Strategy for uncovering complex determinants of hypertension using animal models.

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Hypertension is a complex, multifactorial disorder resulting from the interaction of multiple genetic and environmental factors. While rodent models of hypertension have proved useful for identifying chromosomal regions containing blood pressure quantitative trait loci (QTLs), the gene(s) responsible for strain-differences in blood pressure remain to be identified. A strategy for identifying the genetic factors underlying blood pressure in animal models is presented, grouped according to the following themes: 1) choice of hypertension model, 2) identification of chromosomal regions containing QTLs, 3) confirming the presence of QTLs and delimiting the chromosomal region containing them, 4) developing a physical map of the QTL-containing region of the chromosome, 5) identification of strong candidate gene(s), and 6) requirements for proving that a gene is responsible, in part, for blood pressure differences.

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