in both directions. Consensus sequences for each sequenced individual were derived using GCG (Genetics Computer Group, Madison, WI) GAP program. The GenBank accession numbers for each sequence are AF176341 and AF224873 to AF224880. Sequences were aligned with GCG PILEUP program using paddlefish, Polyodon spathula (GenBank accession number AF176340), as the outgroup taxon. Parsimony analyses on the alignments were conducted with PHYLIP v3.57c (Felsenstein 1993) on phylogenetically informative characters only, with gaps being treated as a fifth character state. Bootstrapping was performed by generating 1000 data sets with the SEQBOOT program. Most-parsimonious trees were constructed using DNAPARS, and a majority rule and combinable competent consensus of these trees were constructed using the CONSENSE program in PHYLIP. The DNADIST program of PHYLIP was used to calculate genetic distances according to the Kimura 2-parameter (Kimura 1980) and maximum likelihood models of sequence evolution. Trees were constructed from these distances with the NEIGHBOR program to create neighbor-joining (Saitou and Nei, 1987) trees.

RESULTS

Polymerase chain reaction resulted in an 838 bp amplicon for the nine sturgeons sequenced. Among the nine individuals, 11 nucleotide positions are polymorphic, of which eight are transitions and three are transversions. Six mitochondrial haplotypes were observed. Genetic distance among all sturgeons sequenced ranged from 0.0 to 0.84%, with a mean of 0.26%. Alignment of the Scaphirhynchus and Polyodon mtDNA sequences resulted in a total of 941 characters, including gaps. Distance analysis resulted in a cladogram similar to the one derived from parsimony analysis (Fig. 1). Neither analysis resulted in a distinct clade for pallid and shovel-nose sturgeons.

DISCUSSION

Although the examined sturgeons had nucleotide polymorphisms at 11 nucleotide sites of the mitocho-

\[ \text{Scaphirhynchus platonychus 641 MT} \]

\[ \text{Scaphirhynchus platonychus 644 MT} \]

\[ \text{Scaphirhynchus platonychus 638 MT} \]

\[ \text{Scaphirhynchus albus 572 LA} \]

\[ \text{Scaphirhynchus albus 115 ND} \]

\[ \text{Scaphirhynchus albus 109 ND} \]

\[ \text{Scaphirhynchus albus 129 IL} \]

\[ \text{Scaphirhynchus albus 560 IL} \]

\[ \text{Scaphirhynchus platonychus 635 MT} \]

Figure 1. Maximum parsimony consensus cladogram generated by PHYLIP from 5 pallid and 4 shovelnose sturgeon D-Loop sequences, using paddlefish as the outgroup taxon. Only bootstrap percentages >50% are provided.
drial D-Loop region, shovelnose and pallid sturgeons are indistinguishable by our results. Because of the limited sample size of each population in our study, no conclusions could be drawn regarding the extent of the variation and possible interpopulational differences. This lack of genetic differentiation between pallid and shovelnose sturgeons has been observed in several other studies. Phelps and Allendorf (1983), using allozyme analysis, observed a lack of genetic evidence supporting pallid and shovelnose sturgeons as different species. PCR-RFLP analysis of nuclear DNA amplicons by Genetic Analysis, Inc. (1994) showed no significant difference between species for the only variable locus. Campton et al. (1995) sequenced approximately 435 bp of mitochondrial DNA of pallid and shovelnose sturgeons from the upper Missouri River and found a difference in haplotype frequencies between shovelnose and pallid sturgeons, but the haplotypes overlapped such that maximum parsimony analysis did not result in two species-congruent clades. Avise (1994) suggested that divergence between genetic and phenotypic data may represent introgressive hybridization or recent divergence of pallid and shovelnose sturgeons. While other nuclear and mitochondrial markers that are commonly used as phylogenetic tools showed low levels of variation when applied to Acipenseriformes (Birstein et al. 1997), the examination of nuclear ribosomal DNA internal transcribed spacer regions or other nuclear markers may yield different results and should be a goal of future research.

ACKNOWLEDGMENTS

We thank the National Fish and Wildlife Laboratory in Ashland, Oregon, for providing samples. D. B. Taylor and R. D. Peterson II provided thoughtful suggestions. This is Journal Paper No. 12837 of the Nebraska Agricultural Research Division.

LITERATURE CITED


