

The Fanconi Anemia Pathway is Functionally Conserved in *Xenopus*

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The majority of FA proteins lack recognizable motifs making predictions about their domain structures and molecular functions challenging. One strategy that could enable recognition of functionally important domains is to compare evolutionary conservation of the protein sequences among different species. Orthologs of the human FA genes *FANCA*, *-C*, *-E*, *-F* and *L* were identified in the *X. laevis* sequence database, with statistically significant E values. The *Xenopus* FA orthologs show striking regional homologies with their human FA counterparts and overall homologies as listed in Table 1.

	FANCA	FANCC	FANCD2	FANCE	FANCF	FANCG	FANCL	FANCD1/ BRCA2
<i>Xenopus laevis</i>	✓	✓	-	✓	✓	-	✓	-
Percent homology to human	53.1%	52.2%	-	41.1%	42.8%	-	79.0%	-

Table 1. (✓) Indicates an ortholog found for the particular gene listed. An (-) indicates no ortholog positively identified. The *X. laevis* genome has not been completely sequenced.

One of the key indicators of FA pathway function is the DNA damage dependent appearance of the ubiquitylated form of FANCD2 (FANCD2-L). To determine if this aspect of FA protein function is mirrored in *Xenopus* cells, FANCD2 ubiquitylation was evaluated in a tadpole derived *Xenopus* cell line (XTC-2). Bands co-migrating with human FANCD2-L and FANCD2-S were detected in XTC-2 lysates, with similar changes in distribution following treatment of XTC-2 cells with cross-linking agents. Finally, XTC-2 cells treated with MMC or DEB contained radials and breaks, the hallmark chromosomal abnormalities of FA. Taken together, these data suggest that the FA pathway is functionally conserved in *Xenopus*.