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Gene targeting of CK2 catalytic subunits

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Abstract

Protein kinase CK2 is a highly conserved and ubiquitous serine–threonine kinase. It is a tetrameric enzyme that is made up of two regulatory CK2 β subunits and two catalytic subunits, either CK2 α /CK2 α , CK2 α /CK2 α' , or CK2 α' /CK2 α' . Although the two catalytic subunits diverge in their C termini, their enzymatic activities are similar. To identify the specific function of the two catalytic subunits in development, we have deleted them individually from the mouse genome by homologous recombination. We have previously reported that CK2 α' is essential for male germ cell development, and we now demonstrate that CK2 α has an essential role in embryogenesis, as mice lacking CK2 α die in mid-embryogenesis, with cardiac and neural tube defects.

Keywords

Protein kinase CK2; Casein kinase II; Homologous recombination; Wnt signaling; Embryonic development

CK2 is a ubiquitous and highly conserved serine–threonine kinase. It is overexpressed in many human cancers, and we have shown that tissue-specific overexpression in transgenic mice leads to malignancy [1, 2]. One of the mechanisms of cellular transformation may be activation of the Wnt pathway, as CK2 is sufficient and necessary for stabilizing the key transcriptional co-factor in Wnt signaling, β -catenin [3–5]. CK2 can be found in transcriptional complexes on Wnt-target genes [6] and is activated by Wnt signaling [7]. In *Xenopus laevis*, CK2 is required for proper development of the dorsal axis of the embryo [5,

8]. In mice, *CK2 β* is required for early embryonic development, and perhaps cell-autonomous growth [9]. We have previously shown that *CK2 α '* is highly expressed in mouse testis and brain and is required for normal male germ cell development [10]; no central nervous system phenotype has been found. In the testis, *CK2 α '* appears to protect developing spermatocytes from apoptosis, and deficiency leads to oligospermia and abnormal development of the sperm head (Fig. 1). We now have found that the more abundant and widely expressed *CK2 α* subunit is required for mouse embryonic development. This report summarizes additional features of these knockout mice, first described in [11].

Methods

Gene targeting

Long-range PCR was used to amplify *CK2 α* genomic DNA from a 129SvEv BAC clone. Arms were cloned into the pPNT targeting vector, which allows for positive and negative selection [12]. This construct (Fig. 2a) was electroporated into TC1 ES cells [13] grown on mitomycin-treated mouse embryonic fibroblast feeders in medium supplemented with 5×10^5 U ESGRO-LIF (Chemicon). Integration of the plasmid was selected for in 260 $\mu\text{g/ml}$ G418 (Gibco), and cells with homologous recombination were enriched using 0.1 μM FIAU. DNA was prepared from surviving ES cell clones, and homologous recombinants were identified by PCR and Southern blot (Fig. 2b). Clones with containing a targeted *CK2 α* allele were microinjected into C57Bl/6 blastocysts. All animal experimentation was performed with approval of the Boston University Medical Center IACUC and with the assistance of the Lab Animal Sciences Center and Transgenic Core Facility. High-grade chimeric mice with nearly 100% agouti coats were bred with wildtype (WT) C57Bl/6 females to test for germline transmission of the targeted *CK2 α* allele. F1 offspring were screened by PCR and Southern blot to identify heterozygous *CK2 α ^{+/-}* mice. These were mated together to attempt to derive homozygous *CK2 α ^{-/-}* offspring. Timed matings were performed and embryos were harvested to determine the developmental phenotypes. Fixed embryos were prepared for light and electron microscopic analysis and in situ hybridization as described [10, 14]. *CK2* expression and activity were determined by in situ hybridization, immuno-blotting, and kinase assay using the *CK2*-specific peptide substrate RRREEETEEE (Sigma-Genosys) [15]. Background kinase activity in the absence of the peptide substrate was subtracted; P values were assessed by ANOVA, and Bonferroni correction was applied for multiple comparisons.

Whole mount in situ hybridization

For in situ hybridization, embryos were fixed in 4% para-formaldehyde/PBS, dehydrated, and stored at -20°C . Prior to hybridization, embryos were rehydrated, bleached in 6% H_2O_2 , permeabilized with 10 $\mu\text{g/ml}$ proteinase K, post-fixed in 4% paraformaldehyde, 0.2% glutaraldehyde in PBT (1 \times PBS, 0.1% Tween), and pre-hybridized. Hybridization was performed at 70°C with digoxigenin-labeled probes transcribed from linearized plasmids (pBS-En-1 for engrailed-1, pSK75-T for brachyury, and pBS-mShh for mouse sonic hedgehog) using a DIG RNA Labeling Kit (Roche). After hybridization, embryos were washed, blocked in 10% lamb serum in PBT, and incubated with antibody in 10% lamb serum and PBT. Embryos were washed and treated with NBT/BCIP (4-nitro blue tetrazolium chloride/5-bromo-4-chloro-3-indolyl-phosphate) and postfixed with 4% paraformaldehyde, 0.1% glutaraldehyde in PBS.

RNA isolation and RT-qPCR

RNA was extracted with Trizol[®] (Invitrogen), DNase I treated, and cDNA was prepared from 1 μg total RNA using the BioRad iScript cDNA Synthesis Kit. Quantitative PCR

(qPCR) was carried out in a 25 μ l iTaq Sybr Green reaction (BioRad), in the presence of 400 nM of each primer in a Stratagene mx3000P real-time PCR machine. Primers included: En1_for (ACACAACCCTGCGATCCTAC); (GATATAGCGGTTTGCCTGGA); HPRT 5' (GTTGGAT ACAGGCCAGACTTTGTTG); HPRT 3' (GAGGGTAGG CTGGCCTATAGGCT); T_for (ATCAAGGAAGGCTTT AGCAAATGGG); and T_rev (GAACCTCGGATTCACA TCGTGAGA). Samples were analyzed in duplicate. Ct was determined for each sample, and copy number was determined using a standard formula: $10^{(Ct - 40)/-3.32}$. When comparing samples, transcript copy number was normalized to the copy number for HPRT.

Results and discussion

Electroporation and positive and negative selection of ES cells led to the identification of clones of cells that had acquired the targeted CK2 α allele, in which the critical ATP-binding residue of CK2 α at lysine 68 was replaced with a neomycin resistance cassette. These were identified by PCR and Southern blot (Fig. 2b). When clones were injected into blastocysts, high grade chimera were obtained. These were bred to obtain heterozygous CK2 $\alpha^{+/-}$ F1 mice. These mice were developmentally and histologically normal and fertile. However, crosses of these failed to yield any CK2 $\alpha^{-/-}$ offspring in more than 30 litters. The ratio of CK2 $\alpha^{+/+}$ to CK2 $\alpha^{+/-}$ offspring was 1:2, consistent with the expected frequency for an embryonic lethal phenotype of CK2 $\alpha^{-/-}$ mice. Thus, timed matings were performed to generate embryos of varying genotypes and ages for analysis. No viable embryos were recovered beyond about e12.5; at e13.5 and e14.5, runted degenerating CK2 $\alpha^{-/-}$ embryos could be seen (Fig. 3a). Embryos up until e10.5 were viable. Some embryos were smaller and were found to have evidence of heart failure and pericardial edema (Fig. 3b) like the syndrome of *hydrops fetalis* that occurs with severe anemia or cardiac defects in humans. In examining earlier embryos, a variety of defects of the developing heart were noted (Fig. 4). In the CK2 $\alpha^{-/-}$ embryos, the formation of the four-chambered heart was markedly defective. An open heart tube persisted, with an enlarged endomyocardial cavity with a thin and disorganized endothelial lining with defective trabeculation and a thin atrial wall. The surface ectoderm and developing pericardium were also abnormal (Fig. 4b).

A second major phenotype was defects in the development of the neural tube and brain. In the CK2 $\alpha^{-/-}$ embryos, neural tube closure failed to occur at the level of the future midbrain in more than 90% of the CK2 $\alpha^{-/-}$ embryos; this was seen in 13% of heterozygous embryos and never observed in control WT embryos (Fig. 5a). Failure of neural tube closure does not interfere with specification of brain regions, as the homeobox gene engrailed-1 (En-1) mRNA was still expressed at the site of the midbrain/hindbrain junction by whole mount in situ hybridization (Fig. 5b). En-1 was similarly expressed in WT and KO embryos by both semiquantitative RT-PCR (Fig. 5b) and quantitative real-time PCR (data not shown). The expression pattern and quantitative expression of sonic hedgehog mRNA, Shh, were also similar in WT and KO embryos, staining both the notochord and floorplate of the neural tubes (Fig. 5c).

Abnormalities of tailbud development were seen in the CK2 $\alpha^{-/-}$ embryos, which typically had broadened shovel-shaped tails, that were well visualized by staining for the T-box gene brachyury (Fig. 6). Brachyury was well-expressed in the abnormal tails, but at higher power, a reduction in anterior (cranial) staining for brachyury mRNA was visible. Additional phenotypes that were noted include underdevelopment of the limb buds, branchial arches, and otic and optic vesicles (not shown).

CK2 $\alpha^{-/-}$ knockout embryos were confirmed to have no CK2 α mRNA or 42 kDa protein but had similar amounts of the 38 kDa CK2 α' protein as their littermate controls (Fig. 7),

suggesting no compensatory mechanism of CK2 α upregulation. Heterozygous CK2 $\alpha^{+/-}$ embryos had about half the CK2 α protein as the WT embryos (Fig. 7). While expression of the CK2 β subunit in the heterozygote and WT embryos was not strikingly different, the null embryos had reduced CK2 β protein. This is similar to what has previously been observed in CK2 α knock-down experiments, where CK2 β mRNA were unchanged ([16], and data not shown). Interestingly, CK2 β subunits are stabilized when integrated in the tetrameric holoenzyme [17], while free β subunits are ubiquitinated and subject to rapid proteosomal degradation [18]. In the null embryos, lack of CK2 α could subject a greater free pool of CK2 β subunit to degradation, leading to reduced steady state CK2 β levels.

Kinase activity measurements on CK2 $\alpha^{+/+}$, CK2 $\alpha^{+/-}$, and CK2 $\alpha^{-/-}$ embryo littermates at e10.5 showed highest activity in the CK2 $\alpha^{+/+}$ embryos, intermediate in the heterozygotes and lowest in the null embryos (Fig. 8); residual CK2 kinase activity in the KOs presumably reflects the presence of CK2 α , and expression of CK2 α likely rescues expression during earlier embryogenesis.

Preliminary data indicated that a variety of potential CK2 targets and pathways were disrupted in the CK2 $\alpha^{-/-}$ embryos, including abnormalities in Wnt pathway genes and proteins (I. Dominguez, unpublished data). These results are very provocative, because deletion of genes in the Wnt pathway also leads to defective development of brain and heart (Fig. 9). The Wnt transcriptional co-factor β -catenin is required for normal heart formation [19, 20], and the Wnt target *cripto* is required for differentiation of cardiogenesis and neural tube formation [21–24]. Wnt1 and Wnt3a are required for brain development [25–29]. The Wnt signaling intermediates of the dishevelled Dvl family are required for normal closure and apposition of the neural folds [6]. Thus, our data are consistent with the hypothesis that regulation of the Wnt pathway by CK2 α is critical in mouse development, as it is in *Xenopus laevis* development [5, 8]. This hypothesis will be validated in future molecular experiments and through rescue experiments designed to determine whether the CK2 $\alpha^{-/-}$ knockout phenotypes can be complemented by expression of elements of the Wnt pathway.

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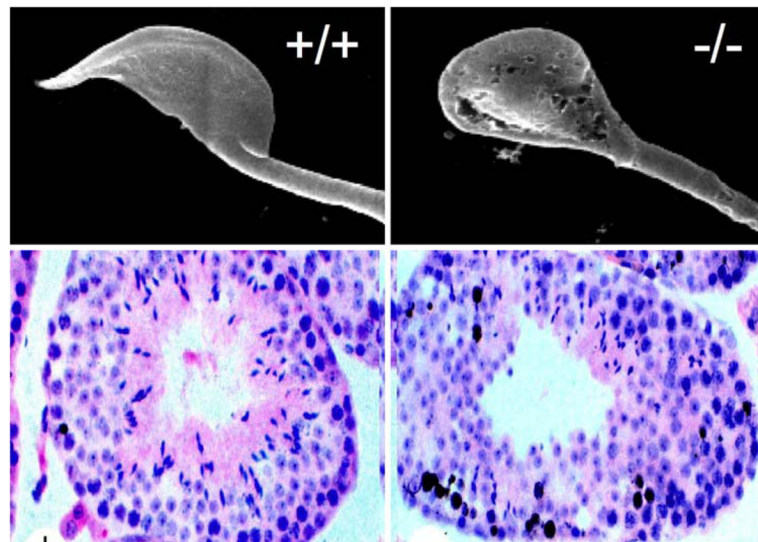


Fig. 1. Male $CK2\alpha^{-/-}$ knockout mice have abnormal sperm development. By scanning electron microscopy (upper panel), defective development of the normally sickle-shaped mouse sperm head is seen. This phenotype is reminiscent of the human globozoospermia (round-headed sperm) syndrome in humans. In cross sections of the seminiferous tubules, the knockouts were found to have an increased number of apoptotic precursor cells, identified by TUNEL staining (lower panel)

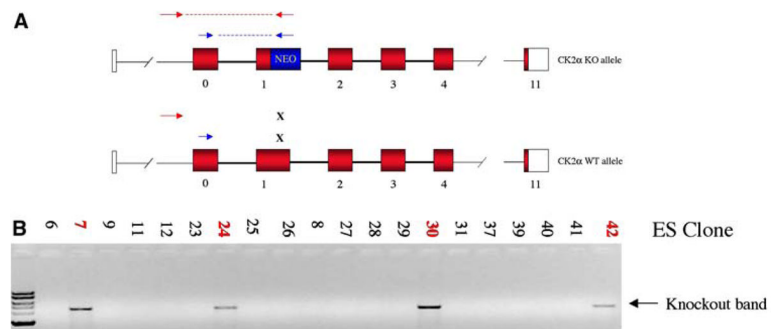


Fig. 2. *CK2a* targeting strategy. A schematic of the targeted and endogenous alleles are shown (a), with the location of PCR primers that detect any recombination event (blue arrows) or homologous recombination (red arrows). These primers were used to screen pools and then individual clones; four clones that have been targeted homologously and selected in G418 and FIAU can be seen, numbers 7, 24, 30, 42 (b)

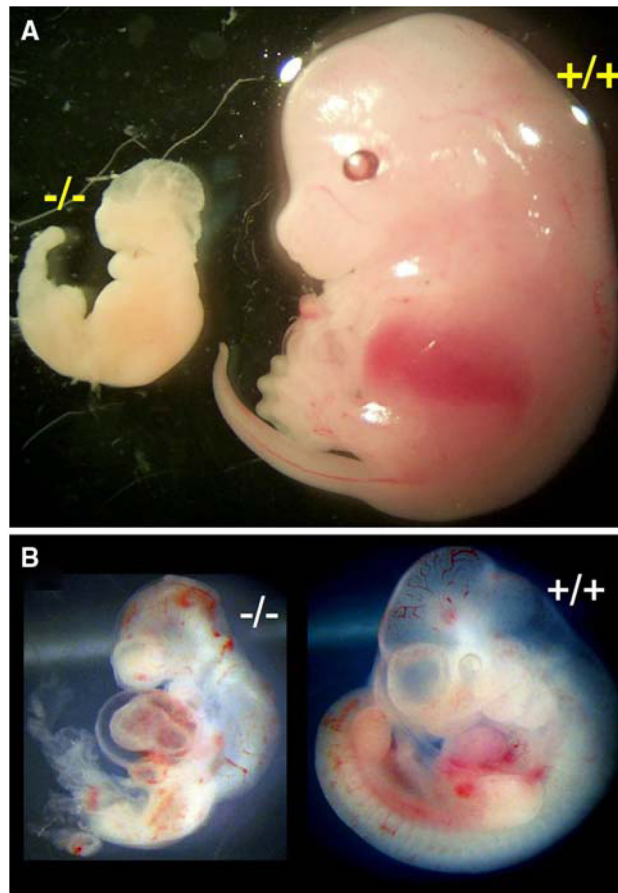


Fig. 3. Abnormal $CK2\alpha^{-/-}$ embryos. Since no viable $CK2\alpha^{-/-}$ pups were found, timed matings were performed to determine the phenotype of the homozygous $CK2\alpha^{-/-}$ embryos. Beyond about embryonic day 12.5, no viable embryos were found, but runted and degenerating embryos were seen (**a**, e14.5). Beginning at e10.5, the $CK2\alpha^{-/-}$ embryos were smaller and some had evidence of heart failure, with a fluid-filled pericardium (**b**)

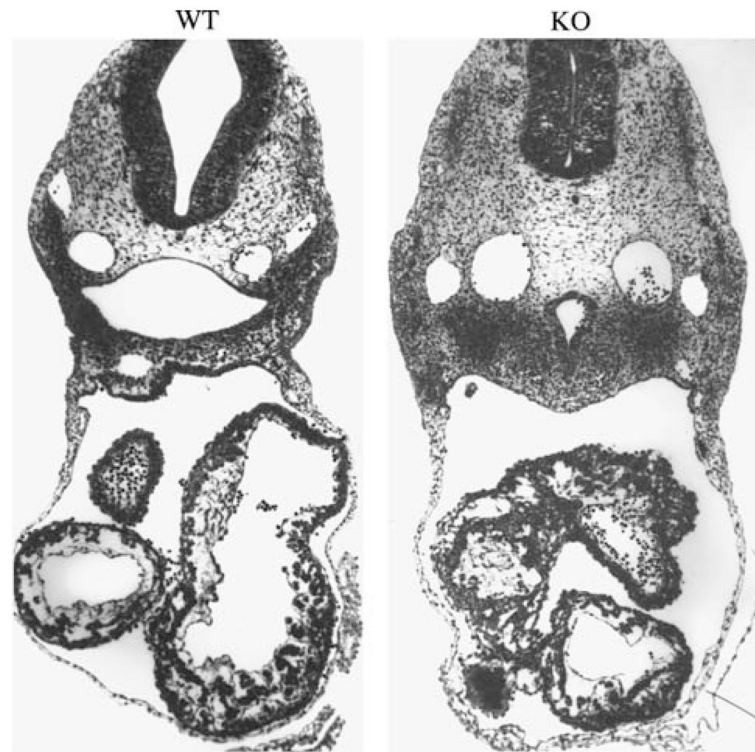


Fig. 4. Cross sections of WT and KO embryos at e10.5 demonstrate the collapse of the open neural tube in the KO, top, and the delayed chambering and reduced trabeculation in the KO heart

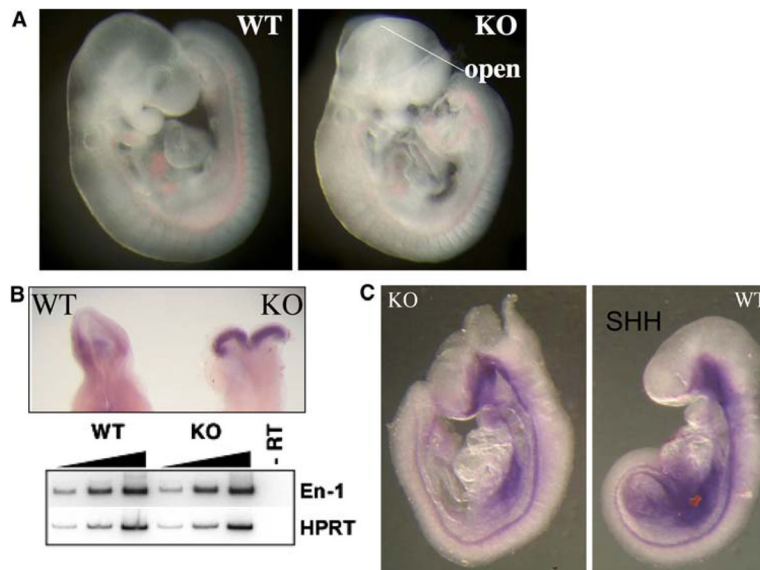


Fig. 5. Neural tube defects. By e9.5, the neural folds should have met and fused along the dorsum of the embryo, but in *CK2α*^{-/-} embryos, this process fails, leading to collapse of the neural tube and failure of brain development to progress (compare WT and KO, panel **a**). The midbrain/hindbrain junction is delineated by in situ hybridization for En-1 mRNA (panel **b**, upper), which is expressed in similar levels by both semiquantitative RT-PCR (panel **b**, lower) and quantitative real-time PCR. The expression pattern and quantitative expression of sonic hedgehog mRNA, *Shh*, were also similar in WT and KO embryos, staining both the notochord and floorplate of the neural tubes (**c**)

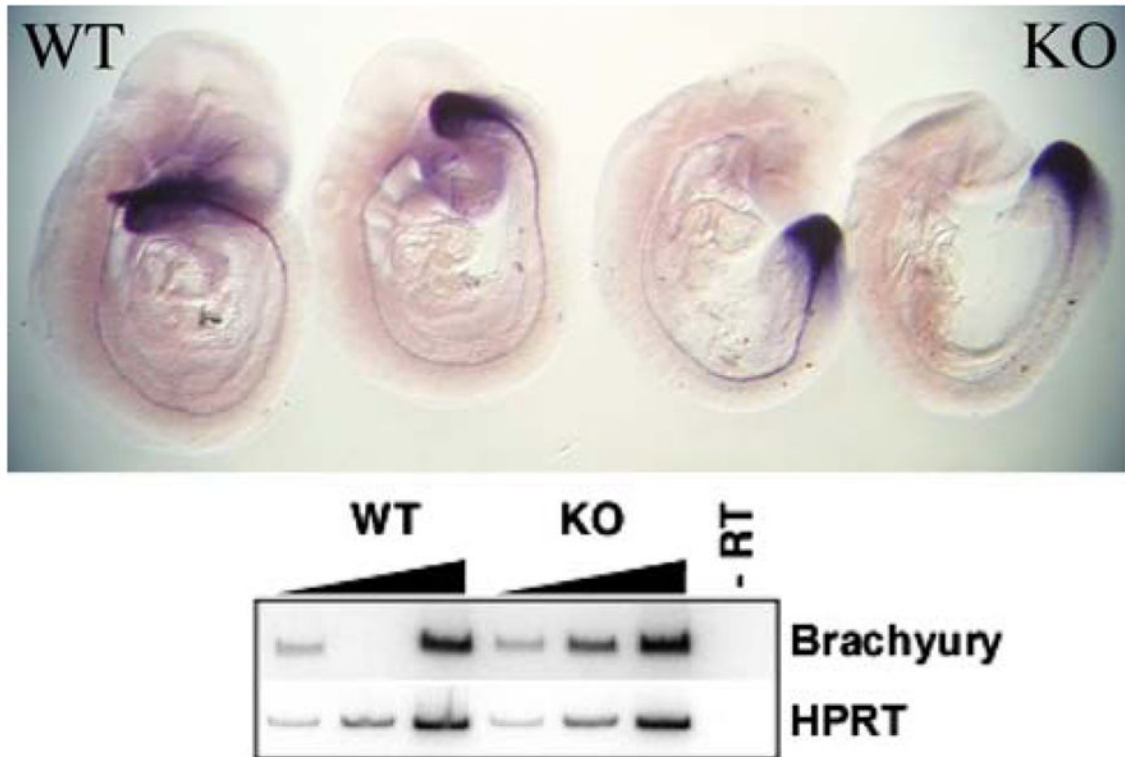


Fig. 6. Abnormal tail bud morphology in the *CK2a* KO embryos. Embryos were stained for brachyury mRNA. As can be seen in the upper panel, the tails, where brachyury is heavily expressed, were broadened in the *CK2a* KO embryos compared to those of the WT embryos. A reduction in the anterior expression of brachyury can be appreciated at higher magnification. Overall expression is similar by both RT-PCR (lower panel) and quantitative real-time PCR

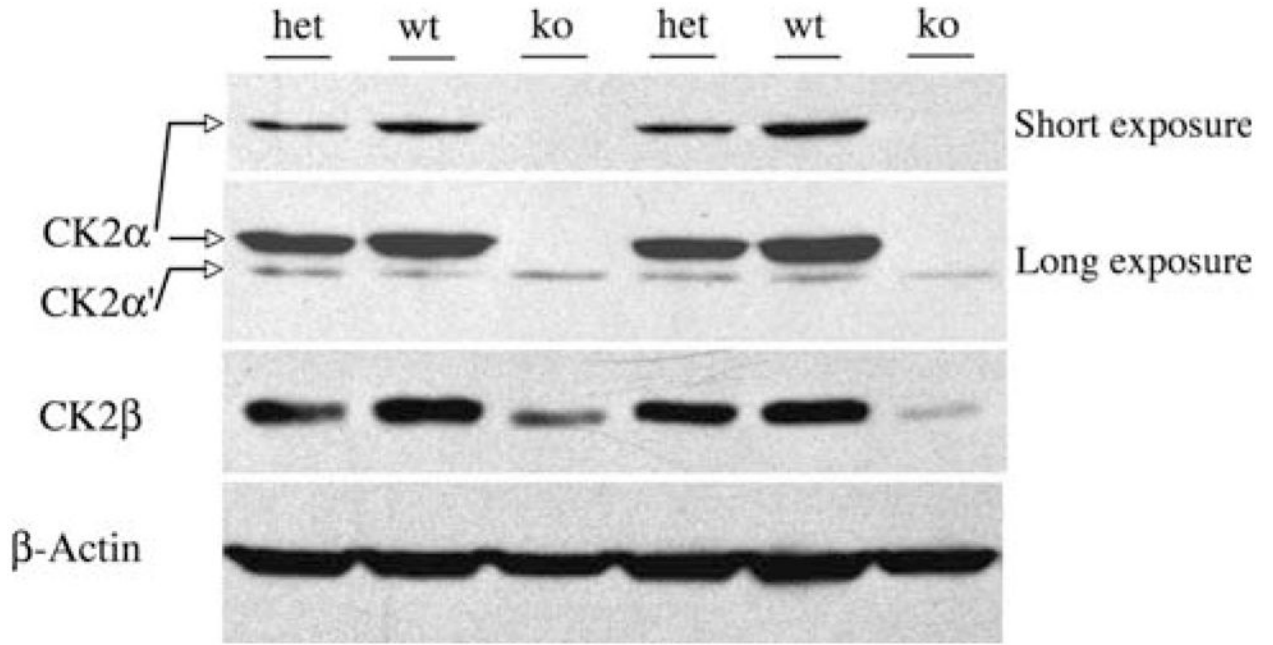


Fig. 7.

Alteration in CK2 subunit proteins in *CK2a* deficient embryos (e10.5). Two sets of embryos are shown, lanes 1–3 and 4–6. As can be seen in the short exposure of equally loaded embryonic proteins (top panel), *CK2a* protein expression is reduced in the *CK2a*^{+/-} heterozygous embryos (het) and lost in the *CK2a*^{-/-} KOs (ko), compared with wildtype *CK2a*^{+/+} (wt) mice. A longer exposure (second panel) confirms the absence of *CK2a* expression in the KOs and demonstrates that *CK2a*' expression is similar in all genotypes. In the third panel, a reduction in *CK2β* protein is seen in the *CK2a*^{-/-} KO embryos. The bottom panel shows the actin control blot for loading

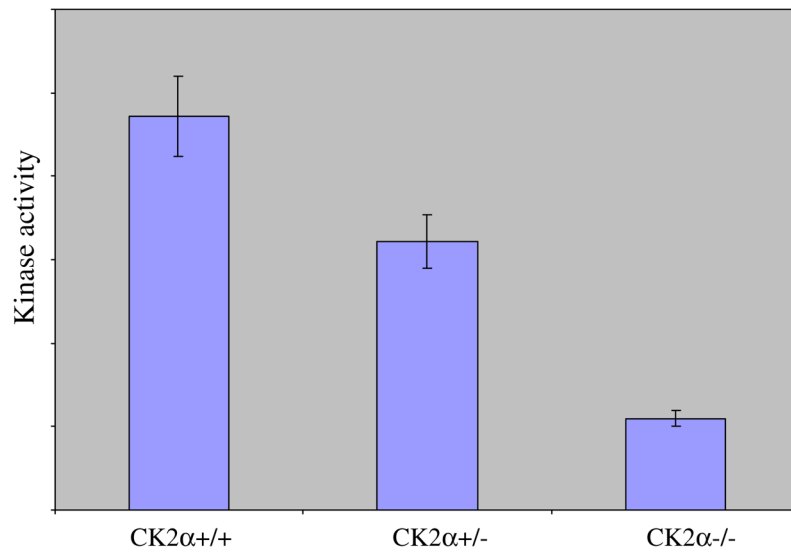
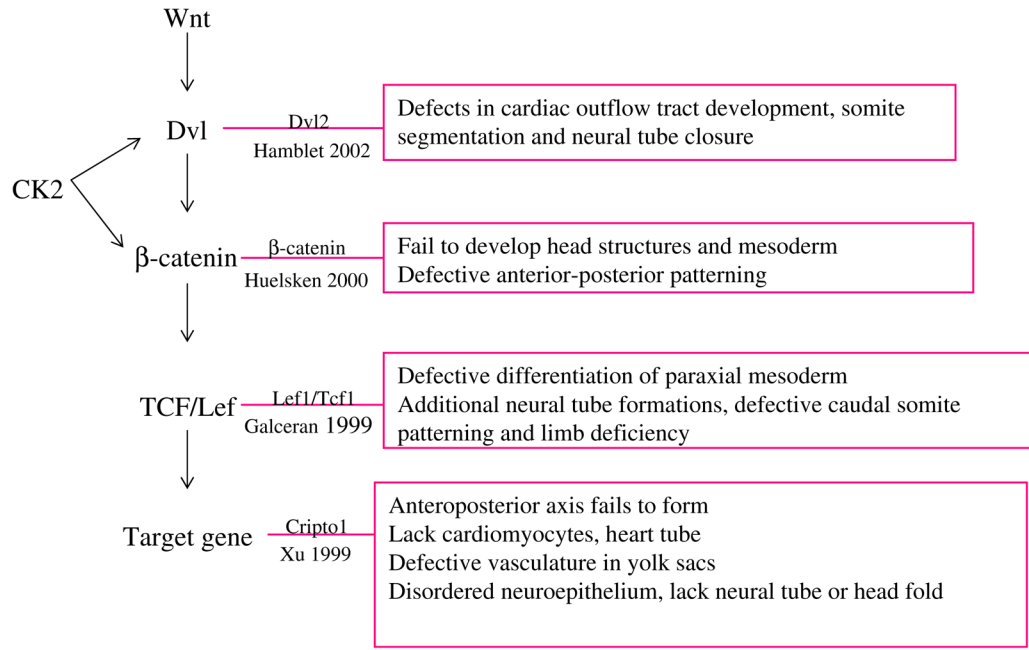


Fig. 8. Reduced CK2 kinase activity in CK2α^{+/-} and CK2α^{-/-} embryos (e10.5). Using the CK2 peptide substrate, kinase activity was reduced by 32% ($P=0.0002$) in the heterozygous embryos and by 77% ($P=0.0001$) in the homozygous deficient embryos, compared to wildtype. Residual CK2 activity is presumably due to the presence of the CK2α gene and protein

**Fig. 9.**

Comparison of CK2 knockout defects and Wnt pathway knockout defects, with a schema to indicate where in the pathway CK2 is believed to act. Both Dvl and β -catenin have been shown to be direct CK2 targets, and thus loss of CK2 is predicted to lead to downregulation of Dvl, β -catenin, and downstream Wnt signaling. Defects of embryos in which Dvl2 [30], β -catenin [19], the transcription factor Lef1/ Tcf1 [31], and the putative Wnt target gene Cripto1 [21] are described