Female mice lacking Xist RNA show partial dosage compensation and survive to term

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X-chromosome inactivation (XCI) compensates for differences in X-chromosome number between male and female mammals. XCI is orchestrated by Xist RNA, whose expression in early development leads to transcriptional silencing of one X chromosome in the female. Knockout studies have established a requirement for Xist with inviability of female embryos that inherit an Xist deletion from the father. Here, we report that female mice lacking Xist RNA can, surprisingly, develop and survive to term. Xist-null females are born at lower frequency and are smaller at birth, but organogenesis is mostly normal. Transcriptomic analysis indicates significant overexpression of hundreds of X-linked genes across multiple tissues. Therefore, Xist-null mice can develop to term in spite of a deficiency of dosage compensation. However, the degree of X-autosomal dosage imbalance was less than anticipated (1.14-fold to 1.36-fold). Thus, partial dosage compensation can be achieved without Xist, supporting the idea of inherent genome balance. Nevertheless, to date, none of the mutant mice has survived beyond weaning stage. Sudden death is associated with failure of postnatal organ maturation. Our data suggest Xist-independent mechanisms of dosage compensation and demonstrate that small deviations from X-autosomal balance can have profound effects on overall fitness.

[Keywords: genome balance; inverse effect; X inactivation; Xist; dosage compensation; knockout mouse; transcriptomics]

Supplemental material is available for this article.

Received April 30, 2016; revised version accepted July 22, 2016.
in extraembryonic tissue [Marahrens et al. 1997]. In contrast, female embryos that inherit a maternal Xist deletion develop normally for two reasons: First, the maternal Xist allele is not expressed during normal development in the early embryo. Second, in the embryo proper, the random XCI process becomes nonrandom such that the X chromosome with an intact copy of Xist is always an inactive X chromosome [Lyon et al. 1964; Takagi 1980; Penny et al. 1996; Marahrens et al. 1997; Senner et al. 2011]. These findings also demonstrate that Xist is essential for not only imprinted XCI but also random XCI. In an embryonic stem (ES) cell model, knocking out Xist on one X chromosome results in a skewed pattern of XCI, with the intact X always adopting the inactive X chromosome state [Penny et al. 1996]. Similarly, a heterozygous deletion of Xist in vivo results in a nonrandom XCI pattern in all cells of the embryo proper and the adult soma [Hoki et al. 2009, 2011].

In spite of these classic studies, the impact of losing both Xist alleles on the developing embryo has never been addressed, as the loss of imprinted XCI causes embryonic lethality before effects on random XCI can be addressed. Of specific interest is whether deviation from a 1:1 X to autosome (X:A) dosage balance has consequences for the developing soma. One recent study showed that conditionally deleting Xist in the blood compartment resulted in a partial inactive X-chromosome reactivation and the development of highly lethal blood cancers with full penetrance, demonstrating that Xist is a potent suppressor of hematologic cancer in adult mice [Yildirim et al. 2013]. On the other hand, in the ex vivo context, cells derived from the ICM, such as mouse ES cells [Lin et al. 2007; Schulz et al. 2014] and embryonal carcinoma (EC) cells [Martin et al. 1978], appear to tolerate some deviation relative to their differentiated male counterparts [Nguyen and Disteche 2006; Lin et al. 2007; Deng et al. 2011; Kharchenko et al. 2011; Yildirim et al. 2012]. This overexpression may explain why, although female mouse ES and EC cells can be maintained indefinitely ex vivo, they have a tendency to lose one X chromosome with prolonged culture. Thus, it is currently believed that full X:A dosage compensation is essential for embryonic development.

Here, we set out to investigate the effects of dosage imbalance on the developing embryo. We asked whether it is possible to create female mice lacking Xist RNA throughout the body. To our surprise, it is. Although X-linked gene expression is significantly increased, the overall increase is far less than expected of two active X chromosomes. These data thereby provide support for inherent genome balance and “inverse effects” as historically observed in plants and flies [Stenberg et al. 2009; Birchler 2013; Sun et al. 2013]. However, they also demonstrate that small deviations from X-autosomal equivalence can have a major impact on survival and fitness.

Results

Female mice lacking Xist RNA undergo embryogenesis and are viable to term

To create a whole-body Xist-null mouse, we used a conditional allele for Xist that would delete the promoter and first three exons upon exposure to Cre recombinase [Fig. 1A; Csankovszki et al. 1999]. To bypass the requirement for Xist during imprinted XCI in placental lineages [Marahrens et al. 1997], we used a Sox2 promoter-driven Cre recombinase [Hayashi et al. 2002] in order to generate mice deficient for Xist only in the epiblast lineage. Previous work showed that Sox2-Cre expression is observed at the blastocyst stage in the ICM but not the trophoderm or primitive endoderm [subjected to imprinted XCI], thereby enabling us to decouple the effects of Xist on random versus imprinted XCI. Heterozygous Xist mutants [Xist\(^{fl/WT}\); Sox2-Cre] were born at normal Mendelian ratios [\(\chi^2, P = 0.6724\)] [Fig. 1B]. The viability of these animals was expected in light of previous work showing skewed XCI patterns in female cells carrying a single Xist knockout allele [Penny et al. 1996; Marahrens et al. 1997]. Indeed, RNA-FISH [fluorescence in situ hybridization] analysis in mouse embryonic fibroblasts (MEFs) showed that >80% of cells in both heterozygous mutants and wild-type controls harbored an Xist cloud [Fig. 1C], consistent with the occurrence of skewed inactivation favoring the wild-type X chromosome. Hence, these heterozygous animals will be used as the “control” group.

We then attempted to generate homozygous Xist mutants by crossing Xist\(^{fl/WT}\); Sox2-Cre neonates to Xist\(^{fl/Y}\) males [Fig. 1D]. To our surprise, we observed live-born pups of the Xist\(^{fl/fl}\); Sox2-Cre genotype, which should in principle have become Xist\(^{-/-}\) upon Cre-mediated excision of the floxed allele around the time of implantation. Litter sizes did not deviate significantly from normal [average litter size of 7.5 pups, with 3.4 females per litter]. We isolated primary tail-tip fibroblasts (TTFs) from Xist\(^{fl/fl}\); Sox2-Cre neonates and performed DNA-FISH using an Xist probe that mapped within the region targeted for deletion. Xist signal was undetectable in at least 92.5% of TTFs [Fig. 1E]. In contrast, as expected, DNA-FISH in control Xist\(^{WT/WT}\); Sox2-Cre TTFs detected the presence of one Xist focus in 88% of cells [Fig. 1F]. Xist RNA-FISH analysis confirmed the absence of the Xist cloud along with loss of the H3K27me3 modification, a classic epigenetic mark associated with the inactive X chromosome [Fig. 1G; Plath et al. 2003]. We also performed RT-qPCR for multiple organs from homozygous mutants and control animals. Xist RNA was almost undetectable in most tissues, including the gut, spleen, kidney, heart, lung, and brain [Fig. 1H]. Residual Xist expression was detected in the livers of all three homozygous mutants but at significantly reduced levels. Thus, we created female mice lacking Xist RNA [referred to here as “mutant"].

Although mutant females were born at regular intervals, their births occurred at only ~25% of the expected Mendelian frequency [\(\chi^2, P = 0.0018\)] [Fig. 1D]. All mutant pups were runted at birth [Fig. 2A], with an average body weight 60% that of female littermates [Fig. 2B].
These mice showed persistent growth retardation and failed to thrive such that, at postnatal day 21 (P21), their average body weight was ~30% that of female littermates (Fig. 2B). With one exception, all Xist-null females died by weaning age, with a median survival of 18 d ± 10.4 d (Fig. 2C). Reducing competition for food by removing male littermates did prolong survival of the Xist-null females, suggesting that a failure to compete for resources might have contributed to their early demise. Nevertheless, these resource-rich mutants still died within the first month of life, with the longest survivor persisting to 24 d. Thus, both inherent physiological defects and external competition contributed to decreased overall fitness.
The reduced number of homozygous females at birth and the progressive loss prior to weaning are consistent with a failure of XCI in the pregastrulation embryo. Indeed, analysis of E8.5 embryos showed that effects began to manifest during this early post-implantation stage. Unlike in neonates, embryos of all genotypes were recovered at approximately equal frequencies at E8.5 (\( \chi^2, P = 0.5653 \)) (Fig. 2D). However, embryos of the \( Xist^{\Delta/\Delta} \); Sox2-Cre genotype already appeared different from \( Xist^{WT/\Delta} \); Sox2-Cre and \( Xist^{\Delta/\Delta} \) control littersmates (Fig. 2G–K). Interestingly, whereas \( Xist^{\Delta/\Delta} \); Sox2-Cre embryos often showed a developmental delay, there was a range of severity, with some embryos appearing only slightly runted, while others showed severe retardation (Fig. 2I–K). Regardless of phenotype, Sox2-Cre efficiently deleted \( Xist \) in all embryos of the \( Xist^{\Delta/\Delta} \); Sox2-Cre genotype, leaving no detectable cells with two intact \( Xist \) alleles and rare cells with one intact allele in each embryo (Fig. 2E,F). By PCR, the intact allele could be detected only faintly, if at all, in null mutant females at E8.5 (Supplemental Fig. S1).

Thus, we conclude that a significant fraction of female mice lacking \( Xist \) RNA is viable to term. This viability of the \( Xist \)-null animals was unexpected for several reasons. First, XCI is tightly coupled to cell differentiation both in

Figure 2. \( Xist \)-null female mice have decreased fitness. (A) Female littermates from homozygous crosses at P3 (d3, left) and P11 (d11, right). Homozygous \( Xist \) mutants are indicated by asterisks. (B) Body weight of \( Xist \) mutants (\( n = 3 \)) and female littermate controls (\( n = 10 \)). Error bars indicate mean ± SEM. (C) Kaplan-Meier survival curve for homozygous \( Xist \) mutants and female littermate controls. (D) Genotype data from homozygous cross at E8.5. The observed number of embryos is listed. (n.s.) Not significant. (E) Representative images for \( Xist \) and chromosome X DNA-FISH to quantify deletion efficiency at E8.5. Data for two \( Xist \)-null mutants are shown. Bar, 10 µm. (F) Quantification for DNA-FISH shown in E. Fifty to 100 nuclei from each animal were counted, depending on the size of the embryo. Data represent mean ± SEM of two \( Xist^{\Delta/\Delta} \) and three \( Xist^{\Delta/\Delta} \); Sox2-Cre embryos. (G–K) E8.5 embryos of various genotypes. E4-2, E5-4, and E2-9 are \( Xist^{\Delta/\Delta} \); Sox2-Cre embryos showing different degrees of developmental defect and/or runting. Bar, 250 µm.
vivo in the epiblast and ex vivo in ES cells [Monk and Harper 1979; Penny et al. 1996]. Furthermore, on the basis of numerous in vivo genetic studies over the past 20 years, it is widely believed that proper dosage compensation is essential for developmental progression and the ultimate survival of female embryos [Marahrens et al. 1997; Hoki et al. 2009, 2011]. Indeed, mice lacking Xist expression due to either a deletion of Xist itself [Marahrens et al. 1997; Kalantry et al. 2009; Namekawa et al. 2010] or mutations of essential regulators all die shortly after implantation [Lee 2000, 2002; Hoki et al. 2009, 2011; Shin et al. 2010]. Deleting effectors of the dosage compensation machinery in other organisms often results in early embryonic lethality as well. For example, female roundworms lacking proteins of the dosage compensation machinery die in early embryonic development, and male fruit flies lacking proteins of the male-specific lethal (MSL) complex or the essential roX RNAs perish during early embryogenesis due to impaired dosage compensation [Cline and Meyer 1996]. Finally, even female mice that are conditionally deleted for Xist only in the blood lineage die from highly lethal blood cancers with full penetrance [Yildirim et al. 2013]. Therefore, the ability of female mice to withstand a near-total loss of Xist across all organs was indeed highly surprising.

The lone survivor is a mosaic of XX and XO cells

One mutant female (F6) survived to adulthood and remained viable at 1 yr of age [Figs. 2C, 3A]. Like other Xist-null females, this animal was also runted at birth but gained substantial weight during the first 2 mo, although she consistently remained smaller than female littermates [Fig. 3B]. Xist RNA-FISH performed on TTFs confirmed the absence of Xist clouds in >95% of cells [Fig. 3C]. However, Xist DNA-FISH revealed that 76% of the diploid fibroblasts carried only one X chromosome [Fig. 3D]. We suggest that the high percentage of “XO” cells in female F6 rescued the lethality associated with biallelic deletion of Xist, as, indeed, XO cells would not require X-linked dosage compensation. In contrast, mutant animals that perished were not evidently XO females [Fig. 3D]. The ability of XO cells to rescue postnatal lethality supports the idea that the death of Xist-null mutants resulted from XCI-related effects and dosage imbalance.

Partial dosage compensation occurs in female mice lacking Xist RNA

Given the ability of Xist-null mutants to survive to term with apparently normal embryogenesis, we investigated whether dosage compensation might have occurred. To this end, we performed RNA sequencing (RNA-seq) for primary TTFs derived from three mutants and three control animals. Scatter plots of gene expression [read counts per million (CPM)] showed that, whereas autosomal gene expression in mutants did not deviate from that in controls, X-linked gene expression showed a net positive change, as evidenced by the offset of red counts from the diagonal [Fig. 4A; Supplemental Fig. S2A]. This observation suggested that the X chromosome was overexpressed in mutants and was supported by the orthogonal RT-qPCR approach that sampled a panel of X-linked genes from three mutants versus controls [Fig. 4B]. Cumulative distribution plots of fold changes from RNA-seq revealed a statistically significant rightward shift for X-linked genes relative to autosomal genes [P < 0.05, Wilcoxon rank sum test] [Fig. 4C; Supplemental Fig. S2B]. This was not observed for X-linked genes when comparing gene expression data from any one control with the average of two other controls. Probability density plots further argued for increased X-linked gene expression in mutant TTFs [filtered for CPM ≥ 1] [Supplemental Fig. S2C].

We then analyzed gene expression changes by binning fold change values in increments of 0.2 [Fig. 4D]. A substantial right shift in X-gene expression was also evident [average fold change 1.36] [Fig. 4D, left panel], whereas this was not observed for autosomal genes [average fold change 1.03] [Fig. 4D, left panel]. Interestingly, although ~12.5% of expressed X-linked genes were up-regulated by ≥1.8-fold, most changes fell between 1.0-fold and 1.8-fold. In fact, the average fold change was only 1.36—a value considerably below the doubling of X-linked expression expected of cells with two active X chromosomes [Fig. 4D, right panel, Supplemental Fig. S2C]. However, our empirical analyses showed that this theoretical doubling does not occur even in undifferentiated female ES cells that carry two active X chromosomes. In actuality, X-linked expression in female ES cells was, on average, 1.8-fold that of the single active X chromosome in male cells [Fig. 4D, right panel], a value in close agreement with previous studies [Nguyen and Disteche 2006; Lin et al. 2007; Deng et al. 2011; Kharchenko et al. 2011; Yildirim et al. 2012].

With the exception of F6 (who is partially XO), none of the mutant females survived beyond P24. Even in a non-nutrient-limiting environment, the Xist-null mice succumbed to sudden death. We examined this lethality more closely by sampling three different tissues [spleen, liver, and brain] from mutant and control females at P1 for RNA-seq. In agreement with data from fibroblasts, comparison of X versus autosomal gene expression changes showed significantly elevated X-linked gene expression in all three tissues [P < 0.05, Wilcoxon rank sum test] [Fig. 4E,F]. As with TTFs, the degree of up-regulation was modest in most X-linked genes. There was some variability in the severity of imbalance, with brain tissue demonstrating the most pronounced changes, while the liver showed the least deviation from control samples [presumably due to residual Xist-expressing cells] [Fig. 1H]. The tempered effect in the liver suggests that this tissue may be less tolerant of Xist loss and select for progenitors that retain at least one copy of Xist. Taken together, our data demonstrate that female mice lacking Xist show partial dosage compensation.

In principle, X-linked up-regulation could result from increased expression from a single X or partial expression from both Xs. To distinguish between these possibilities, we performed RNA-FISH for three X-linked genes—Med14, Msn, and Atrx—in mutant and control TTFs [Fig. 5]. Med14, a gene identified to be up-regulated in
the mutant TTF lines, showed significantly increased biallelic expression from 4.2% of control cells to up to 30% of mutant cells (P = 0.044) (Fig. 5). We also noted an increase in biallelic Msx expression (up to 13.3%) in the mutant TTF line, whose RNA-seq showed up-regulated bulk Msx RNA relative to controls (7.4%). This was not observed in mutant TTFs that did not demonstrate increased bulk Msx levels (mutants 2 and 3). Similarly, expression of Atrx RNA remained mostly monoallelic, correlating with minimal changes in Atrx levels observed by RNA-seq analysis. These results demonstrate a correlation between X-linked up-regulation and occurrence of biallelic expression and also imply the presence of an Xist-independent mechanism of dosage compensation in mice.

**X up-regulation tends to occur in regions with normally high Xist density**

We asked whether commonalities existed among X-linked genes that were up-regulated (≥1.2-fold, CPM ≥ 1) across the four cell/tissue types profiled. In each tissue type, hundreds of X-linked genes were up-regulated [Fig. 6C; Supplemental Tables S1, S2]. There was extensive overlap between biological replicates and between tissue types [Fig. 6A,B]. Gene ontology (GO) analysis for up-
Figure 4. Partial dosage compensation in Xist-null female mice. (A) Scatter plot for normalized read counts of all X-linked [red] and autosomal [black] genes in primary TTFs derived from control [Xist\textsuperscript{WT}; Sox2-Cre] versus Xist-null mutant [Xist\textsuperscript{+/−}; Sox2-Cre] mice. (B) RT-qPCR validation of RNA-seq data. Expression was normalized to β-actin. Data represent mean ± SEM of two replicate experiments. Data for six animals [three controls and three Xist-null mutants] are shown individually. (C) Cumulative distribution plots for fold changes in X-linked [red] and autosomal [black] genes in a control TTF line [relative to the average of other controls] [left], Xist-null TTF line [relative to the average of all controls] [middle], and female undifferentiated ES cells [relative to male ES cells] [right]. Only genes with CPM ≥ 1 were considered. P-values were given by Wilcoxon’s rank sum test. (D) [left] Distribution of X-linked [red] versus autosomal [white] fold changes in Xist-null TTFs relative to control cells. To minimize the effects due to noise, only genes with CPM ≥ 1 were considered. Fold changes are binned in steps of 0.2 (i.e., label of 0.2 on the X-axis includes all genes with fold changes between 0.0 and 0.2). Average fold changes of X-linked or autosomal genes are indicated. (Right) Distribution of X-linked [red] versus autosomal [white] fold changes in XX female ES cells relative to XY male ES cells. Average fold changes of X-linked or autosomal genes are indicated. (E) Cumulative distribution plots for fold changes in X-linked and autosomal genes [black] for the spleen [left], liver [middle], and brain [right] of the P1 Xist-null mutant relative to the average of age-matched control females. n = 2. Only genes with CPM ≥ 1 were considered. P-values were given by Wilcoxon’s rank sum test. (F) Distribution of X-linked versus autosomal fold changes for the spleen [left], liver [middle], and brain [right] of the Xist-null mutant from D relative to age-matched control females. n = 2. Only genes with CPM ≥ 1 were considered. Average fold changes of X-linked or autosomal genes are indicated.
regulated genes revealed consistent enrichment (adjusted \( P < 0.05 \)) of factors implicated in chromatin regulation, chromatin modification, and chromatin/chromosome organization for TTFs, the liver, and the brain [Supplemental Fig. S3]. The cluster of transcription elongation factor A-like genes (\( \text{Tceal5, Tceal6, Tceal7, and Wbp5} \)) on the X chromosome was enriched in the brain. Interestingly, genes known to escape X inactivation were also up-regulated. At the genome-wide level, differential expression analysis identified 266, 290, and 98 differentially expressed genes (DEGs) from the spleen, liver, and brain, respectively (false discovery rate < 0.05) (Supplemental Table S3A–C). GO analysis for DEGs did not identify significant enrichment for any processes in the liver and brain. However, DEGs in the spleen were highly enriched for proteases (Supplemental Table S3D).

The overlap in up-regulated X-linked genes across different cell/tissue types suggested that some chromosomal domains may be more prone to dosage imbalance in the absence of \( \text{Xist} \). To test this idea, we divided the X chromosome into 1-Mb bins and computed the frequency of gene up-regulation in each 1-Mb segment [Fig. 6D; Supplemental Fig. S4]. Up-regulated genes were found throughout the chromosome, and their occurrence was correlated with gene density \( (r = 0.53–0.68) \) [Supplemental Fig. S5]. Up-regulated genes were also generally correlated with regions with high-level \( \text{Xist} \) RNA binding, as determined by correlation analysis with published CHART-seq data sets [Simon et al. 2013]. Thus, up-regulated genes fell within or near regions targeted by \( \text{Xist} \) RNA in female cells undergoing XCI.

\textbf{Maturation defects of the spleen and heart}

Finally, to investigate proximal causes of death, we analyzed tissues from moribund pups and age-matched controls at P1 and P23. Mutants appeared grossly normal except for a general reduction in organ size, in keeping with the smaller stature of these animals [Fig. 7A; data not shown]. This indicated that body patterning and organogenesis were largely normal in spite of impaired dosage compensation. Hematoxylin and eosin (H&E) staining of the kidney, lung, and brain did not reveal any remarkable differences between \( \text{Xist} \)-null females and controls [Supplemental Fig. S6A,B]. In mice, postnatal developmental staging could be performed using the kidney, where the nephrogenic zone [consisting of immature glomeruli and nephrons undergoing proliferation] at P1 normally gives way to mature cortex and fully formed glomeruli by P23 [Little et al. 2007; Rinkevich et al. 2014; Romagnani et al. 2015]. This postnatal transition occurred in the kidneys of both mutant and control females [Fig. 7B]. Thus, \( \text{Xist} \)-deficient kidneys could in fact progress normally on a postnatal developmental time scale.

However, in spite of the capacity to progress postnatally, mutant females displayed abnormalities in several organs. First, the spleen failed to show the development of distinctive red and white pulp zones that was observed in controls on day 23 [Fig. 7C]. In fact, between days 1 and 23, mutant spleens remained the same size grossly and were disproportionately small. There was also a lack of histological organization [Fig. 7C, note the lack of red
and white pulp). The splenic phenotype is consistent with hematologic abnormalities observed in mouse models that either overexpress Xist or conditionally delete Xist in the blood compartment (Savarese et al. 2006; Yildirim et al. 2013) and further supports a critical role of Xist expression and dosage compensation for hematopoietic cells.

We also noticed abnormalities in the liver, with a darkening suggestive of hepatic congestion (Fig. 7A). Histologic analysis confirmed a hepatopathy consistent with...
venous congestion (Fig. 7D). Such venous congestion is often associated with right-sided cardiac failure. Interestingly, histologic examination of the heart revealed overall features of developmental delay at both day 1 and day 23 (Fig. 7E). During normal mouse development, the perinatal heart usually increases in size through hypertrophy of individual myocytes as the cytoplasm undergoes a dramatic enlargement (Naqvi et al. 2014; Alkass et al. 2015; Soonpaa et al. 2015). However, we observed overall smaller sizes of the heart that correspond to histologically immature cardiomyocytes in the mutant animals. Cells demonstrated a much higher nuclear to cytoplasmic ratio and had correspondingly more densely packed nuclei typical of prenatal embryonic hearts (Fig. 7E). Mutant cardiomyocytes therefore demonstrated features of an earlier development state. Aberrant development of cardiac tissue might thus have been inadequate to support the increasing circulatory demands of the neonates. We propose that aberrant postnatal development in the cardiac and hematologic compartments at least partially explains the observed sudden death of Xist-deficient females.

Figure 7. Xist-null mutants are grossly normal but show developmental defects of the spleen and heart. (A) Xist-null mutant and female control littersmates at P1. (B) H&E stainings for kidneys from one mutant and one control animal at P1 (top panel) and P23 (bottom panel). For each animal, H&E stainings are shown at two magnifications. Bars: lower magnification (4× or 10× objectives), 250 µm; higher magnification (20× objectives), 100 µm. (NZ) Nephrogenic zone; (CB) comma-shaped body, (SB) S-shaped body. (C) H&E stainings for spleens from one mutant and one control animal at P1 (day 1) and P23 (day 23). Bars (20× objective), 100 µm. (RP) Red pulp, (WP) white pulp. (D) H&E stainings for livers from one mutant and one control animal at P1 (day 1). Bars (20× objective), 100 µm. (E) H&E stainings for cardiac muscle from one mutant and one control animal at P1 (day 1) and P23 (day 23). Bars (40× objective), 25 µm.
Discussion

Work by Takagi and Abe [1990] previously showed that the persistent presence of two active X chromosomes is detrimental to early mouse development. The nature of their mouse model [involving a truncated X chromosome], however, made it difficult to distinguish between the effects of partial X monosomy during imprinted XCI versus increased dosage of X-linked genes during random XCI. $Xist$-null ES cells have been reported to demonstrate slower differentiation kinetics compared with their female wild-type counterparts, but no other phenotypes have been noted [Schulz et al. 2014]. Here, our goal was to examine the effects of total-body $Xist$ loss by decoupling the known effects on imprinted XCI in extraembryonic tissues [Marahrens et al. 1997] from those on random XCI in the soma. Surprisingly, deleting both copies of $Xist$ during early embryogenesis did not preclude female embryonic development and organogenesis. A quarter of the $Xist$-null mice survived to term. Since the conditional deletion was driven by a Sox2-Cre recombinase, the loss most likely occurred prior to the initiation of XCI in pre-gastrulation embryos. Indeed, $Xist$ ablation is mostly complete by E8.5, and the recovery of $Xist^{+/+}$, Sox2-Cre embryos already displaying developmental defects at this stage points to loss of $Xist$ at early time points, either before or around the time of XCI initiation [Fig. 2]. This is further supported by extremely skewed XCI patterns in heterozygous $Xist$ mutants [Fig. 1C], indicative of a primary choice for the wild-type X to become the inactive X chromosome. Nevertheless, we cannot rule out deleterion events occurring after the establishment of XCI in rare cells where Cre recombinase might persist briefly. Although the proportion of cells with pre-XCI versus post-XCI deletion events could vary between embryos, we suspect that a large number of cells in any embryo never initiated XCI through an $Xist$-dependent mechanism.

Another surprising finding to emerge from this study is that, while hundreds of X-linked genes were consistently overexpressed across multiple organs and tissues, the magnitude of X-linked overexpression fell far short of the expected doubling that would be commensurate with two active X chromosomes. In plants and fruit flies, the expected doubling that would be commensurate with two active X chromosomes is 100% overexpression across multiple organs and tissues, the magnitude of X-linked overexpression ranged only between 10% and 30% overall, this small deviation from dosage equivalence resulted in significantly decreased overall organismal fitness.

Materials and methods

Animal studies

$Xist^{+/+}$ mice (in a 129Sv/Jae background) were a gift from R. Jaenisch [Csankovszki et al. 1999]. Tg[Sox2-Cre]1Amc/J animals [jax 004783] were procured from the Jackson Laboratory. All progeny are maintained on a 129Sv/Jae and C57BL/6 mixed background. Genotypings of the $Xist^{WT}$ and $Xist^{−/+}$ alleles were carried out using the 370/389 primer pair. Sox2-Cre genotyping was performed using the Cre-3F/3R primer pair. For harvesting of embryos, pregnant females were humanely sacrificed at 8.5 d post-coitum [dpc] for $Xist^{WT}$, Sox2-Cre or 14.5 dpc [for $Xist^{−/+}$]. The morning of copulation plug detection was considered 0.5 dpc. Sexing of embryos was performed by PCR using the NS18/19 [Tsx1] and Zfy1.8b/YNL5.5 [Zfy1] primer pairs and was confirmed by DNA-FISH using a Y-chromosome BAC probe [see below]. Primers are listed in Supplemental Table S4. Embryonic fibroblasts were isolated using standard procedures. Mouse husbandry and experiments were carried out as stipulated by the Massachusetts General Hospital Institutional Animal Care and Use Committee [IACUC].

Isolation of TTFs

One centimeter of tail tissue was snipped from neonates between P1 and P3. Tissue was rinsed sequentially in betadine solution, 70% ethanol, and 2× penicillin/streptomycin and minced finely. The slurry was incubated with TrypLE Select [Thermo Fisher Scientific] for 30 min at 37°C, plated, and cultured at physiological O2 (4.0% O2, 5.0% CO2).

DNA-FISH, RNA-FISH, and immunostaining

For TTFs, cells were grown on glass coverslips and fixed in 4% paraformaldehyde before permeabilization with 0.2% Triton-X in PBS at room temperature. For E8.5 embryos, cells were dispersed using TrypLE Select [Thermo Fisher Scientific] and immobilized onto glass slides by centrifugation [Shandon Cytospin]. Cells were pre-extracted in ice-cold cytokeskeletal buffer with 0.5% Triton-X and then fixed with 4% paraformaldehyde. DNA-FISH and RNA-FISH were performed according to established protocols [Zhang et al. 2007; Sunwoo et al. 2015]. The
probes used for RNA-FISH were Xist-, Med14-, and Msn-labeled oligo probes; the probe for Atrx was nick translation of BAC RP23-450B21. The probes used for DNA-FISH were RP24-386011 for chromosome 8, RP24-148H21 for chromosome X, and RP24-332J21 for chromosome Y (all BAC probes labeled by nick translation) and nick translation of PCR product from Xist1.3F/Xist1.3R primers for the Xist locus between loxP sites [Supplemental Table S4]. Mouse monoclonal H3K27me3 anti-body (1:300 in 1% BSA/PBS, Active Motif, 39535) was used for immunostaining. Images were acquired with a Nikon Eclipse 90i microscope and a Hamamatsu CCD camera. Image analysis was performed using Volocity (Perkin-Elmer).

RNA isolation from mouse tissues, reverse transcription, and qPCR

Mouse tissues (~100 mg) were collected into RNALater (Qiagen) at the time of dissection and mechanically homogenized in Trizol using a Tissue Lyzer II (Qiagen) at 25 Hz twice for 2 min. RNA is isolated by phenol–chloroform extraction. For reverse transcription, cDNA was prepared using SuperScript III [Thermo Fisher Scientific] with random hexamers (Promega). qPCR was performed using iTaq Universal SYBR Green Supermix (Bio-Rad), and relative gene expression was calculated by the standard curve method. The primers used are listed in Supplemental Table S4.

Strand-specific RNA-seq

Four micrograms of total RNA [RIN value ≥8] from fibroblasts or mouse tissues was depleted of ribosomal RNA (RibopMinus eukaryote kit version 2, Thermo Fisher Scientific) as per the manufacturer’s recommendations, DNase-treated for 30 min at room temperature, and purified using an RNasy minulete cleanup kit (Qiagen). Eluted RNA was then quantified (Quant-iT Ribogreen RNA assay, Thermo Fisher Scientific), and 30 ng of RNA was fragmented in 6 mM MgCl₂ buffer for 10 min at 94°C before first strand [SuperScript III, Thermo Fisher Scientific] and second strand [NEBNext Ultra Directional RNA second strand synthesis module, New England Biolabs] cDNA synthesis. Adaptor oligos were ligated to the cDNA library [NEBNext Chip-seq library master mix, New England Biolabs]. Libraries were amplified with multiplexing barcodes [NEBNext Multiplex Oligos for illumina, New England Biolabs] and quantified [Kapa library quantification kit, Kapa Biosystems] before 50-nucleotide paired-end sequencing was performed on an Illumina HiSeq 2000 or HiSeq 2500. All sequencing data can be accessed via Gene Expression Omnibus under accession number GSE84665.

RNA-seq analysis

Sequencing reads were first checked for quality by FastQC [http://www.bioinformatics.babraham.ac.uk/projects/fastqc] before alignment with TopHat2 [Kim et al. 2013] to the mouse reference genome [GRCm38/mm10]. Read counting was performed using HTSeq-count [Anders et al. 2015] against all ENSEMBL transcripts [ENSEMBL release 84]. Normalization and differential expression analysis were performed using the EdgeR package [Robinson et al. 2010]. For analyzing distributions of gene expression fold changes on chromosome X and autosomes, only genes with CPM ≥ 1 were considered. For undifferentiated ES cell analysis, a published RNA-seq data set [Gendrel et al. 2014] (SRA124266) was downloaded from the European Nucleotide Archive and processed similarly for analysis.

Histopathology

Tissues were fixed in 10% neutral buffered formalin [Fisher Scientific] overnight and stored in 70% ethanol for further processing. Sections were stained with H&E. Images were acquired using a Nikon Eclipse 90i microscope and a Q-imaging MicroPublisher RTV color camera. Image analysis was performed with Volocity [Improvement, Perkin-Elmer].

Acknowledgments

We thank R. Jaenisch for Xist<sup>fl/fl</sup> mice, R. Mostoslavsky, K. Hochedlinger, W. Bender, B. Payer, and the Lee laboratory for valuable advice and feedback; D. Lessing, T. Dial, and B. del Rosario for critical reading of the manuscript, and W. Press for mouse colony maintenance. This work was supported by grant funding from the Agency for Science, Technology, and Research of Singapore [to L.Y.], the National Institutes of Health [DA-R01-36895 to J.T.L.], and the Rett Syndrome Research Trust [to J.T.L.]. J.T.L. is also an Investigator of the Howard Hughes Medical Institute.

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