Both native progestagens and synthetic progestins have important effects on reproduction that are mediated through progesterone receptors (PRs). They regulate gamete maturation and can serve as precursors for other steroid hormones in vertebrates and act as reproductive pheromones in some fishes. There are four known PRs, including the nuclear progesterone receptor (nPR) and three membrane progesterone receptors (mPRα, mPRβ, and mPRγ). The objectives of this study were to clone these receptors and investigate their tissue distribution in the fathead minnow (FHM), a species widely distributed in the United States with well-characterized reproductive morphology and endocrinology that is used by the Environmental Protection Agency as an aquatic toxicological model. Full-length coding sequences were obtained through traditional cloning strategies using total RNA extracted from ovary (nPR, mPRα, and mPRβ) or gill (mPRγ). The open reading frame for nPR consists of 1,923 nucleotides and encodes a protein that is 640 amino acids long. Phylogenetic comparison of the predicted amino acid sequence of FHM nPR with other vertebrates indicates that it is 53-80% identical with other teleosts, 38-46% identical with avian and frog nPR, and 34-44% with mammalian nPR. The open reading frames for each of the three membrane PRs are 1,065 nucleotides in length and are predicted to code for proteins with 354 amino acids. Comparison of the predicted amino acid sequence for FHM mPRα with that in other species indicates that it is 77-94% identical with other teleosts, 56-57% identical to avian and frog species, and 51-55% identical with mammals. The predicted amino acid sequence for FHM mPRβ is also highly similar to that in other vertebrates and was found to be 66-88% identical with other teleosts, 52-54% identical to avian and frog species, and 54-56% identical with mammals. Comparison of the predicted amino sequence for mPRγ in FHM with other teleosts, avian and frog species, and mammals indicates identities of 68-83%, 58-76%, and 49-53%, respectively. Expression of each of the PRs was evaluated by reverse-transcription PCR in male and female adult FHM tissues, including brain, head kidney, heart, gill, liver, muscle, ovary, pituitary, spleen, and testis. In both sexes, nPR transcript was detected in brain, gonad, pituitary, and spleen. Surprisingly, nPR mRNA was detected in the male, but not the female, kidney. Of the four receptors, mPRα transcript was the most widely expressed and was detected in all tissues examined in both sexes. In both male and female FHM, mPRβ mRNA was detected only in the brain, gonad, and gill. Expression of mPRγ mRNA was detected in male and female gill and kidney, and in female intestine. In conclusion, we have successfully identified the coding sequences for each of the four known PRs in FHM and investigated tissue-specific expression of each in adults of both sexes. The differential expression of mPRα, mPRβ, and mPRγ may indicate unique roles for each of these receptors regulating reproduction and other important physiological processes, such as osmoregulation, in fish.