

Correction

Correction: Transcriptional Profiling of Wnt3a Mutants Identifies Sp Transcription Factors as Essential Effectors of the Wnt/ β -catenin Pathway in Neuromesodermal Stem Cells

The PLOS ONE Staff

The genotypes displayed in Figure 4 are incorrect. The genotype of the embryo depicted in Figure 4B should read $Sp5^{lacZ/lacZ}; Wnt3a^{+/+}$. The genotype of the tail shown at the top of Figure 4E is $Sp5^{lacZ/+}; Wnt3a^{+/+}$, and in Figure 4F, the second bar on the left represents the genotype $Wnt3a^{+/-}$.

Please see the corrected Figure 4 here.

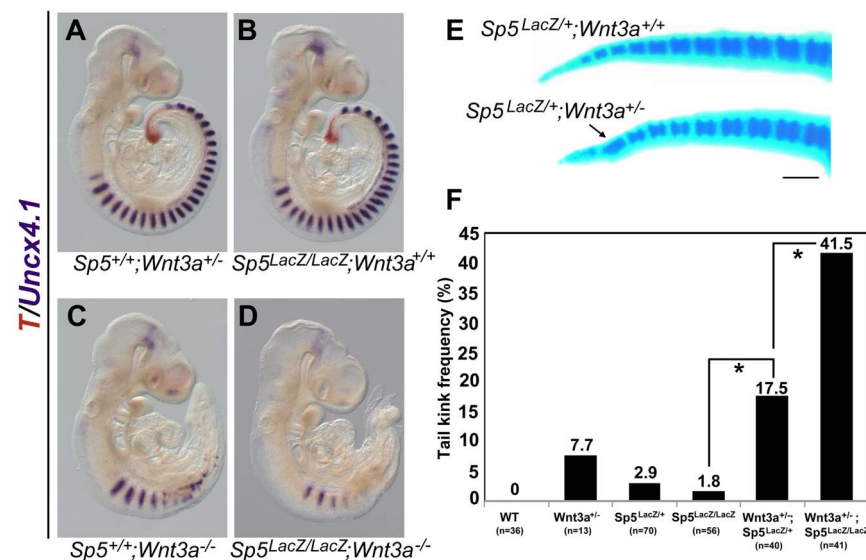


Figure 4. Genetic interactions between Sp5 and Wnt3a during tail development. (A-D) Two-color WISH illustrating Uncx4.1 (purple) and T (orange) in $Sp5^{+/+}; Wnt3a^{+/-}$ (A), $Sp5^{lacZ/lacZ}; Wnt3a^{+/+}$ (B), $Sp5^{+/+}; Wnt3a^{-/-}$ (C), and $Sp5^{lacZ/lacZ}; Wnt3a^{-/-}$ double mutants (D) at E9.5. Double mutants ($n = 8$) display fewer and less-defined Uncx4.1 expressing anterior somites as compared to stage-matched $Wnt3a$ null embryos. (E) At E18.5, $Sp5^{lacZ/+}; Wnt3a^{+/-}$ animals (bottom) display abnormal, fused tail vertebrae (arrow) compared to $Sp5^{lacZ/+}; Wnt3a^{+/+}$ mice (top). (F) Frequency of tail kinks (expressed as %) observed in $Wnt3a^{+/-}$ heterozygotes at 6 weeks of age increased dramatically as the $Sp5$ gene dosage was reduced. The number of animals examined (n) is indicated below each genotype. *, statistical significance ($p < 0.0001$, Chi-squared t-test). Scale bar = 500um (E). doi:10.1371/journal.pone.0087018.g004

Reference

1. Dunty WC Jr, Kennedy MWL, Chalamalasetty RB, Campbell K, Yamaguchi TP (2014) Transcriptional Profiling of Wnt3a Mutants Identifies Sp Transcription Factors as Essential Effectors of the Wnt/ β -catenin Pathway in Neuromesodermal Stem Cells. PLoS ONE 9(1): e87018. doi:10.1371/journal.pone.0087018

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