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Several methods, such as quantitative trait locus mapping, gene expression profiling, and proteomics, have been used in various mouse models of anxiety to identify genes that regulate anxiety or play a role in maintaining pathological anxiety. We first discuss briefly the evolutionary background of anxiety, which justifies cross-species approaches.

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neighborhoods (also called genomic contexts) in microbes may provide insight into determining functionally related or co-regulated sets of genes, suggest annotations of previously un-annotated genes, and help to identify horizontal gene transfer events across microbial species.

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