MicroRNAs are noncoding RNA species of 22 nts that induce post-transcriptional gene silencing through base-pairing with their target mRNAs. MicroRNA primary transcripts contain a local hairpin structure that is cleaved by the Microprocessor complex, thereby releasing the microRNA precursor (pre-miRNA). It was recently suggested that intronic pre-miRNAs and spliced protein-coding mRNA can derive independently from the same transcription unit. We bioinformatically predicted the transcription units of all miRNA genes in 13 species using EST and mRNA data. We observed a group of 28 miRNA genes from 5 different vertebrates which share an intriguing genomic location: the pre-miRNAs are located on exon-intron junction (active splice sites) in their hosting transcript. Several of these pre-miRNAs are far more conserved than their hosting transcript, and the hosting transcript itself has features of non-coding gene: short transcript, very few and poorly conserved exons, insignificant open reading frame. The orthologous miRNAs in other relative species are fully located on exon or intron. Using these miRNAs we suggest a model of a competition between the Microprocessor complex and the Spliceosome, in which only the spliced RNA or the pre-miRNA, but not both, can derive from the common transcript. We also hypothesize that hairpin internal splice site evolved recently in specific lineages, possibly as way to negatively regulate miRNA expression. Preliminary experimental results indeed showed that Drosha (a Microprocessor component) over-expression caused an elimination of inclusion of an exon overlapping with pre-miRNA.