



PARTIAL CHARACTERIZATION OF THE PITX1 GENE OF EMPETRICHTHYINE FISHES (GOODEIDAE).

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Abstract

Vertebrate pelvic appendages are complex structures comprising many different tissues. Nevertheless, taxa including sticklebacks (Gasterosteidae, Teleostei) and manatees (Sirenia, Mammalia) have independently lost these structures as a result of defects in a common, cis-acting, upstream regulatory element (pel) of the *Pituitary homeobox transcription factor 1* (*PITX1*) gene. Here we began investigating whether independent pelvic loss in the Empetrichthyinae (Goodeidae, Teleostei) was caused by similar *PITX1* regulatory defects. Toward this end we desired to sequence *PITX1* from *Crenichthys baileyi* and the goodeine *Goodea atripinnis* (a related clade with pelvic fins) using standard molecular protocols. Multiple, overlapping sets of primers were developed within the four exons of this nuclear gene using comparative bioinformatics approaches with publicly available sequence data for *Oryzias latipes* and *Fundulus heteroclitus*. Most primer combinations did not successfully amplify products of the predicted size. Partial sequences were successfully determined for exon 2, intron 2 and exon 3. Comparisons of exons 2 (89 bp) and 3 (148 bp) of *Crenichthys* and *Goodea* revealed 96 and 97% sequence identity, respectively. These same exons shared 84 and 92% identity with *Oryzias*, and 96 and 96% identity with *Fundulus*. These coding regions yielded no significant hits on other genes. We have successfully sequenced part of the *PITX1* gene of goodeids with and lacking pelvic fins.

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Abstract

Vertebrate pelvic appendages are complex structures comprising many different tissues. Nevertheless, taxa including sticklebacks (Gasterosteidae, Teleostei) and manatees (Sirenia, Mammalia) have independently lost these structures as a result of defects in a common, cis-acting, upstream regulatory element (pel) of the *Pituitary homeobox transcription factor 1 (PITX1)* gene. Here we began investigating whether independent pelvic loss in the Empetrichthyinae (Goodeidae, Teleostei) was caused by similar *PITX1* regulatory defects. Toward this end we desired to sequence *PITX1* from *Crenichthys baileyi* and the goodeine *Goodea atripinnis* (a related clade with pelvic fins) using standard molecular protocols. Multiple, overlapping sets of primers were developed within the four exons of this nuclear gene using comparative bioinformatics approaches with publicly available sequence data for *Oryzias latipes* and *Fundulus heteroclitus*. Most primer combinations did not successfully amplify products of the predicted size. Partial sequences were successfully determined for exon 2, intron 2 and exon 3. Comparisons of exons 2 (89 bp) and 3 (148 bp) of *Crenichthys* and *Goodea* revealed 96 and 97% sequence identity, respectively. These same exons shared 84 and 92% identity with *Oryzias*, and 96 and 96% identity with *Fundulus*. These coding regions yielded no significant hits on other genes. We have successfully sequenced part of the *PITX1* gene of goodeids with and lacking pelvic fins.

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TEILWEISE CHARAKTERISIERUNG DES PITX1 GENES VON EMPETRICHTHYINE FISCHEN (GOODEIDAE).

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Abstrakt

Wirbeltier-Anhänge sind komplexe Strukturen, die viele verschiedene Gewebe umfassen. Trotzdem haben Taxa, einschließlich Sticklebacks (Gasterosteidae, Teleostei) und Manatees (Sirenia, Mammalia) diese Strukturen infolge von Defekten in einem gemeinsamen, cis-agierenden, vorgeschalteten regulatorischen Element (pel) des *Hypophysen-Homeobox-Transkriptionsfaktors 1* (*PITX1*) -Gen Hier begannen wir zu untersuchen, ob ein unabhängiger Beckenverlust in den Empetrichthyinae (Goodeidae, Teleostei) durch ähnliche *PITX1*- Regulationsdefekte verursacht wurde. Zu diesem Zweck *wünschten* wir, *PITX1* von *Crenichthys baileyi* und die Goodeine *Goodea atripinnis* (eine *verwandte* Clade mit Beckenflossen) unter Verwendung von Standard-Molekülprotokollen zu sequenzieren. Mehrere, überlappende Sätze von Primern wurden innerhalb der vier Exons dieses nuklearen Gens mit vergleichenden bioinformatischen Ansätzen mit öffentlich verfügbaren Sequenzdaten für *Oryzias latipes* und *Fundulus heteroclitus* *entwickelt* . Die meisten Primer-Kombinationen haben die Produkte der vorhergesagten Größe nicht erfolgreich verstärkt. Die Teilsequenzen wurden erfolgreich für Exon 2, Intron 2 und Exon 3 bestimmt. Vergleiche von Exons 2 (89 bp) und 3 (148 bp) von *Crenichthys* und *Goodea* zeigten eine 96 bzw. 97% Sequenzidentität. Diese gleichen Exons teilten 84 und 92% *Identität* mit *Oryzias* und 96 und 96% *Identität* mit *Fundulus* . Diese kodierenden Regionen ergaben keine signifikanten Hits für andere Gene. Wir haben erfolgreich einen Teil des *PITX1*- Gens von Goodeiden mit und fehlenden Beckenflossen sequenziert.

Empfohlenes Zitat

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