptional hub for DNA transcription into mRNA.

ERα-associated demethylase enzyme LSD1, which does not influence interchromosomal gene interaction — is required for the subsequent colocalization of the gene pairs with nuclear speckles (structures composed of high concentrations of specific proteins involved in messenger-RNA splicing), thereby probably leading to mRNA maturation (Fig. 1).

Transcriptional coactivators are multiprotein complexes that, collectively, have diverse enzymatic activities⁷. So it is tempting to specu-

late that, together with LSD1, distinct enzymes of a coactivator complex mediate actin polymerization (which might facilitate gene movement within the nucleus), interchromatin interactions and chromatin interface with transcription 'factories' — structures that generate mRNAs at higher rates. Ultimately, it is likely that coactivators and other receptor-associated proteins work together to orchestrate the formation of an ERα-activated transcriptional supercomplex comprising

ERα itself, coactivators, mRNA-splicing factors, transcription factories and two or more oestrogen-regulated genes (Fig. 1).

The possibility of ERα-regulated genes converging into distinct hubs gives rise to some interesting questions. How common is the above process among other genes regulated by nuclear receptors? What signals define how one gene finds its appropriate partner gene? Do these transcriptional hubs contain functionally related genes, or is their organization simply spatial? Could it be that sequences close to a gene, or possibly specific chromatin modifications at each ERα-regulated locus, provide proper pairing information?

Many ERs are located in stretches of DNA between genes, far away from known coding sequences. Do these sites also engage with interchromatin loci pairs, and, if so, to what extent do they influence the transcription of the partner locus? Do large-scale structural rearrangements induced by oestrogen, or other signals that activate oestrogen receptors, affect genome-wide expression of genes that are not directly regulated by ERα? These are some of the intriguing questions that remain. But with the availability of sophisticated techniques such as those used by Nunez *et al.*³, there is hope that the mysterious relationship between higher-order nuclear architecture, chromatin organization and gene expression will soon be revealed.

David M. Lonard and Bert W. O'Malley are in the Department of Molecular and Cellular Biology, Baylor College of Medicine, One Baylor Plaza, Houston, Texas 77030, USA.
e-mail: berto@bcm.tmc.edu

1. Kumaran, R. I., Thakar, R. & Spector, D. L. *Cell* **132**, 929–934 (2008).
2. Speicher, M. R. & Carter, N. P. *Nature Rev. Genet.* **6**, 782–792 (2005).
3. Nunez, E. *et al.* *Cell* **132**, 996–1010 (2008).
4. Nègre, N., Lavrov, S., Hennetin, J., Bellis, M. & Cavalli, G. *Methods Enzymol.* **410**, 316–341 (2006).
5. Carroll, J. S. & Brown, M. *Mol. Endocrinol.* **20**, 1707–1714 (2006).
6. Simonis, M., Kooren, J. & de Laat, W. *Nature Methods* **4**, 895–901 (2007).
7. Lonard, D. M. & O'Malley, B. W. *Mol. Cell* **27**, 691–700 (2007).

PLANT BIOLOGY

Scent of a rose

What Chinese roses lack in resistance to cold and disease, they make up for with repeated blooming and a distinctive fragrance. It isn't surprising, then, that plant breeders, fascinated with this ancient rose family, brought it to Europe in the nineteenth century to generate the now popular hybrid tea roses, among many others. But how did the distinctive scent of Chinese roses evolve? Gabriel Scalliet and colleagues now provide the answer (G. Scalliet *et al.* *Proc. Natl Acad. Sci. USA* **105**, 5927–5932; 2008).

Unlike their European counterparts, the main scent component of Chinese roses and their descendants is dimethoxytoluene. In the final steps of its formation, two methyl groups are sequentially added to a precursor molecule in reactions catalysed by enzymes called OOMT1 and OOMT2. These enzymes are almost identical in amino-acid

sequence, yet they target different substrates.

Scalliet and colleagues pinpoint the crucial amino-acid residues of the enzymes that confer substrate specificity: a tyrosine in OOMT1 and a phenylalanine in OOMT2. Swapping these single residues between the two enzymes switched their substrate specificity, most probably by changing the steric and hydrophobic properties of their substrate-binding sites, where these residues reside. Moreover, OOMT2 could methylate the target of OOMT1 *in vitro*, albeit with lower efficiency.

Two nearly identical enzymes with nearly identical activities, that can both perform similar reactions, although together they are more efficient than alone — these are hallmarks of the products of duplicated genes, which arise when a gene doubles in number and one of the copies then undergoes a

minor mutation. Indeed, Scalliet *et al.* show that, although all of the 13 European rose species they examined carry an OOMT-like gene, only the Chinese species, which are evolutionarily younger, carry two types of this gene. The authors' further phylogenetic analysis strongly hints that, in Chinese species, the second OOMT gene arose through a duplication event.

Roses are not unique in acquiring new functions through gene duplication; this is thought to be a fundamental mechanism for generating diversity between and within organisms. But it isn't always possible to trace such changes, which makes Scalliet and colleagues' work of interest not only to plant biologists but also to evolutionary scientists.

Sadaf Shadan