Conditional transgenic technologies

A D S Ryding, M G F Sharp and J J Mullins
Molecular Physiology Group, University of Edinburgh Medical School, Wilkie Building, Teviot Place, Edinburgh EH8 9AG, UK
(Requests for offprints should be addressed to A D S Ryding; Email: alisdair.ryding@ed.ac.uk)

Abstract
Transgenic technology has been revolutionised by the development of techniques that allow temporo-spatial control of gene deletion or expression in transgenic animals. The ability to switch gene expression ‘on’ or ‘off’ in restricted tissues at specific times allows unprecedented flexibility for exploring gene function in both health and disease. As use of these techniques grows in all areas of biomedical research, an understanding of this topic is essential. In this review we examine the theory, application and limitations of these strategies, with particular reference to endocrine research.

Journal of Endocrinology (2001) 171, 1–14

Introduction
Conventional transgenic technologies (gene overexpression or knockouts) are invaluable for modelling genetic disorders and answering specific questions in relation to developmental biology. However, this ‘all or nothing’ approach is inflexible and cannot be used to answer more subtle questions about gene function. Frequently, a genetic change has developmental consequences that either preclude or complicate studies on adult animals (e.g. embryonic lethality). Furthermore, conventional knockout strategies affect every cell in an animal, so that it is often impossible to distinguish primary and secondary changes in a complex phenotype. In order to tease out more precise information about the role of a gene in a specific cell type at a critical stage of disease or development, a more sophisticated approach is required. Building on conventional transgenic techniques, conditional technologies allow flexible temporo-spatial control of gene expression. In these systems the switching ‘on’ or ‘off’ of a particular gene is conditional on a specific stimulus. Such techniques are increasingly applied to endocrine problems, providing elegant models to study physiology and disease. An appreciation of the principles involved is essential for researchers in this field.

This review will concentrate on the theory, application and problems of established conditional transgenic strategies. A basic knowledge of conventional transgenesis is assumed, and a good review of this is provided by Bronson & Smithies (1994).

Conditional overexpression

Tetracycline responsive system
The ideal conditional overexpression system should allow the investigator to switch transgene expression on and off, rapidly, reversibly, at any point during development or postnatal life, and only in the desired cell type. Many systems have been developed harnessing the inherent responsiveness of specific promoters to various stimuli, such as heat shock and steroid hormones (Gossen et al. 1993). However, in most cases the effects of the stimulus are too profound and non-specific to offer any practical in vivo application.

Pioneering work by Bujard and Gossen has established the tetracycline transactivator system as a reliable tool for regulated transgene expression. This exploits pathways that control the expression of a tetracycline resistance gene in E. coli. This gene is constitutively repressed by tetracycline repressor (tetR), a protein that binds specifically to tetracycline operator (tetO) sequences within the promoter, rendering the gene transcriptionally silent. Repression is relieved by tetracycline, which avidly binds tetR (Fig. 1a and b). In this way, tetracycline resistance is controlled in a simple on/off manner by tetracycline itself (Gossen et al. 1993).

Because tetR and tetO interact specifically with each other and do not overlap with eukaryotic systems, they avoid many of the problems that have beset previous attempts to regulate transgene expression. Two modifications have been made to suit transgenic purposes (Gossen & Bujard 1992). First, tetR has been converted

Journal of Endocrinology (2001) 171, 1–14
0022–0795/01/0171–001 © 2001 Society for Endocrinology Printed in Great Britain
into a transcriptional activator by fusing it with the activation domains of the herpes simplex virus VP16 protein. VP16 is a virally encoded factor that recruits cellular transcription factors and potently activates viral transcription (Herr 1998). The hybrid molecule is termed the tetracycline transcriptional activator (tTA). The second modification is the use of a cytomegalovirus (CMV)-derived minimal promoter, fused with tetO sequences to control transgene expression. This chimaeric promoter is transcriptionally silent in basal conditions, and is induced in the presence of tTA and tetracycline (Fig. 1c). Tetracycline inactivates tTA and causes transgene downregulation (Fig. 1d).

Many variants of the tTA system have been designed with specific properties: these are summarised in Table 1. Reverse tTA (rtTA) is a mutagenised version which binds tetO in the presence of doxycycline and activates transcription (Gossen et al. 1995) (Fig. 1c and d). In other words, the effects of doxycycline are the opposite of tTA. The major advantage of this is that gene induction occurs ...
rapidly because the low levels of doxycycline required for transcriptional activation are readily achieved. In contrast, the kinetics of gene induction by tTA are somewhat slower, since clearance of doxycycline can take days in animals. However, a limitation is that rtTA retains some affinity for tetO sequences even in the absence of doxycycline: this leads to low level basal expression, which may not be acceptable (e.g. expression of toxins) (Keyvani et al. 1999, Imhof et al. 2000). To overcome this problem, tet-repressors have been designed. Two constructs, rTS\textsuperscript{aad} and tTR, are available in which the repressor domain of tetR has been substituted with a mammalian equivalent. These repress transcriptional activity at tetO sequences in the absence of tetracycline (Freundlieb et al. 1995, Rossi et al. 1998, Sander et al. 2000). Used in combination with rtTA, complete suppression of transgene expression can be achieved in vivo without compromising inducibility (Zhu et al. 2001). An obvious disadvantage of this approach is that triple transgenic animals are required. An alternative method has been to engineer improvements in rtTA by a combination of random mutagenesis, use of minimal transactivating domains and codon optimisation for mammalian cells. The variant RtTA\textsuperscript{2S-M2} was generated in this manner. This has virtually no background activity, enhanced doxycycline sensitivity and improved transcript stability (Urlinger et al. 2000a,b). However, evidence of improved performance in transgenic mice is still preliminary. Finally, substitution of the VP16 moiety of rtTA with the transactivation domain of the mammalian transcription factor E2F4 appears to be tolerated better by mammalian cells (Akagi et al. 2001).

The tetracycline analogues, doxycycline and anhydro-tetracycline, tend to be used in preference to tetracycline itself due to higher tTA binding affinities and lower toxicities (Gossen & Bujard 1993, Efrat et al. 1995, A-Mohammadi et al. 1997).

**Tet-regulated transgenic mice** Use of this system in mice requires the generation of two independent transgenic lines: one carrying the transgene of interest under the control of the tetO-CMV promoter, and the other an (r)tTA transgene. Crossing the lines generates a proportion of progeny with both transgenes, allowing regulation of the gene of interest through the administration of tetracycline (Fig. 2).

Initial studies in mice transgenic for tTA or rtTA crossed with luciferase or β-galactosidase reporter strains demonstrated both the practicality and problems of this approach (Furth et al. 1994, Kistner et al. 1996). Between different transgenic lines, reporter expression varied, probably reflecting variation in chromosomal integration sites and transgene copy number. In many lines, significant leaky expression was found. However, in selected lines basal expression levels were close to the limits of detection. Expression could be induced up to 100 000-fold in certain tissues and, in rtTA transgenics, kinetic studies showed significant induction within hours of oral doxycycline administration. With tTA, transgenic changes in expression occurred over days, due to the reasons mentioned above. Transgene expression could be switched on and off repeatedly without adverse effect. Histological analysis revealed mosaic expression of β-galactosidase within tissues when tTA was under the control of a CMV promoter (Furth et al. 1994), but this problem has not been seen using a strong tissue–specific promoter (Kistner et al. 1996).

Tissue-specific promoters allow expression of the transactivator to be restricted to a particular tissue or cell type. Defining the site of expression of the transactivator determines the site of transgene expression, because the minimal promoter itself confers no tissue specificity. It should be noted that the expression pattern of a promoter can be strongly influenced by the chromosomal context in which it integrates. Therefore, it is important to screen for ectopic expression. This can be done by screening for expression of the transgene itself, or using transgenic reporter lines (e.g. β-galactosidase) which allow visualisation of the expression pattern. An alternative approach is to use a bi-directional minimal promoter to drive expression of both the transgene and the reporter in the same animal (Baron et al. 1995, Yamamoto et al. 2000). This avoids the need to cross to additional lines, and gives an indirect measure of transgene expression.

The fine regulation of transgenes afforded by this system has been used to great advantage in numerous studies. This is best exemplified by experiments where neonatal lethality has been by-passed by delaying expression to later
time-points. For example, overexpression of the BCR-ABL1 oncogene (BCR-ABL) during development is lethal. Huetter et al. (2000) used the tTA system to induce BCR-ABL expression in B-lymphocytes in adult animals, resulting in acute leukaemia. Silencing transgene expression allowed complete resolution of the leukaemia, a process that could be reversed many times. Conditional activation of toxic transgenes has also been used to ablate specific cell populations: Lee et al. (1998) conditionally expressed diptheria toxin A chain in cardiac cells leading to cell ablation and progressive cardiomyopathy. By contrast, Efrat et al. (1995) conditionally transformed islet β-cells with SV40 T antigen creating pancreatic tumours from which cell lines were derived.

Additional regulatory control can be built into experiments. For example, Redfern et al. (1999) created a modified kappa opioid receptor that only recognises a synthetic ligand, spiradoline. This modified G protein-coupled receptor activates Gi signalling in response to spiradoline. Using tissue-specific promoters, enhanced Gi signalling was targeted to the heart, liver and salivary gland in separate transgenic lines. In long-term experiments, chronic Gi signalling led to dilated cardiomyopathy which was partially reversible (Redfern et al. 2000). Bond et al. (2000) recently described a method of using the tTA system to control native gene expression. In this way, a reversible cell-specific ‘virtual knockout’ was generated. By homologous recombination, a tetracycline-based control cassette was placed in the 5′ untranslated region of the SK3 gene (encoding a subunit of a Ca2+-activated K+ channel). Expression of tTA was under the control of the native regulatory elements of SK3. Expression of SK3 itself was in turn contingent upon expression of tTA, and could be abolished by administering doxycycline. However, disruption of the native locus led to elevated expression of the conditional allele in the brain in the basal state, although the pattern of expression was not altered. This allowed them to either augment or switch off SK3 expression.

Despite these impressive studies, certain limitations are increasingly recognised, such as leaky expression, cellular toxicity, unstable transcripts and insensitivity to doxycycline in certain tissues (Baron et al. 1997, Urlinger et al. 2000a). It is hoped that developments such as the RfTA2′-M2 variant will circumvent these problems. In addition, it should be noted that the genetic background of mice can influence the occurrence of such difficulties (Zhu et al. 2001). Another drawback is the need to generate two separate transgenic lines for each study. Schultz et al. (1996) have used a single construct containing all the necessary regulatory sequences and transgene on one plasmid. Theoretically, this approach is less time consuming and avoids the segregation of control elements during breeding. However, the use of double transgenic lines is more flexible if one wishes to make use of several different tissue-specific transactivator lines to study the effects of a single transgene.

The wealth of transactivators and tetracycline analogues available with different properties theoretically allows independent regulation of more than one transgene in a single animal using combinations of the tetracycline system. The feasibility of this has been demonstrated in cell lines (Baron et al. 1999) although not in vivo.

It should also be noted that the various components of this system are now commercially available, making it highly accessible.

**Ecdysone-inducible overexpression**

Ecdysone is a steroid hormone that triggers metamorphosis in insects. It mediates pleiotropic effects via a heterodimeric receptor, comprising the ecdysone receptor (EcR) and the product of the ultraspiracle gene (USP) which together bind ecdysone response elements (ERE) to enhance transcription of genes required for metamorphosis. No et al. (1996) have adapted this system for mammalian cells in a manner analogous to the tet system described above. A novel transactivator was generated by fusion of a truncated EcR with transcriptional activation domains of the glucocorticoid receptor and the herpes simplex virus VP16. This hybrid retains specificity for binding ecdysone and ERE, but has enhanced transcriptional activity. In addition, a novel ecdysone-specific response element was constructed that allowed inducible gene expression without cross reactivity with endogenous mammalian nuclear hormone receptors. The retinoid X receptor (RXR) is the mammalian homologue of USP, and functions effectively with the hybrid EcR (Fig. 3).
Experiments in transfected cells and transgenic mice have demonstrated the potential use of this system. Mice transgenic for hybrid EcR and RXR under the control of T-lymphocyte promoters were crossed with reporter mice bearing an ecdysone-inducible β-galactosidase transgene. Basal reporter expression was minimal, but could be rapidly induced by intraperitoneal injection of a synthetic ecdysone analogue, muristerone A. Muristerone has not been found to exert any teratogenic or physiological effects in mice. More recently, a widely available natural plant steroid, ponasterone A, has been shown to be a potent and innocuous inducing agent (Saez et al. 2000). The use of synthetic RXR ligands synergises with muristerone induction (Saez et al. 2000), although the use of such compounds may have unwanted physiological effects. Hoppe et al. (2000a) have simplified the system using a chimaeric Drosophila/Bombyx ecdysone receptor which transactivates transgenes without the need for RXR at all.

In vitro comparison of the ecdysone and tetracycline induction systems demonstrated lower basal expression, greater inducibility and more rapid induction kinetics with ecdysone (No et al. 1996). In the uninduced state, there may even be transcriptional repression of the transgene which makes this system less leaky than tet-based ones (Rossant & McMahon 1999). However, direct in vivo comparison has not been carried out.

So far this technology has been used most extensively in cell culture systems and examples of ecdysone-based transgenics are sparse. Albanese et al. (2000) have successfully targeted expression of an ecdysone-responsive β-galactosidase transgene to the mammary gland. Similarly, Saez et al. (2000) directed inducible luciferase expression to the skin with a human keratin 5 promoter. Other in vivo work has been limited to adenoviral-mediated transfer of ecdysone-inducible constructs to the heart and carotid bodies (Hoppe et al. 2000b).

Until further studies are reported, the advantages of this system cannot be evaluated. However, the benefit of having more than one inducible system available is the potential for combination transgenics with multiple independently regulated transgenes.

Cytochrome P-450 induction system

An inherent drawback of the systems described above is the requirement for doubly-transgenic animals. Use of endogenous mammalian gene regulatory systems can avoid this complexity. For example, the mouse metallothionein promoter has been used for many years to regulate transgene expression (Palmiter et al. 1983). Transcription at this promoter is induced by heavy metal ions such as zinc and cadmium. However, there is invariably high-level constitutive expression in a broad range of tissues, and the degree of transgene induction is relatively poor (Joseph et al. 1999). For these reasons, this system will not be discussed further. In contrast, the cytochrome P-450 system is highly inducible and provides more stringent control of gene expression.

Cytochrome P-450 mono-oxygenases are enzymes involved in metabolising and detoxifying lipophilic xenobiotics (Gonzalez & Nebert 1990). Expression of some P-450 enzymes is directly regulated by the availability of their substrate. In other words, exposure to a specific compound will induce expression of the cytochrome responsible for its metabolism. One such cytochrome, CYP1A1 (encoding aryl hydrocarbon (benzo[a]pyrene) hydroxylase (E.C.1.14.14.1)) is induced by aryl hydrocarbons and the enhancer/promoter sequences of this gene have been used successfully for conditional transgene expression.

CYP1A1 is not expressed constitutively and it is regulated entirely at a transcriptional level (Ryu et al. 1996). Induction requires binding of aryl hydrocarbon compounds to aryl hydrocarbon receptors (AHR) in the cytoplasm. AHR–ligand complexes shuttle to the nucleus where they bind to the aryl hydrocarbon nuclear translocator (ARNT), forming a heterodimer–ligand complex. Both AHR and ARNT are ligand-dependent basic helix-loop-helix transcription factors that bind aromatic hydrocarbon-responsive elements (AhREs) several hundred base pairs upstream of the cyp1a1 promoter (Fig. 4). AhRE binding induces chromatin remodelling at

This system has been characterised in transgenic mice and rats using various portions of the cyp1a1 enhancer promoter. Small parts of the promoter region fail to control transgene expression adequately (Jones et al. 1991, Schachter et al. 1994, Smith et al. 1995a) whilst more extensive portions which include all the known enhancer/promoter sequences allow tightly regulated expression (Campbell et al. 1996, Kantachuvesiri et al. 2001). As for any transgene, the site of chromosomal integration has a profound effect on the level of baseline expression: many transgenic lines may have to be screened in order to identify a suitable one. Transgene expression can be induced in a dose-dependent manner as much as 10 000-fold (Jones et al. 1991). Expression is predominantly in the liver, but also adrenal, kidney, intestine, spleen, lung, pancreas, skin and the reproductive organs (Campbell et al. 1996, Kantachuvesiri et al. 2001). Within each tissue, expression is regulated in a cell-type specific manner (Campbell et al. 1996). The widespread expression reflects the tissue distribution of AHR, and ARNT: this may be less than ideal for some applications.

In our laboratory, we have used the rat cyp1a1 enhancer/promoter sequences to control mouse Ren2 cDNA (encoding renin) expression in rats (Kantachuvesiri et al. 2001). This has created an inducible model of hypertension. Background expression levels are undetectable in non-induced rats. Blood pressure can be titrated in a dose-dependent manner to produce either malignant or chronic phase hypertension. Furthermore, the renin–angiotensin system and blood pressure return to normal in the absence of inducer, making this an extremely flexible model for studying hypertension, vascular injury and repair.

One prerequisite for a useful regulatory system is that the inducer must be innocuous, and that spillover activation of other loci is inconsequential. Most AHR-binding compounds have deleterious effects, but indole–3-carbinol (I3C) is an exception. This is a naturally occurring aryl hydrocarbon found in brassicae. It has anticarcinogenic, antioestrogenic, hypocholesterolaemic and immunomodulatory effects which are poorly understood (Dunn & LeBlanc 1994, Bradlow et al. 1999, Exon & South 2000). I3C itself is a weak inducer of cyp1a1 but derivatives formed in the stomach are much more potent: up to 24 different active metabolites have been found in rats fed I3C (Stresser et al. 1995). Since it is readily absorbed and metabolised, induction of cyp1a1 occurs within hours (Stresser et al. 1995). It also induces other members of the aryl hydrocarbon battery including CYP1A2, CYP2B1/2 and CYP3A1/2, and inhibits both the activity and expression of flavin mono-oxygenase 1 (Katchamart et al. 2000): thus, metabolism of other xenobiotics is undoubtably affected and this may interfere with pharmacological studies. Furthermore, in vitro studies on a hepatoma cell line indicated that induction of CYP1A1 with an I3C derivative can lead to oxidative DNA damage (Park et al. 1996). Despite these multiple effects, chronic oral administration in adult rats and mice has been shown to be safe.

The simplicity and robustness of this system make it eminently suitable for overexpression of secreted soluble proteins. However, limited tissue specificity restricts its broader application.

**Conditional genetic deletion: somatic cell mutagenesis**

Embryonic lethality in many conventional gene knockouts impedes attempts to study gene function in older animals. One way of avoiding this is to ablate specific genes at later stages of development or adulthood using recombinases. Two members of the α integrase family of site-specific recombinases, Cre and Flp, have proved invaluable for conditional transgenic use.

Cre (causes recombination) recombinase of the P1 bacteriophage directs recombination between loxP (locus of crossover) sites. Its function is to maintain phase-encoding plasmids as monomers. In a similar manner the Flp integrase of *Saccharomyces cerevisiae* mediates recombination between FRT (FLP recombination target) sites within yeast plasmids (Kimby et al. 1993). In each case, the only requirements for DNA rearrangement are the integrase and the recombination sites: no additional cellular factors are necessary. Both loxP and FRT sites are 34 bp DNA sequences comprising two 13 bp palindromes separated by an asymmetric 8 bp core. The recombinases catalyse DNA strand exchange between two aligned recombination sites, resulting in deletion, duplication, integration, inversion or translocation of sequences, according to the orientation of the recombination sites and the number of molecules involved (Fig. 5).

Application of these techniques in mice allows deletion of genetic material in selected cells at a specific time. In this way, one can avoid the complications of embryonic lethality and developmental compensatory changes. At its most simple, this requires incorporation of two recombination sites within a gene of interest, and then expression of a recombinase in only those cells in which one wishes deletion to occur. Because this technology relies on homologous recombination in embryonic stem cells, its use is restricted to mice.
Cre-lox system

Modification of a specific gene with loxP sites flanking the region of interest is achieved using standard gene targeting vectors in embryonic stem (ES) cells. Such an allele is said to be 'floxed' (flanked by loxP) and depending on the exact position of the lox P sites and selection markers, may or may not be fully functional. Mice derived from these targeted ES cells can be bred to homozygosity for the floxed allele, and crossing with other mice transgenic for Cre recombinase under the control of a specific promoter allows time- or tissue-specific deletion of the floxed segment (Fig. 6). In this way, the activity of the gene can be modified in a limited range of cells at a particular developmental stage, whilst the genetic content of the rest of the animal is essentially unaltered. Crossing to a different Cre transgenic mouse line allows the generation of a different temporo-spatial pattern of recombination, and possibly phenotype (Fig. 6).

This strategy has been used extensively since Lakso et al. (1992) first described the Cre-mediated activation of an SV40 T antigen transgene in lens cells leading to tumour formation. Tissue specificity is determined by the choice of promoter driving Cre recombinase expression. Many tissue-specific Cre transgenic and floxed mice strains are becoming available, and a database cataloguing such animals is available at http://www.mshri.on.ca/nagy/cre.htm: from this it can be seen that many important endocrine tissues can be selectively targeted, although the list is far from complete. Tissue-specific Cre-lox techniques have yielded unexpected insights into endocrine physiology in recent years. Table 2 gives published examples of Cre-loxP-mediated gene deletion in endocrine tissues or target tissues. Cre-lox strategies can also facilitate cell fate-mapping studies. Using Cre recombination to genetically tag the progeny of pancreatic stem cells, Herrera (2000) demonstrated separate developmental lineages for α and β cells.

Ideally one would wish to control not only the site of recombination but also the timing. Several strategies have been designed to address this, using inducible forms of Cre recombinase. Fusion of the ligand-binding domain (LBD) of a mutated oestrogen receptor to Cre results in a hybrid that is active in the presence of tamoxifen, but not endogenous steroids (Metzger et al. 1995). The LBD allows sequestration of hybrid Cre in the cytosol by heat-shock proteins. Tamoxifen liberates the recombinase, allowing recombination to proceed at a specified time in tissues expressing Cre. Similar hybrids have been developed using modified progesterone and glucocorticoid
receptor LBDs, responsive to RU486 and dexamethasone respectively (Kellendonk et al. 1996, Brocard et al. 1998). Validation of ligand-activated Cre in transgenic mice demonstrated no detectable recombination in the absence of tamoxifen (Feil et al. 1996) but almost 100% recombination in Cre-expressing cells after 3 days of exposure (Brocard et al. 1997). However, in some cases incomplete and ligand-independent recombination have been observed (Schwenk et al. 1998, Kellendonk et al. 1999). New forms of tamoxifen and RU486-inducible Cre are now available with enhanced ligand sensitivity and low background activity (Indra et al. 1999, Kuhbandner et al. 2000, Imai et al. 2001, Wunderlich et al. 2001). Thus ligand-activated Cre shows great promise for controlling the timing of recombination. Since tamoxifen is only given for a brief time, no lasting complications arise, and it has even been used with pregnant mice (Danielian et al. 1998).

An alternative strategy for inducing Cre activity is to use an inducible promoter. Tetracycline-regulated expression of Cre has been used by several groups. For example, Shin et al. (1999) successfully ablated endothelin B receptors (EDNBRB) in mice at various time-points and were able to define a critical developmental period in which EDNBRB is essential. Tetracycline-inducible tissue-specific knockouts are also possible (Saam & Gordon 1999, Utomo et al. 1999). Kuhn et al. (1995) have used an interferon-inducible promoter to control Cre expression,

Table 2

<table>
<thead>
<tr>
<th>Disrupted gene</th>
<th>Tissue-specificity</th>
<th>Phenotype</th>
<th>Reference</th>
</tr>
</thead>
<tbody>
<tr>
<td>C/ebp</td>
<td>Liver</td>
<td>Impaired gluconeogenesis and bilirubin metabolism</td>
<td>Lee et al. (1997)</td>
</tr>
<tr>
<td>Glucocorticoid receptor</td>
<td>Glia</td>
<td>Altered HPA regulation</td>
<td>Tronche et al. (1999)</td>
</tr>
<tr>
<td>Glucokinase</td>
<td>Liver</td>
<td>Defective glycogen synthesis</td>
<td>Postic et al. (1999)</td>
</tr>
<tr>
<td>GLUT4, ICFl</td>
<td>Pancreatic β cells</td>
<td>Fatal hyperglycaemia</td>
<td>Abel et al. (2001)</td>
</tr>
<tr>
<td>Insulin receptor</td>
<td>Adipose tissue</td>
<td>Hepatic and skeletal muscle insulin resistance</td>
<td>Yakar et al. (2001)</td>
</tr>
<tr>
<td>Insulin receptor</td>
<td>Liver</td>
<td>Skeletal muscle insulin resistance</td>
<td>Yakar et al. (1999)</td>
</tr>
<tr>
<td>Insulin receptor</td>
<td>Pancreatic β cells</td>
<td>Normal postnatal growth</td>
<td>Kulkarni et al. (1999)</td>
</tr>
<tr>
<td>PTHrP</td>
<td>Skeletal muscle</td>
<td>Impaired insulin release: impaired glucose tolerance</td>
<td>Brüning et al. (1998)</td>
</tr>
<tr>
<td>RXRa</td>
<td>Global</td>
<td>Perinatal lethality: aberrant endochondral bone formation</td>
<td>He et al. (2001)</td>
</tr>
<tr>
<td>SF1</td>
<td>Adipose tissue</td>
<td>Obesity resistance</td>
<td>Imai et al. (2001)</td>
</tr>
<tr>
<td></td>
<td>Anterior pituitary</td>
<td>Impaired lipolysis</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>Hypogonadotrophic hypogonadism</td>
<td>Zhao et al. (2001)</td>
</tr>
</tbody>
</table>

Figure 6 Tissue-specific gene ablation using Cre-lox. Mouse lines expressing Cre (blue) in a tissue-restricted manner, such as the brain or liver, can be crossed to a line containing a floxed allele. Cre-mediated recombination results in allele deletion in the brain or liver alone, leading to altered function (red).
and this has been used successfully to delete the low density lipoprotein receptor–related protein in hepatocytes
(Rohlmann et al. 1998). Adenoviral delivery of Cre can also be used to determine the timing of recombination in
certain tissues: after systemic delivery most recombination
occurs within the liver, none in the central nervous
system, and intermediate levels in other tissues (Wang et al.
1996, Akagi et al. 1997). However, immune responses to
adenovirus limit the permanence of Cre expression (Akagi
et al. 1997).

Cre-lox has been used most extensively for small-scale
DNA rearrangements affecting single loci. However, it
can also orchestrate chromosomal rearrangements, such as
deletion of large regions, or translocations (Smith et al.
between loxP sites in cis can extend up to at least
60 centimorgan (cM) in ES cells in vitro. In vitro, a
cardiac-specific 2cM deletion has been demonstrated
(Zheng et al. 2000). Such manipulations are very attractive
for loss of heterozygosity studies and screens for tumour
suppressor genes. Both deletion and duplication of regions
within the Hox gene cluster has been achieved by induc-
ing unequal exchanges between homologous chromo-
somes at loxP sites (Herault et al. 1998). Such exchanges
can be engineered to cause whole chromosome loss by
generating acentric/dicentric chromosomes (Lewandoski
& Martin 1997). Anti-parallel loxP sites have been used to
invert regulatory elements within the HoxD complex,
resulting in dysregulation of limb and gut development
(Kmita et al. 2000).

It is clear from most Cre-lox mouse experiments that
there are several potential pitfalls. First, expression of Cre
within a particular cell type or tissue is rarely uniform,
leading to mosaic recombination. In certain instances this
may be desirable or at least inconsequential, in so far as it
models random somatic mutagenesis (e.g. carcinogenesis).
However, for some physiological studies, even remnant
levels of wild-type product may not be acceptable.
Determining the extent of recombination is essential for inter-
preting experiments. In tissues of heterogeneous cell type,
Southern blotting may be an inadequate method of analysis
because it does not indicate the cell type in which
recombination has occurred. In situ PCR for the floxed
allele or immunohistochemistry for Cre expression are
alternatives that give some indication of cell specificity
(Selbert et al. 1998). Reporter strains for Cre activity such
as ROSA26-βgeo (Mao et al. 1999, Soriano 1999) in
which an activatable floxed βgeo has been knocked-in to
the ubiquitously expressed ROSA26 locus, give a clear
indication of the sites and extent of recombination for a
particular Cre transgenic. Alternative reporter strains with
activatable enhanced green fluorescent protein (GFP) are
also available (Kawamoto et al. 2000, Mao et al. 2001).
‘Double-reporter’ lines have been developed that consti-
tutively express LacZ throughout development and adult-
hood: Cre-mediated recombination inactivates the LacZ
transgene whilst activating a second reporter such as GFP
or alkaline phosphatase (Lobe et al. 1999, Novak et al.
2000). A major assumption of reporter strains is that they
accurately reflect recombination for other floxed loci.
However, recombination efficiency is known to vary be-
tween different target loci (Holzenberger et al. 2000a)
so results obtained in this manner can only be a guide.
One solution is to design the initial targeting vector in such
a way that recombination leads to activation of a reporter
gene (Knita et al. 2000, Moon & Cappechi 2000). This has
the advantage of giving a direct read-out of recombination
efficiency within the animal under study.

A second problem is that of transcriptional interference
by vector-derived sequences, such as the neo selection
cassette, or even the loxP sites. Tronche et al. (1999) found
that the floxed glucocorticoid allele gave rise to levels of
expression twice as high as wild type, whilst others have
found underexpression (Fiering et al. 1995, Olson et al.
1996, McDevitt et al. 1997, Nagy et al. 1998, Holzenberger et al. 2000a,b). Such alleles are referred to as
‘knockdown’ or ‘hypomorph’. Intermediate expression
levels may be informative (Meyers et al. 1998,
Holzenberger et al. 2000b), but this is unpredictable.
Cryptic splicing of plasmid sequences can also create
abnormal transcripts (Yu et al. 1998) which may have
unexpected effects (Meyers et al. 1998, Forlino et al. 1999).
Vectors can be designed to allow the removal of unwanted
plasmid sequences from cultured ES cells prior to blasto-
cyst injection (Xu et al. 1999). However, the extended
period of culture required may theoretically interfere with
ES cell pluripotency. Alternatively, mice expressing Cre in
the testes have been used successfully for excision of floxed
plasmid sequence in germline chimaeras (O’Gorman et al.

In most circumstances, mammalian cells appear
surprisingly tolerant of Cre recombinase expression and
DNA rearrangements. However, several studies have
indicated that Cre can act efficiently at endogenous
pseudo-loxP sites identified within mammalian genomes
(Thyagarajan et al. 2000). Schmidt et al. (2000) found that
mice expressing Cre in spermatids were sterile due to gross
chromosomal rearrangements that may have been caused
by this mechanism. Although this problem has not been
reported in somatic cells its occurrence may have less
dramatic consequences and it has therefore escaped
attention. For this reason it would seem sensible to
restrict Cre expression as far as possible: one approach has
been to design self-excising Cre cassettes (Bunting et al.
1999).

Despite these caveats, Cre-lox technology has
revolutionised genetic analysis of mice and is now well
established as a routine genetic tool. It should be
considered the first choice for conditional gene deletion
experiments.
FLP recombinase

The uses of Flp mirror those already established for Cre; conditional gene knockouts, transgene activation, selection cassette removal, chromosomal rearrangement and mapping studies. The same cautions regarding mosaicism and ectopic expression are also pertinent. However, use of Flp in transgenic mice is at a less advanced stage than that of Cre and a direct comparison between the two is not possible at this time.

Dymecki (1996) has demonstrated dose-dependent Flp-mediated recombination in a FRT–lacZ reporter strain, and elegantly used Wnt1 promoter-driven Flp to fate-map neuronal migrations in the developing brain (Dymecki & Tomaszewicz 1998, Rodriguez & Dymecki 2000). Exhaustive analysis of the pattern and extent of Flp expression/recombination events demonstrated high levels of recombination (>90%) in a highly restricted cell-type specific pattern (Rodriguez & Dymecki 2000). Vooijs et al. (1998) conditionally ablated the retinoblastoma gene in anterior pituitary cells, leading to adenoma formation. In this study, a modified form of Flp was used, and the efficiency of recombination was far less than 100%.

Concern that the recombination efficiency of Flp is inferior to that of Cre has been allayed somewhat since the development of an enhanced, mutant form (FLPe) (Buchholz et al. 1998). This exhibits fourfold greater activity than wild type, and maximally excises a target gene in a broadly expressing reporter line (Rodriguez et al. 2000). No ubiquitously expressing reporter lines for Flp are currently available, and this is another disadvantage compared with Cre.

As for Cre, an oestrogen–LBD–Flp hybrid has been developed to allow rapidly inducible recombination activity (Logie & Stewart 1995, Logie et al. 1998). However, activity of the hybrid is only 50% that of the wild-type enzyme.

Use of Flp and Cre in combination allows sophisticated manipulation of loci: for example, removal of unwanted plasmid sequences from a conditional allele at the ES cell stage with Flp/FRT, and subsequent deletion by Cre in vivo (Moon & Cappechi 2000). Meyers et al. (1998) ingeniously used both to create an allelic series at the Fgf8 locus. A floxed hypomorphic allele could be knocked out completely using conditional Cre, or reverted back to wild type using Flp. One can easily envisage many more situations where multiple simultaneous or sequential conditional mutations are created using recombinase combinations, either at single or multiple loci. However, whilst Flp/FRT is an increasingly attractive system, it does not yet have the track record of Cre-lox.

Discussion and Conclusions

The phenotypic modification of monogenic disorders by the genetic background of inbred laboratory animals has been recognised for many years. Under identical environmental conditions, such observations may be attributable to one or more ‘modifier loci’ that increase or decrease the severity of a phenotype (Nadeau 2001). Formal identification and analysis of modifiers may provide a novel insight into the biology of a disease, for which there are numerous examples in the literature (Kantachuvesiri et al. 1999, Nadeau 2001).

Genetic background is of great importance in conditional transgenic experiments because it may influence not only the primary pathology but also the efficiency of the conditional system itself. For example, evidence already suggests that the regulation of the rtTA system differs between mouse strains (Zhu et al. 2001). In a similar manner, one might anticipate that the efficiency of Cre recombination is strain dependent, although this has not been formally investigated. Complications of this nature may have unpredictable and misleading consequences, particularly when different conditional models on different inbred backgrounds are intercrossed (genetic multiplexing). For this reason every effort should be made to maintain pure genetic backgrounds.

The availability of reliable conditional transgenic technologies is set to revolutionise our understanding of physiology and disease. This comes at an opportune time, when advances in genome sequencing, array technology and miniaturised physiological assessment will provide both the raw material and the means for analysis. Conditional techniques should be seen as supplementing rather than supplanting conventional transgenesis, which remains an invaluable tool.

Theoretically one may choose to overexpress or delete genes in specified tissues at will. Choosing between the available systems depends very much on the goals of the experiment and available expertise. However, some systems have well-established track records and should probably be the first choice unless there are special experimental considerations. In practice, these experiments are a considerable investment of time and resources without guarantee of success. Problems still remain to be resolved, such as mosaic, ectopic and leaky expression, necessitating careful characterisation and quantification of transgene expression patterns (e.g. using reliable reporter lines or built-in reporters). With the growing availability of complementary transgenic lines (e.g. Cre/Flp, floxed/FRT, tet/ecdysone) convenient inter-crossing experiments of ever greater complexity will be possible.

Acknowledgements

We acknowledge the support of the Wellcome Trust and the British Heart Foundation. A R is the holder of a Wellcome Trust Cardiovascular Initiative Clinical Training Fellowship (062859/HS). M S ia a BHF Basic Science Lecturer and J M is a Wellcome Trust Principal Research
Fellow. Thanks are due to Mark Lawson for assistance with figures.

References


Buchholz F, Refaely Y, Trumpp A & Bishop JM 2000 Inducible chromosomal translocation of AML1 and ETO genes through Cre/loxP-mediated recombination in the mouse. EMBO Reports 1 133–139.


www.endocrinology.org


O’Gorman S, Dagenais NA, Qian M & Marchuk Y 1997 Protamine-Cre recombinase transgenes efficiently recombine target sequences in the male germ line of mice, but not in embryonic stem cells. PNAS 94 14602–14607.


Park J-YK, Shigenaga MK & Ames BN 1996 Induction of cytochrome P4501A1 by 2,3,7,8-tetrachlorodibenzo-p-dioxin or indolo(3,2-c)carbazole is associated with oxidative DNA damage. PNAS 93 2322–2327.


Tomita S, Sinal CJ, Yim SH & Gonzalez FJ 2000 Conditional disruption of the aryl hydrocarbon receptor nuclear translocator (Ahr) gene leads to loss of target gene induction by the aryl hydrocarbon receptor and hypoxia-inducible factor 1 alpha. *Molecular Endocrinology* **14** 1674–1681.


Received 4 June 2001
Accepted 5 July 2001