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(71) Applicant (for all designated States except US):
TRUSTEES OF BOSTON UNIVERSITY [US/US];
One Sherbron Street, Boston, MA 02215 (US).

(72) Inventors; and

(75) Inventors/Applicants (for US only): **HERRERA, Victoria, L.M.** [US/US]; 175 Briar Lane, Westwood, MA 02090 (US). **RUIZ-OPAZO, Nelson** [CL/US]; 175 Briar Lane, Westwood, MA 02090 (US).

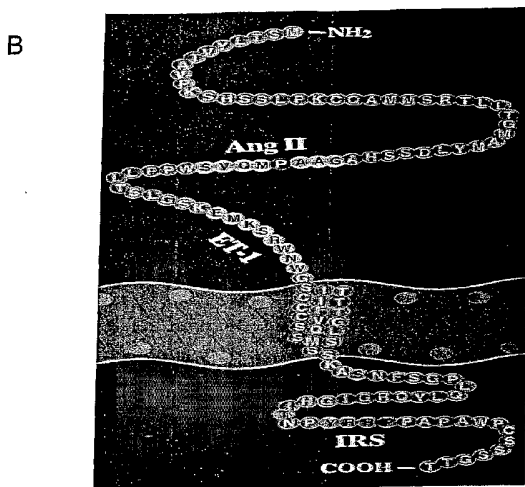
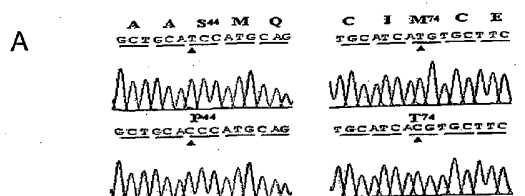
(74) Agents: **EISENSTEIN, Ronald, I.** et al.; Nixon Peabody LLP, 100 Summer Street, Boston, MA 02110 (US).

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[Continued on next page]

(54) Title: ROLES FOR DUAL ENDOTHELIN-1/ANGIOTENSIN II RECEPTOR (DEAR) IN HYPERTENSION AND ANGIO-GENESIS



(57) Abstract: The present application is directed to the identification of mutations and/or polymorphisms in the Dual Endothelin-1/Angiotensin II Receptor (Dear) that indicate susceptibility to, or show current affliction with, hypertension. Additionally, the present invention discloses methods for the modulation of angiogenesis via the regulation of Dear.

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ROLES FOR DUAL ENDOTHELIN-1/ANGIOTENSIN II RECEPTOR (DEAR) IN HYPERTENSION AND ANGIOGENESIS

CROSS-REFERENCE TO RELATED APPLICATION

[001] This application claims the benefit under 35 U.S.C. 119(e) of U.S. Provisional Patent Application Serial No. 60/628,447, filed November 16, 2004 and U.S. Provisional Patent Application Serial No. 60/694,268, filed June 27, 2005, the contents of which are herein incorporated by reference in their entirety.

GOVERNMENT SUPPORT

[002] This invention was made with Government Support under Contract No. HL69937 awarded by the National Institutes of Health. The Government has certain rights in the invention.

FIELD OF THE INVENTION

[003] The present application is directed to the identification of mutations and/or polymorphisms in the Dual Endothelin-1/Angiotensin II Receptor (Dear) that indicate susceptibility to, or show current affliction with, hypertension. Additionally, the present invention discloses methods for the modulation of angiogenesis via the regulation of Dear.

BACKGROUND OF THE INVENTION

[004] The Dual Endothelin-1/Angiotensin II Receptor (Dear) was originally isolated from an adult rat brain cDNA library using an AngII antisense oligonucleotide probe and also, independently, with an ET-1 oligonucleotide, see Molecular Medicine 4: 96-108, 1998. Structural analysis of the receptor revealed putative single predicted transmembrane domain and distinct ET-1 and AngII putative binding domains. Functional analysis has shown that both ET-1 and AngII bind to Dear and induce coupling to a Ca²⁺ mobilizing transduction system.

[005] ET-1 is a potent vasoconstrictor peptide involved in diverse physiological functions such as blood pressure regulation, mitogenesis and apoptosis (Lariviere, R. et al.

Can J Physiol Pharmacol. 81, 607-621 (2003), and angiogenesis (Salani, D. *et al. Am. J. Pathol.* 157, 1537-1547 (2000); Sullivan, D.C. & Bicknell, R. *British Journal of Cancer* 89, 228-231 (2003)), and has been implicated in several pathophysiological conditions such as hypertension, cardiac failure (Lariviere, R. *et al. Can J Physiol Pharmacol.* 81, 607-621 (2003); Ikeda, T. *et al. Hypertension* 34, 514-519 (1999); Touyz, R.M. & Schiffrin, E.L. *Can J Physiol Pharmacol.* 81, 533-541 (2003)), and more recently tumor angiogenesis, invasion and metastases (Bagnato, A. & Spinella, F. *Trends in Endocrinology and Metabolism* 14, 44-50 (2002); Grant, K., Loizidou, M. & Taylor, I. *British Journal of Cancer* 88, 163-166 (2003)).

[006] AngII exhibits similar physiological responses to ET-1, such as blood pressure regulation, proliferation, apoptosis and angiogenesis (Watanabe, T. *et al. Hypertension* 45, 163-169 (2005), and has also been implicated in tumor angiogenesis (Escobar, E. *et al. Curr Vasc Pharmacol* 2, 385-399 (2004)). Separate receptors have been identified for binding by either ET-1 or AngII which are believed to be responsible for the physiological responses observed.

[007] Accordingly, despite known roles for ET-1 and AngII, the role of Dear is currently unknown. It is believed that Dear regulates pathways distinct from those triggered by either ET-1 or AngII binding to ET_A, ET_B or AT₁ and AT₂ receptors respectively. However, due to its ability to bind to both ET-1 and AngII, and the important role these molecules play in angiogenesis, hypertension and tumor progression, a better understanding of Dear's role is needed. The present invention discloses newly discovered roles for Dear and presents methods to screen for, diagnose, prognose and treat various diseases and disorders such as hypertension, pathological angiogenesis and tumor growth/metastasis.

[008] The genomes of all organisms undergo spontaneous mutation in the course of their continuing evolution, generating variant forms of progenitor genetic sequences (Gusella, *Ann. Rev. Biochem.* 55, 831-854 (1986)). A variant form may confer an evolutionary advantage or disadvantage relative to a progenitor form or may be neutral. In some instances, a variant form confers an evolutionary advantage to the species and is eventually incorporated into the DNA of many or most members of the species and effectively becomes the progenitor form. However, often times the variant form confers a disadvantage that may make an individual susceptible to certain diseases or disorders. An understanding of these

variants may provide for better diagnosis of existing diseases or disorders, prognosis of the risk of obtaining certain diseases or disorders, and improved, more targeted treatments.

[009] The knowledge of specific mutations and/or polymorphisms that are disease or disorder associated help identify patients most suited to therapy with particular pharmaceutical agents (this is often termed "pharmacogenetics"). Pharmacogenetics can also be used in pharmaceutical research to assist the drug selection process. Polymorphisms are used in mapping the human genome and to elucidate the genetic component of diseases. The following references show background details on pharmacogenetics and other uses of polymorphism detection: Linder et al. (1997), *Clinical Chemistry*, 43, 254; Marshall (1997), *Nature Biotechnology*, 15, 1249; International Patent Application WO 97/40462, Spectra Biomedical; and Schafer et al. (1998), *Nature Biotechnology*, 16, 33.

I. Hypertension

[0010] Hypertension, or high blood pressure, is the most common chronic illness in America. The American Heart Association estimates that more than 62 million Americans over the age of six suffer from high blood pressure, and that only a minority of these people have their blood pressure under control. Left untreated, hypertension can lead to stroke, heart attack, kidney damage, congestive heart failure, and death. Uncontrolled mild-to-moderate hypertension will reduce the life expectancy of a typical 35-year-old person by 16 years. Even the mildest form of high blood pressure, "borderline hypertension," can cut one's life span by a few years and impact negatively on the quality of life.

[0011] The existence of a genetic component to hypertension is known from twin studies, which have revealed a greater concordance of blood pressure in monozygotic twins than in dizygotic twins. Similarly, biological siblings show greater concordance of blood pressure than adoptive siblings raised in the same household. Such studies have suggested that up to about 40% of the variations in blood pressure in the population are genetically determined. However, to date, a reliable genetic marker for hypertension has not been identified. Although significant gains have been made with respect to treatment, hypertension prevails as a major risk factor for heart and kidney disease, and stroke prompting the lowering of the BP level at which to start treatment.

[0012] Thus, a genetic marker for predicting one's susceptibility to hypertension is needed, as well as, a reliable method to diagnose hypertension is needed. Additionally, treatment strategies targeting the normalization of mutant genes contributing to genetic hypertension (hypertension genes) are needed.

II. Angiogenesis

[0013] Angiogenesis is a process of tissue vascularization that involves both the growth of new developing blood vessels into a tissue (neo-vascularization) and co-opting of existing blood vessels to a target site. Blood vessels are the means by which oxygen and nutrients are supplied to living tissues and waste products are removed from living tissue. Angiogenesis can be a critical biological process. For example, angiogenesis is essential in reproduction, development and wound repair. Conversely, inappropriate angiogenesis can have severe negative consequences. For example, it is only after solid tumors are vascularized as a result of angiogenesis that the tumors have a sufficient supply of oxygen and nutrients that permit it to grow rapidly and metastasize.

[0014] Angiogenesis-dependent diseases and disorders are those diseases and disorders affected by vascular growth. Such diseases represent a significant portion of diseases for which medical treatment is sought, and include inflammatory disorders such as immune and non-immune inflammation, chronic articular rheumatism and psoriasis, disorders associated with inappropriate or inopportune invasion of vessels such as diabetic retinopathy, macular degeneration, neovascular glaucoma, restenosis, capillary proliferation in atherosclerotic plaques and osteoporosis, and cancer associated disorders, such as solid tumors, solid tumor metastases, angiofibromas, retrolental fibroplasia, hemangiomas, Kaposi sarcoma, cancers which require neovascularization to support tumor growth, etc.

[0015] While methods to inhibit unwanted angiogenesis are known, few have proven clinically useful. For example, a number of therapeutic strategies exist for inhibiting aberrant angiogenesis, which attempt to reduce the production or effect of VEGF. For example, anti-VEGF or VEGF receptor antibodies (Kim ES et al. (2002), PNAS USA 99: 11399-11404), and soluble VEGF "traps" which compete with endothelial cell receptors for VEGF binding (Holash J et al. (2002), PNAS USA 99: 11393-11398) have been developed. Classical VEGF "antisense" or aptamer therapies directed against VEGF gene expression have also been proposed (U.S. published application 2001/0021772 of Uhlmann et al.). The anti-angiogenic

agents used in these and similar non-VEGF targeted therapies have typically been unsuccessful. The results achieved with available anti-angiogenic therapies have therefore been generally unsatisfactory.

[0016] Thus, methods to reduce or eliminate unwanted angiogenesis are needed.

[0017] Conversely, in situations where angiogenesis is desired, such as, for example, reproduction, development, wound repair and areas of ischemia or infarction, the stimulation of angiogenesis is useful. Current methods to initiate or up-regulate angiogenesis have also typically been clinically unsuccessful and are thus needed.

[0018] Furthermore, because ET-1 is also associated with breast cancer growth and pro-malignant potential, inhibition of Dear will also be useful in decreasing tumor growth and potential to metastasize, independent of its effects on angiogenesis.

SUMMARY OF THE INVENTION

[0019] The inventors of the present invention have discovered that mutations and/or polymorphisms in Dear that enhances the expression and/or the affinity of ET-1 binding to Dear can accurately predict susceptibility to hypertension. Mutations and/or polymorphisms in Dear and human homologues thereof are encompassed in the present invention. Thus, in one embodiment of the present invention, it is possible to predict susceptibility to hypertension, to diagnose current hypertension and/or provide prognosis of the hypertension by analyzing Dear gene and/or protein. The presence of a mutation and/or polymorphism that (1) enhances Dear expression and/or (2) enhances the affinity of ET-1 binding to Dear, compared to a wild type control, is indicative of one's susceptibility to and/or current affliction with hypertension.

[0020] In addition, Dear plays a role in angiogenesis, tumor growth and pro-malignant potential. In particular, the inventors have shown that inhibitors of Dear, such as anti-Dear antibodies, decreased tumor progression and pro-malignant potential in both a rat and mouse model of cancer. Thus, in another embodiment of the present invention, methods to inhibit angiogenesis and/or tumor growth and/or pro-malignant potential are disclosed. In this embodiment, an individual is administered a compound that inhibits Dear activation, such as for example, a small molecule inhibitor, competitive inhibitor, antibody, antibody fragment,

siRNA, aptamer, etc. Preferably, these are used in conjunction with inhibitors to other angiogenesis-associated agents such as VEGF, placental growth factors etc.

[0021] Non-limiting examples of pathological angiogenesis or disorders treated by the methods of the present invention include, inflammatory disorders such as immune and non-immune inflammation, chronic articular rheumatism and psoriasis, disorders associated with inappropriate or inopportune invasion of vessels such as diabetic retinopathy, macular degeneration, neovascular glaucoma, restenosis, capillary proliferation in atherosclerotic plaques and osteoporosis, and cancer associated disorders, such as solid tumors, solid tumor metastases, angiofibromas, retrolental fibroplasia, hemangiomas, Kaposi sarcoma and the like cancers which require neovascularization to support tumor growth. In a preferred embodiment of the present invention, the methods are directed to inhibiting tumor angiogenesis and/or pro-malignant potential in a mammal with cancer, such as, for example, breast cancer.

[0022] In a related embodiment, the present invention discloses methods to stimulate angiogenesis in tissues in need thereof. In this embodiment, activators of Dear are administered to an individual, such as, for example, small molecules, antibodies, antibody fragments, or other activators known to those of skill in the art.

[0023] As an example, stimulation of angiogenesis may be beneficial in diabetes-induced ischemia, poor circulation, myocardial infarction, aortic aneurysm, arterial disease of the lower extremities, cerebrovascular disease, etc.

BRIEF DESCRIPTION OF THE DRAWINGS

[0024] Figures 1A-1C. Molecular characterization of Dahl S and Dahl R Dear variants. (Figure 1A) Comparative nucleotide sequence of Dahl S and Dahl R cDNAs spanning the T²⁸¹⁴ (Dahl S)/C²⁸¹⁴ (Dahl R) and T²⁹⁰¹ (Dahl S)/C²⁹⁰¹ (Dahl R) nucleotide transitions. Amino acid substitutions resulting from the corresponding nucleotide transitions detected S44 substitution in Dahl R Dear for P44 and M74 substitution in Dahl R Dear for T74 (amino acid numbering as per Ruiz-Opazo et al. 1998) (Figure 1B) Schematic structure of the Dahl R Dear. The following functional domains are highlighted: putative AngII binding site, AngII (aa 41-48); ET-1 binding site, ET-1 (aa 60-67); amino acid S44 and M74 substituted in the Dahl S Dear by P44 and T74 respectively; potential cAMP-dependent protein kinase

phosphorylation sites (S91, T108 in green); a potential internalization recognition sequence (IRS) (Figure 1C) Western blot analysis detects equivalent levels of Dahl S (S) and Dahl R (R) *Dear* variants in Dahl S and Dahl R rat kidney membranes isolated from male and female rats. MW, 14.4 kDa molecular weight marker.

[0025] Figures 2A-2C. Functional characterization of Dahl S and Dahl R *Dear* variants. Saturation binding curves of ligand binding studies of Dahl S (○) and Dahl R (●) *Dear* expressed in Cos1 cells with radiolabeled ^{125}I -AngII (Figure 2A) and ^{125}I -ET-1 (Figure 2B). Values are presented as Mean $\pm$ standard deviation from five independent experiments. (Figure 2C) Detection of the 14 kDa *Dear* protein (◀) by western blot analysis (ab) of Dahl R (Kid-R) and Dahl S (Kid-S) kidney (Kid) membranes; control non-transfected Cos1 cell membranes (Cos1-c), Cos1 cell membranes expressing the Dahl R S44P/M74T variant (Cos1-R) and Cos1 cell membranes expressing the Dahl S S44/M74 variant (Cos1-S). ^{125}I -AngII west-western blot analysis (*AngII) detects binding only to Dahl S kidney membranes (Kid-S) and Cos1 cell membranes expressing the Dahl S S44/M74 variant (Cos1-S) while ^{125}I -ET-1 west-western blot analysis (*ET-1) reveals binding to both Dahl R (Kid-R) and Dahl S (Kid-S) kidney membranes as well as to Cos1 cell membranes expressing the Dahl R S44P/M74T (Cos1-R) and Dahl S S44/M74 (Cos1-S) molecular variants.

[0026] Figures 3A-3D. Scatchard plots of saturation data for Dahl S and Dahl R *Dear* variants. Scatchard plots of ^{125}I -AngII (Figure 3A) and ^{125}I -ET-1 (Figure 3B, Figure 3C) saturation binding data of Dahl S (○) and Dahl R (●) *Dear* expressed in Cos1 cells. Figure 3D: Saturation binding curves of ligand binding studies of mouse *Dear* expressed in Cos-1 cells. ○, mean $\pm$ sem ^{125}I -ET-1 binding; ●, mean $\pm$ sem ^{125}I -AngII binding.

[0027] Figures 4A-4C. Detection and genetic analysis of *Dear* variants. (Figure 4A) Detection of the *Dear* gene variants by single strand conformation polymorphism (SSCP) analysis in different rat strains. A 137 bp PCR product spanning the S44P substitution reveals the S44P/M74T variant in Dahl R (R) and LEW strains while the S44/M74 variant is detected in Dahl S (S), BN, WKY and SHR genomic DNAs. F1 denotes F1 [RxS] subjects. Interval mapping with bootstrap-analysis for chromosome-2 in male (Figure 4B) and female (Figure 4C) cohorts using Map Manager QTXb17 program. Horizontal lines (—) mark LRS values for significance of linkage. For (Figure 4B) from top to bottom: LRS = 18.4 (LOD = 4.00) for highly significant, LRS = 10.6 (LOD = 2.30) for significant, LRS = 4.1 (LOD = 0.89) for

suggestive; for (Figure 4C) from top to bottom: LRS = 16.6 (LOD = 3.61) for highly significant, LRS = 9.9 (LOD = 2.15) for significant, LRS = 3.9 (LOD = 0.85) for suggestive. — Likelihood ratio statistic; — regression coefficient for additive effect; — regression coefficient for dominance effect. Histograms represent the bootstrap-based confidence intervals for the detected QTLs.

[0028] Figure 5: *Dear* expression and schematic representation of the targeting vector. Figure 5A shows a restriction map of wild type 129SVJ mouse *Dear* (WT allele), the *Dear* targeting vector for homologous recombination (KO construct), and the mutant allele. (1) is a probe for Southern-blot analysis, which is a 1.5 kb S-B restriction fragment which detects a 5.2kb *SphI* restriction digest fragment in targeted allele (2) and a 8.0 kb fragment in the wild type allele (3); P1 (4) is a forward primer flanking integration site; P2 (5) is a reverse pGKNeo-specific primer; successful targeting event yields expected 5.5 kb P1-P2 PCR product. S, *SacI*; B, *BamHI*; N, *NsiI* restriction enzymes.

[0029] Figure 5B shows a Northern blot analysis which detects mouse *Dear* mRNA in all tissues tested with higher levels in kidney and aorta. The three different-sized *Dear* mRNAs most likely represent different polyadenylation signals. 28S and 18S ribosomal markers are noted to the left. H, heart, B, brain, K, kidney, Li, liver, Sp, spleen, Lu, lung, Ao, aorta, Te, testis, Ut, uterus.

[0030] Figure 5C shows a Southern blot analysis for detection of *Dear*-inactivation in mice by homologous recombination. Evidence of inactivation is characterized by predicted 5.2 kb *SphI* restriction digest fragment of genomic DNA detected as a lower hybridizing band in heterozygous (+/-) DNA samples compared with absence in wild type (+/+) samples.

[0031] Figure 5D shows PCR genotyping of E11.5 mouse embryos. Results (lower panel) show a 153 bp allele in wild type, *Dear*^{+/+} (+/+) and heterozygous *Dear*^{+/-} (+/-), but not in *Dear*^{-/-} (-/-) embryos. The upper panel shows inactivated (5.5 kb) allele in *Dear*^{+/-} and *Dear*^{-/-} but not in *Dear*^{+/+} embryos.

[0032] Figure 5E: Deduced amino acid sequence for mouse *Dear* cDNA (bottom sequence) compared with rat *Dear* sequence; Ab, peptide sequence used for anti-*Dear* antibody; AngII, angiotensin II binding site¹, ET-1, endothelin-1 binding site¹, TM-1, predicted transmembrane domain; IRS, internalization recognition sequence; (-), identical

sequence; (*), adjusted gap for better alignment; bold lettering denotes non-conservative amino acid differences.

[0033] Figure 5F: Western blot analysis of *Dear*^{+/+} (+/+) and *Dear*^{+/-} (+/-) deficient mouse kidney membranes using the anti-mouse *Dear* specific anti-peptide antibody (upper panel); presence of a non-specific cross-reacting high molecular weight protein demonstrates equal amounts of protein analyzed (lower panel).

[0034] Figures 5G-5I: Analysis of blood pressure (Fig. 5G), heart rate (Fig. 5H) and body weight (Fig. 5I) in heterozygous *Dear*^{+/-} adult mice. Systolic blood pressure (SBP, mmHg) and mean heart rate (bpm, in beats per minute) in *Dear*^{+/+} (□) and *Dear*^{+/-} (■) deficient male (M) and female (F) mice. Body weight in grams (g) comparing male *Dear*^{+/+} (◇) and *Dear*^{+/-} (◆) mice, and female *Dear*^{+/+} (○) and *Dear*^{+/-} (●) mice from 4-6 months (m) of age. *, $P < 0.05$; **, $P < 0.01$.

[0035] Figures 6A-I: Comparative anatomical analysis of *Dear*^{+/+} (left side) and *Dear*^{+/-} (right side) mouse embryos. Figure 6A shows adjacent E12.5 embryos revealing prominent yolk-sac collecting vessels in *Dear*^{+/+} (left side) but absent in the smaller *Dear*^{+/-} embryo (right side); both embryos still attached to placentas respectively.

[0036] Figure 6B shows adjacent E11.5 mouse embryos revealing well-developed yolk-sac collecting vessels in *Dear*^{+/+} while absent in *Dear*^{+/-} embryo.

[0037] Figure 6C shows that compared to E10.5 *Dear*^{+/+}, E10.5 *Dear*^{+/-} mouse embryo exhibits a lack of yolk-sac collecting vessels; embryo translucency allows detection of incomplete vascular network, blood filled heart and some cranial region vascularization.

[0038] Figure 6D shows adjacent E12.5 mouse embryos distinguishing normal *Dear*^{+/+} from darkened, resorbed *Dear*^{+/-} embryo.

[0039] Figure 6E shows E11.5 *Dear*^{+/-} mouse embryo exhibiting a hypoplastic phenotype compared with age-matched, larger dysmorphic null phenotype in Figure 6B.

[0040] Figure 6F shows E10.5 *Dear*^{+/-} mouse embryo exhibiting a hypoplastic phenotype compared with a slightly larger E10.5 dysmorphic null phenotype in Figure 6C.

[0041] Figure 6G shows high magnification of E9.5 *Dear*^{+/+} (left panel) mouse embryo showing vascular network development from cranial to caudal region with prominent blood-filled dorsal aortae (∇) and heart (→), in contrast to E10.5 *Dear*^{-/-} embryo (right panel) with rudimentary and abnormal vascular plexus in cranial region, an isolated blood filled heart (→), and non-detection blood-filled dorsal aortae.

[0042] Figure 6H shows an analysis of mouse embryos revealing distinct blood-filled cardiac ventricles and vascular network throughout the body in the larger *Dear*^{+/+} embryo, in contrast to *Dear*^{-/-} embryo with an enlarged single-chamber blood-filled heart, minimal peripheral vascular network, absent eye pigmentation, and abnormal brain region development.

[0043] Figure 6I shows cleared, fixed E11.5 mouse embryos shown in Figure 6B, revealing marked developmental delay in *Dear*^{-/-} embryo particularly in brain region development and heart chamber formation.

[0044] Figures 7A-7L shows histologic analysis of Masson-trichrome stained mouse embryos. Figure 7A: E10.5 *Dear*^{-/-} yolk sac revealing sparse blood islands in primary vascular plexus with a dilated vessel (→), but absent collecting vessels. Figure 7B: E10.5 *Dear*^{+/+} embryo yolk-sac revealing large blood island-filled collecting vessels (→) and primary vascular plexus. Figure 7C: Analysis of E12.5 *Dear*^{-/-} embryos reveals abnormal hyper-convoluted neuroepithelium with disorderly demarcation of major brain regions. Central ventral section is devoid of organogenesis with no recognizable liver and gut differentiation. Figure 7D: Analysis of littermate E12.5 *Dear*^{+/+} embryo contrasts the dysmorphic phenotype in the *Dear*^{-/-} mutant. Note prominent organogenesis: gut, liver, heart, brain and dorsal aorta. Figure 7E: High magnification of *Dear*^{-/-} neuroepithelial segment (proximal * in Figure 7C) revealing thin-walled perineural vessels (→) and a hyper-cellular neuroepithelium. Figure 7F: In contrast, high magnification of *Dear*^{+/+} neuroepithelial segment (proximal * in Figure 7C) revealing perineural vessels (→) filled with blood islands and exhibiting relatively thicker walls. Figure 7G: Higher magnification of *Dear*^{-/-} neuroepithelium segment (distal * in FIGURE 7C) showing marked cellularity with poor differential layering, absent penetrating capillaries, although a few nucleated rbcs are detected within the neuroepithelium. Figure 7H: Higher magnification of *Dear*^{+/+} neuroepithelium (distal * in Figure 7D) revealing differential layering and numerous

penetrating capillaries ($\rightarrow$) with nucleated rbc's. Figures 7I-J: Analysis of fetal-placental connections (f-pl con/xn) (bar = 160 μ m) and Figures 7K-L: fetal-placental junctions (f-pl jxn) in E11.5 embryos shows abnormal vascular development and decreased embryonic blood cells in *Dear*^{-/-}, (bar = 20 μ m).

[0045] Figures 8A-F: Histological analysis of *Dear*^{+/+} (+/+) (Figures 8A, 8C and 8E) and *Dear*^{-/-} (-/-) mouse embryos (Figures 8B, 8D and 8F). Masson-trichrome stained E11.5 embryos showing deficient development of dorsal aorta (da), vasculature (vasc) and yolk sac, as well as heart and brain in *Dear*^{-/-} (bar = 160 μ m).

[0046] Figures 9A-F: Smooth muscle cell α -actin immunostaining of E12.5 mouse embryos (embryo (Fig. 9A-B); bar = 160 μ m) demarcating angiogenesis (angiog; Fig. 9C-D) in perineural region and formation of vascular network (vasc net; Fig. 9E-F) in the caudal region detects deficient vascular development in *Dear*^{-/-} embryos; bar = 20 μ m.

[0047] Figures 10A and 10B: Analysis of mouse *dear* expression pattern in wild type (+/+) E9.5 and E12.5 embryos detects *Dear* expression in the heart, extra-embryonic and embryonic vasculature, and neural tube. sc, spinal cord, ao, aorta, bi, blood islands; neuroepith, neuroepithelium; bar = 20 μ m.

[0048] Figures 11A-11E: Analysis of *Dear*-inhibition on tumor growth. In *Dear*^{+/-} mice (■), decreased tumor mass (mg) (Figure 11A) and tumor volume (mm³) (Figure 11B) of melanoma cell-induced subcutaneous tumors were observed in females but not in males compared with age-matched *Dear*^{+/+} control mice (□). Figure 11C: Anti-rat *Dear* anti-peptide specific antibody treatment (○) results in decreased tumor volume in radiation-induced rat mammary tumors. Figure 11D: Anti-rat *Dear* DNA vaccine treatment (◇) also results in decreased tumor volume in radiation-induced rat mammary tumors. Figure 11E: Representative histological analysis of Masson-trichrome stained tumor sections comparing mock-treated (mock-Rx) vector controls, anti-*Dear* anti-peptide specific antibody treatment (ab-Rx) and anti-rat *Dear* DNA-vaccine (DNA-vac) shows changes in tumor pattern, microvascular invasion and nuclear grade in anti-*Dear* treated tumors; bar = 20 μ m. Values are presented as mean $\pm$ sem. *, $P < 0.05$; **, $P < 0.01$; ***, $P < 0.001$

DETAILED DESCRIPTION OF THE INVENTION

I. Hypertension

[0049] In one embodiment of the present invention, a method for determining an individual's susceptibility to hypertension is disclosed, as well as a diagnostic and/or prognostic method to determine the condition of the hypertension. An individual is screened for mutations and/or polymorphisms in Dear that correlate to an increase expression of Dear and/or enhancement of Dear-activation or Dear-signaling by AngII, ET-1, VEGF-signal peptide (VEGFsp) or other Dear-ligand as compared to a control. The presence of such a mutation and/or polymorphism in the test sample, as compared to the normal control, is indicative of an individual's susceptibility to hypertension. The presence of such a mutation and/or polymorphism in the test sample, as compared to the normal control, can also be indicative of a current state of hypertension.

[0050] As used herein, the term Dear encompasses Dear and human homologues thereof. In one embodiment, the term "human homologue to Dear" refers to a DNA sequence that has at least about 50% homology to SEQ ID NO:1 and more preferably at least about 60% homology or identity, including all intervals up (i.e. 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, etc.). In one embodiment, the term "human homologue to Dear protein" refers to an amino acid sequence that has 50% homology to SEQ ID NO: 2, more preferably at least about 60% homology, still more preferably, at least about 70% homology, even more preferably, at least about 75% homology, yet more preferably, at least about 80% homology, even more preferably at least about 85% homology, still more preferably, at least about 90% homology, and more preferably, at least about 95% homology, intervals of the same are also encompassed (i.e., 55%, 60%, 70%, 75%, 80%, 85%, 90%, 95%, 98%, etc.).

[0051] "Homology" or "identity" or "similarity" refers to sequence similarity between two peptides or between two nucleic acid molecules. Homology and identity can each be determined by comparing a position in each sequence which may be aligned for purposes of comparison. When an equivalent position in the compared sequences is occupied by the same base or amino acid, then the molecules are identical at that position; when the equivalent site occupied by the same or a similar amino acid residue (e.g., similar in steric and/or electronic nature), then the molecules can be referred to as homologous (similar) at that position. Expression as a percentage of homology/similarity or identity refers to a

function of the number of identical or similar amino acids at positions shared by the compared sequences. A sequence which is "unrelated" or "non-homologous" shares less than 40% identity, though preferably less than 25% identity with a sequence of the present application.

[0052] In comparing two sequences, the absence of residues (amino acids or nucleic acids) or presence of extra residues also decreases the identity and homology/similarity. The term "homology" describes a mathematically based comparison of sequence similarities which is used to identify genes or proteins with similar functions or motifs. The nucleic acid and protein sequences of the present application may be used as a "query sequence" to perform a search against public databases to, for example, identify other family members, related sequences or homologs. Such searches can be performed using the NBLAST and XBLAST programs (version 2. 0) of Altschul, et al. (1990) J Mol. Biol. 215:403-10. BLAST nucleotide searches can be performed with the NBLAST program, score=100, wordlength=12 to obtain nucleotide sequences homologous to nucleic acid molecules of the application. BLAST protein searches can be performed with the XBLAST program, score=50, wordlength=3 to obtain amino acid sequences homologous to protein molecules of the application. To obtain gapped alignments for comparison purposes, Gapped BLAST can be utilized as described in Altschul et al., (1997) Nucleic Acids Res. 25(17):3389- 3402. When utilizing BLAST and Gapped BLAST programs, the default parameters of the respective programs (e.g., XBLAST and BLAST) can be used. See <http://www.ncbi.nlm.nih.gov>.

[0053] As used herein, "identity" means the percentage of identical nucleotide or amino acid residues at corresponding positions in two or more sequences when the sequences are aligned to maximize sequence matching, i.e., taking into account gaps and insertions. Identity can be readily calculated by known methods, including but not limited to those described in (Computational Molecular Biology, Lesk, A. M., ea., Oxford University Press, New York, 1988; Biocomputing: Informatics and - 14 Genome Projects, Smith, D. W., ea., Academic Press, New York, 1993; Computer Analysis of Sequence Data, Part I, Griffin, A. M., and Griffin, H. G., eds., Humana Press, New Jersey, 1994; Sequence Analysis in Molecular Biology, von Heinje, G., Academic Press, 1987; and Sequence Analysis Primer, Gribskov, M. and Devereux, J., eds., M Stockton Press, New York, 1991; and Carillo, H., and Lipman, D., SIAM J. Applied Math., 48: 1073 (1988)). Methods to determine identity are designed to give the largest match between the sequences tested. Moreover, methods to

determine identity are codified in publicly available computer programs. Computer program methods to determine identity between two sequences include, but are not limited to, the GCG program package (Devereux, J., et al., *Nucleic Acids Research* 12(1): 387 (1984)), BLASTP, BLASTN, and FASTA (Altschul, S. F. et al., *J. I Molec. Biol.* 215: 403-410 (1990) and Altschul et al. *Nuc. Acids Res.* 25: 3389-3402 (1997)). The BLAST X program is publicly available from NCBI and other sources (BLAST Manual, Altschul, S., et al., NCBI NLM NIH Bethesda, Md. 20894; Altschul, S., et al., *J. Mol. Biol.* 215: 403-410 (1990)). The well known Smith Waterman algorithm may also be used to determine identity.

[0054] Once an individual is known to be susceptible to hypertension, currently available methods to reduce or prevent a rise in blood pressure may be used. Examples of currently available methods to reduce and/or prevent hypertension include, for example, diet, exercise, multidrug regimens including combinations of antihypertensive drugs such as beta blockers, diuretics, calcium antagonists, angiotensin II active agents, heart rate-reducing nondihydropyridine calcium antagonists, and angiotensin-converting enzyme (ACE) inhibitors. Alternatively, compounds that modulate Dear function may be administered. Where the individual already has hypertension knowing the basis for that hypertension can be used to determine treatment regime.

[0055] Methods to detect the presence or absence of mutations and/or polymorphisms in genes such as Dear are known to those of skill in the art and certain embodiments are as follows:

Preparation of Samples

[0056] Mutations and/or polymorphisms are detected in a target nucleic acid from an individual being analyzed. For example, for assay of genomic DNA, virtually any biological sample (other than pure red blood cells) is suitable. For example, convenient tissue samples include whole blood, semen, saliva, tears, urine, fecal material, sweat, buccal, skin and hair. For assay of cDNA or mRNA, the tissue sample must be obtained from an organ in which the target nucleic acid is expressed, see for example, Figure 5B, which shows Dear expression in heart, brain, kidney, liver, spleen, lung, aorta, testis, and uterus.

[0057] Many of the methods described below require amplification of DNA from target samples. This can be accomplished by e.g., PCR. See generally PCR Technology: Principles

and Applications for DNA Amplification (ed. H. A. Erlich, Freeman Press, NY, N.Y., 1992); PCR Protocols: A Guide to Methods and Applications (eds. Innis, et al., Academic Press, San Diego, Calif., 1990); Mattila et al., Nucleic Acids Res. 19, 4967 (1991); Eckert et al., PCR Methods and Applications 1, 17 (1991); PCR (eds. McPherson et al., IRL Press, Oxford); and U.S. Pat. No. 4,683,202 (each of which is incorporated by reference for all purposes).

[0058] Other suitable amplification methods include the ligase chain reaction (LCR) (see Wu and Wallace, Genomics 4, 560 (1989), Landegren et al., Science 241, 1077 (1988), transcription amplification (Kwoh et al., Proc. Natl. Acad. Sci. USA 86, 1173 (1989)), and self-sustained sequence replication (Guatelli et al., Proc. Nat. Acad. Sci. USA, 87, 1874 (1990)) and nucleic acid based sequence amplification (NASBA). The latter two amplification methods involve isothermal reactions based on isothermal transcription, which produce both single stranded RNA (ssRNA) and double stranded DNA (dsDNA) as the amplification products in a ratio of about 30 or 100 to 1, respectively.

Detection of Mutations and/or Polymorphisms in Target DNA

[0059] The identity of bases occupying mutated or polymorphic sites can be determined in an individual (e.g., a patient being analyzed) by several methods, which are described in turn.

Allele-Specific Probes

[0060] The design and use of allele-specific probes for analyzing mutations and/or polymorphisms is described by e.g., Saiki et al., Nature 324, 163-166 (1986); Dattagupta, EP 235,726, Saiki, WO 89/11548. Allele-specific probes can be designed that hybridize to a segment of target DNA from one individual but do not hybridize to the corresponding segment from another individual due to the presence of different mutated or polymorphic forms in the respective segments from the two individuals. Hybridization conditions should be sufficiently stringent that there is a significant difference in hybridization intensity between alleles, and preferably an essentially binary response, whereby a probe hybridizes to only one of the alleles. Some probes are designed to hybridize to a segment of target DNA such that the polymorphic site aligns with a central position (e.g., in a 15 mer at the 7 position; in a 16 mer, at either the 8 or 9 position) of the probe. This design of probe achieves good discrimination in hybridization between different allelic forms.

[0061] Allele-specific probes are often used in pairs, one member of a pair showing a perfect match to a reference form of a target sequence and the other member showing a perfect match to a variant form. Several pairs of probes can then be immobilized on the same support for simultaneous analysis of multiple mutations and/or polymorphisms within the same target sequence.

Tiling Arrays

[0062] The mutations and/or polymorphisms can also be identified by hybridization to nucleic acid arrays, some example of which are described by WO 95/11995 (incorporated by reference in its entirety for all purposes). The same array or a different array can be used for analysis of characterized mutations and/or polymorphisms. WO 95/11995 also describes subarrays that are optimized for detection of a variant form of a precharacterized mutation and/or polymorphism. Such a subarray contains probes designed to be complementary to a second reference sequence, which is an allelic variant of the first reference sequence. The second group of probes is designed by the same principles as described above except that the probes exhibit complementarity to the second reference sequence. The inclusion of a second group (or further groups) can be particularly useful for analyzing short subsequences of the primary reference sequence in which multiple mutations are expected to occur within a short distance commensurate with the length of the probes (i.e., two or more mutations within 9 to 21 bases).

Allele-Specific Primers

[0063] An allele-specific primer hybridizes to a site on target DNA overlapping a mutation and/or polymorphism and only primes amplification of an allelic form to which the primer exhibits perfect complementarity. See Gibbs, Nucleic Acid Res. 17, 2427-2448 (1989). This primer is used in conjunction with a second primer which hybridizes at a distal site. Amplification proceeds from the two primers leading to a detectable product signifying the particular allelic form is present. A control is usually performed with a second pair of primers, one of which shows a single base mismatch at the polymorphic site and the other of which exhibits perfect complementarity to a distal site. The single-base mismatch prevents amplification and no detectable product is formed. The method works best when the mismatch is included in the 3'-most position of the oligonucleotide aligned with the mutation

and/or polymorphism because this position is most destabilizing to elongation from the primer. See, e.g., WO 93/22456.

Direct-Sequencing

[0064] The direct analysis of the sequence of mutation and/or polymorphisms of the present invention can be accomplished using either the dideoxy-chain termination method or the Maxam-Gilbert method (see Sambrook et al., Molecular Cloning, A Laboratory Manual (2nd Ed., CSHP, New York 1989); Zyskind et al., Recombinant DNA Laboratory Manual, (Acad. Press, 1988)).

Denaturing Gradient Gel Electrophoresis

[0065] Amplification products generated using the polymerase chain reaction can be analyzed by the use of denaturing gradient gel electrophoresis. Different alleles can be identified based on the different sequence-dependent melting properties and electrophoretic migration of DNA in solution. Erlich, ed., PCR Technology, Principles and Applications for DNA Amplification, (W. H. Freeman and Co, New York, 1992), Chapter 7.

Single-Strand Conformation Mutation and/or Polymorphism Analysis

[0066] Alleles of target sequences can be differentiated using single-strand conformation mutation and/or polymorphism analysis, which identifies base differences by alteration in electrophoretic migration of single stranded PCR products, as described in Orita et al., Proc. Nat. Acad. Sci. 86, 2766-2770 (1989). Amplified PCR products can be generated as described above, and heated or otherwise denatured, to form single stranded amplification products. Single-stranded nucleic acids may refold or form secondary structures which are partially dependent on the base sequence. The different electrophoretic mobilities of single-stranded amplification products can be related to base-sequence difference between alleles of target sequences.

Antibody Detection Methods

[0067] According to another aspect of the present invention an antibody specific for an allelic variant (mutation and/or polymorphism) of human Dear polypeptide is used to detect the presence or absence of Dear mutations and/or polymorphisms.

[0068] Antibodies can be prepared using any suitable method. For example, purified polypeptide may be utilized to prepare specific antibodies. The term "antibodies" is meant to include polyclonal antibodies, monoclonal antibodies, and the various types of antibody constructs such as for example F(ab')₂, Fab and single chain Fv. Antibodies are defined to be specifically binding if they bind the allelic variant of Dear with a K_a of greater than or equal to about 10⁷ M⁻¹. Affinity of binding can be determined using conventional techniques, for example those described by Scatchard et al., Ann. N.Y. Acad. Sci., 51:660 (1949).

[0069] Polyclonal antibodies can be readily generated from a variety of sources, for example, horses, cows, goats, sheep, dogs, chickens, rabbits, mice or rats, using procedures that are well-known in the art. In general, antigen is administered to the host animal typically through parenteral injection. The immunogenicity of antigen may be enhanced through the use of an adjuvant, for example, Freund's complete or incomplete adjuvant. Following booster immunizations, small samples of serum are collected and tested for reactivity to antigen. Examples of various assays useful for such determination include those described in: Antibodies: A Laboratory Manual, Harlow and Lane (eds.), Cold Spring Harbor Laboratory Press, 1988; as well as procedures such as countercurrent immuno-electrophoresis (CIEP), radioimmunoassay, radioimmunoprecipitation, enzyme-linked immuno-sorbent assays (ELISA), dot blot assays, and sandwich assays, see U.S. Pat. Nos. 4,376,110 and 4,486,530.

[0070] Monoclonal antibodies may be readily prepared using well-known procedures, see for example, the procedures described in U.S. Pat. Nos. 4,902,614, 4,543,439 and 4,411,993; Monoclonal Antibodies, Hybridomas: A New Dimension in Biological Analyses, Plenum Press, Kennett, McKearn, and Bechtol (eds.), (1980).

[0071] Monoclonal antibodies to variant forms of Dear can be produced using alternative techniques, such as those described by Alting-Mees et al., "Monoclonal Antibody Expression Libraries: A Rapid Alternative to Hybridomas", Strategies in Molecular Biology 3: 1-9 (1990) which is incorporated herein by reference. Similarly, binding partners can be constructed using recombinant DNA techniques to incorporate the variable regions of a gene that encodes a specific binding antibody. Such a technique is described in Larrick et al., Biotechnology, 7: 394(1989).

[0072] Once isolated and purified, the antibodies may be used to detect the presence of variant Dear in a sample using established assay protocols, see for example "A Practical

Guide to ELISA" by D. M. Kemeny, Pergamon Press, Oxford, England. As is known to those of skill in the art, a suitable control sample (i.e. a sample with wild type or non-mutated and/or polymorphic Dear) is used as a control.

[0073] Also encompassed are methods for the determination of expression levels. For example, the overexpression of Dear is an indication that an individual is susceptible to or is currently afflicted with hypertension. Methods for analyzing expression levels are known to those of skill in the art. In one aspect of the invention, Dear levels present in a test biological sample are measured by analyzing the level of Dear mRNA in a test sample and comparing this level to the level of Dear in a control sample. In another embodiment, Dear levels present in a test biological sample are measured by contacting the test sample, or preparation thereof, with an endogenous control 18S rRNA. A preferred embodiment of the present invention is the use of laser capture microdissection and RT-PCR for the analysis of Dear mRNA from tissue samples. Laser capture microdissection is known to those of skill in the art and described, for example, in Simon et al. (1998) Trends in Genetics 14:272 and Emmert-Buck et al. (1996) Science 274:998-1001.

[0074] In another aspect of the invention, Dear levels present in a test biological sample are measured by contacting the test sample, or preparation thereof, with an antibody-based binding moiety that specifically binds to Dear protein, or to a portion thereof. The antibody-based binding moiety forms a complex with Dear that can be detected, thereby allowing the levels of Dear to be measured.

[0075] Any means known to those skilled in art can be used to assess Dear levels. For example, in some embodiments Dear expression levels are assayed by measuring levels of Dear via mass spectrometry, ELISA, MR, CT, PET targeted at Dear or immunohistochemistry.

[0076] In a further embodiment, the invention provides for kits that comprise means for measuring Dear in a biological sample.

Definitions

[0077] "Dear", "DEAR", or "*Dear*" as used herein and throughout is the Dual Endothelin-1/Angiotensin II Receptor.

[0078] Polymorphism refers to the occurrence of two or more genetically determined alternative sequences or alleles in a population. A polymorphic marker or site is the locus at which divergence occurs. Preferred markers have at least two alleles, each occurring at frequency of greater than 1%, and more preferably greater than 10% or 20% of a selected population. A polymorphic locus may be as small as one base pair. Polymorphic markers include restriction fragment length polymorphisms, variable number of tandem repeats (VNTR's), hypervariable regions, minisatellites, dinucleotide repeats, trinucleotide repeats, tetranucleotide repeats, simple sequence repeats, and insertion elements such as Alu. The first identified allelic form is arbitrarily designated as the reference form and other allelic forms are designated as alternative or variant alleles.

[0079] The allelic form occurring most frequently in a selected population is sometimes referred to as the wild type form. Diploid organisms may be homozygous or heterozygous for allelic forms. A diallelic polymorphism has two forms. A triallelic polymorphism has three forms.

[0080] A single nucleotide polymorphism occurs at a polymorphic site occupied by a single nucleotide, which is the site of variation between allelic sequences. The site is usually preceded by and followed by highly conserved sequences of the allele (e.g., sequences that vary in less than {fraction (1/100)} or {fraction (1/1000)} members of the populations).

[0081] A single nucleotide polymorphism usually arises due to substitution of one nucleotide for another at the polymorphic site. A transition is the replacement of one purine by another purine or one pyrimidine by another pyrimidine. A transversion is the replacement of a purine by a pyrimidine or vice versa. Single nucleotide polymorphisms can also arise from a deletion of a nucleotide or an insertion of a nucleotide relative to a reference allele.

II. Angiogenesis

A. Inhibiting Angiogenesis

[0082] In another embodiment of the present invention, a method of inhibiting angiogenesis in a tissue of an individual having a disease or disorder dependent or modulated by angiogenesis, wherein the disease or disorder can be treated by the inhibition of

angiogenesis is disclosed. Generally, the method comprises administering to the tissue a composition comprising an angiogenesis-inhibiting amount of Dear inhibitor.

[0083] In a related embodiment, the methods of the present invention provide for a method of inhibiting angiogenesis in a tissue of an individual at risk for developing an angiogenic disease or disorder.

[0084] Where the growth of new blood vessels is the cause of, or contributes to, the pathology associated with a disease, inhibition of angiogenesis will reduce the deleterious effects of the disease. Examples include tumors, rheumatoid arthritis, diabetic retinopathy, inflammatory diseases, restenosis, and the like. Where the growth of new blood vessels is required to support growth of a deleterious tissue, inhibition of angiogenesis will reduce the blood supply to the tissue and thereby contribute to reduction in tissue mass based on blood supply requirements. Examples include growth of tumors where neovascularization is a continual requirement in order that the tumor growth beyond a few millimeters in thickness, and for the establishment of solid tumor metastases. Another example is coronary plaque enlargement.

[0085] The invention provides for a method for the inhibition of angiogenesis in a tissue, and thereby inhibiting events in the tissue which depend upon angiogenesis.

[0086] The treatment will involve the administration of a Dear inhibitor. The treatment may involve a combination of treatments, including, but not limited to a Dear inhibitor in combination with other angiogenic inhibitors, chemotherapy, radiation, surgery, or other treatments known to those of skill in the art to inhibit angiogenesis. Examples of angiogenic inhibitors that may be used in combination with the Dear inhibitor of the present invention are: direct angiogenesis inhibitors, Angiostatin, Bevacizumab (Avastin), Arresten, Canstatin, Combretastatin, Endostatin, NM-3, Thrombospondin, Tumstatin, 2-methoxyestradiol, and Vitaxin; and indirect angiogenesis inhibitors: ZD1839 (Iressa), ZD6474, OSI774 (Tarceva), CI1033, PKI1666, IMC225 (Erbix), PTK787, SU6668, SU11248, Herceptin, and IFN- α , CELEBREX® (Celecoxib), THALOMID® (Thalidomide), and IFN- α .

[0087] Thus, in connection with the administration of a Dear inhibitor, a compound which inhibits angiogenesis indicates that administration in a clinically appropriate manner results in a beneficial effect for at least a statistically significant fraction of patients, such as

improvement of symptoms, a cure, a reduction in disease load, reduction in tumor mass or cell numbers, extension of life, improvement in quality of life, or other effect generally recognized as positive by medical doctors familiar with treating the particular type of disease or condition.

[0088] Examples of Dear inhibitors include, but are not limited to, molecules which block the binding of AngII, ET-1 and/or other ET-1 or AngII-like ligands to Dear, compounds which interfere with downstream signaling events of Dear, or other compounds or agents that inhibit activation of the receptor. Such compounds include antibodies that bind to Dear and prevent binding of AngII, ET-1 or other mimetic ligands. Preferably, the antibody is a humanized antibody. Preferably, the antibody is a single chain antibody or F(ab)² fragment. Other inhibitors including small molecules that bind to the Dear domain that binds to ET-1, soluble Dear receptors, peptides containing the Dear ET-1 and/or AngII binding domains, etc.

[0089] There are a variety of diseases or disorders in which angiogenesis is believed to lead to negative consequences, referred to as pathological angiogenesis, including but not limited to, inflammatory disorders such as immune and non-immune inflammation, chronic articular rheumatism and psoriasis, disorders associated with inappropriate or inopportune invasion of vessels such as diabetic retinopathy, neovascular glaucoma, restenosis, capillary proliferation in atherosclerotic plaques and osteoporosis, and cancer associated disorders, such as solid tumors, solid tumor metastases, angiofibromas, retrolental fibroplasia, hemangiomas, Kaposi sarcoma and the like cancers which require neovascularization to support tumor growth. In a preferred embodiment of the present invention, the methods are directed to inhibiting angiogenesis in a mammal with cancer.

[0090] As described herein, any of a variety of tissues, or organs comprised of organized tissues, can support angiogenesis in disease conditions including skin, muscle, gut, connective tissue, joints, bones and the like tissue in which blood vessels can invade upon angiogenic stimuli.

[0091] The individual treated in the present invention in its many embodiments is desirably a human patient, although it is to be understood that the principles of the invention indicate that the invention is effective with respect to all mammals, which are intended to be included in the term "patient". In this context, a mammal is understood to include any

mammalian species in which treatment of diseases associated with angiogenesis is desirable, particularly agricultural and domestic mammalian species.

[0092] In a preferred embodiment, the present invention is directed to methods of inhibiting angiogenesis in a tissue of a mammal having pathological angiogenesis as in cancer, and in particular breast cancer and the administration of the Dear inhibitor eliminates or reduces the presence of the cancer.

B. Enhancing Angiogenesis

[0093] In an alternative embodiment of the present invention, Dear activators are used to stimulate angiogenesis in tissues or organs in need of neovascularization or additional blood supply. In these instances, delivery of a Dear activator alone or in combination with other angiogenesis stimulators may be beneficial.

[0094] Any condition that would benefit from increased blood flow are encompassed such as, for example, gangrene, diabetes, poor circulation, arteriosclerosis, atherosclerosis, coronary artery disease, myocardial ischemia, myocardial infarction, aortic aneurysm, arterial disease of the lower extremities, cerebrovascular disease, etc. In this manner, the methods of the invention may be used to treat peripheral vascular diseases by administering Dear activators to promote vascularization. Likewise, the Dear activators are useful to treat a diseased or hypoxic heart, particularly where vessels to the heart are partially or completely obstructed. Other organs with arterial sclerosis may benefit from Dear activation. Likewise, organs whose function may be enhanced by higher vascularization may be improved by an activation of Dear. This includes kidneys or other organs which need an improvement in function. In the same manner, other disorders which could benefit from increased blood flow include ischemic bowel disease, cerebro vascular disease, impotence of a vascular basis, and the like. Additionally, formation of new blood vessels in the heart is critically important in protecting the myocardium from the consequences of coronary obstruction. Administration of a Dear activator into ischemic myocardium can enhance the development of collaterals, accelerate the healing of necrotic tissue and prevent infarct expansion and cardiac failure.

[0095] Additionally, Dear activators are useful to prepare a transplant site for tissues or organs of interest by increasing vascularization. Such organ transplants include, but are not

limited to, pancreas, kidney, heart, lung, liver, etc. Dear activators may also be used in combination with other implants as a surgical adhesion barrier.

[0096] Following in vitro fertilization, the embryo is implanted in a female for gestation. The methods of the invention can be used to prepare the uterine vascularized bed for embryo implantation. In this embodiment, Dear activators are introduced prior to implantation so as to promote blood vessel formation in the uterine wall prior to implantation of the embryo, thus promoting fetal-maternal vascular plexus. Likewise, Dear activators can also enhance fetal-maternal vascular plexus formation, and/or robust placental vasculature for successful pregnancy/gestation of both natural and in vitro fertilized embryos.

[0097] Skilled artisans are able to determine when therapy is beneficial and where therapy is contraindicated. In general, patients with known tumors or pathological angiogenesis should not be given the Dear activators of the present invention.

[0098] III. Tumor pro-malignant potential: decreasing pro-malignant potential of tumors. In another embodiment of the present invention, a method of decreasing the pro-malignant potential of a tumor is disclosed. Generally, the method consists of administering to the tumor, systemically or locally, a composition comprising a Dear inhibitor at a dose which decreases pro-malignant parameters such as, but not all inclusive, nuclear pleomorphism, nuclear hyperchromasia, vascular invasion, mosaic tumor vessels, chaotic tumor vessels, tumor metastasis, etc.

Formulations

[0099] The Dear activators and inhibitors of the present invention may be administered to an individual via intravenous (I.V.), intramuscular (I.M.), subcutaneous (S.C.), intradermal (I.D.), intraperitoneal (I.P.), intrathecal (I.T.), intrapleural, intrauterine, rectal, vaginal, topical, intratumor and the like. The Dear modulators (either activators or inhibitors) can be administered parenterally by injection or by gradual infusion over time and can be delivered by peristaltic means.

[00100] Administration may be by transmucosal or transdermal means. For transmucosal or transdermal administration, penetrants appropriate to the barrier to be permeated are used in the formulation. Such penetrants are generally known in the art, and include, for example,

for transmucosal administration bile salts and fusidic acid derivatives. In addition, detergents may be used to facilitate permeation. Transmucosal administration may be through nasal sprays, for example, or using suppositories. For oral administration, the compounds of the invention are formulated into conventional oral administration forms such as capsules, tablets and tonics.

[00101] For topical administration, the pharmaceutical composition (inhibitor or activator of Dear activity) is formulated into ointments, salves, gels, or creams, as is generally known in the art.

[00102] The activators and inhibitors of Dear are conventionally administered intravenously, as by injection of a unit dose, for example. The term "unit dose" when used in reference to a therapeutic composition refers to physically discrete units suitable as unitary dosage for the subject, each unit containing a predetermined quantity of active material calculated to produce the desired therapeutic effect in association with the required diluent; i.e., carrier, or vehicle.

[00103] The compositions are administered in a manner compatible with the dosage formulation, and in a therapeutically effective amount. The quantity to be administered and timing depends on the subject to be treated, capacity of the subject's system to utilize the active ingredient, and degree of therapeutic effect desired. Precise amounts of active ingredient required to be administered depend on the judgment of the practitioner and are peculiar to each individual.

[00104] The Dear activators and inhibitors useful for practicing the methods of the present invention are of any formulation or drug delivery system containing the active ingredients, which is suitable for the intended use, as are generally known to those of skill in the art. Suitable pharmaceutically acceptable carriers for oral, rectal, topical or parenteral (including inhaled, subcutaneous, intraperitoneal, intramuscular and intravenous) administration are known to those of skill in the art. The carrier must be pharmaceutically acceptable in the sense of being compatible with the other ingredients of the formulation and not deleterious to the recipient thereof.

[00105] As used herein, the terms "pharmaceutically acceptable", "physiologically tolerable" and grammatical variations thereof, as they refer to compositions, carriers, diluents

and reagents, are used interchangeably and represent that the materials are capable of administration to or upon a mammal without the production of undesirable physiological effects.

[00106] Formulations suitable for parenteral administration conveniently include sterile aqueous preparation of the active compound which is preferably isotonic with the blood of the recipient. Thus, such formulations may conveniently contain distilled water, 5% dextrose in distilled water or saline. Useful formulations also include concentrated solutions or solids containing the compound which upon dilution with an appropriate solvent give a solution suitable for parental administration above.

[00107] For enteral administration, a compound can be incorporated into an inert carrier in discrete units such as capsules, cachets, tablets or lozenges, each containing a predetermined amount of the active compound; as a powder or granules; or a suspension or solution in an aqueous liquid or non-aqueous liquid, e.g., a syrup, an elixir, an emulsion or a draught. Suitable carriers may be starches or sugars and include lubricants, flavorings, binders, and other materials of the same nature.

[00108] A tablet may be made by compression or molding, optionally with one or more accessory ingredients. Compressed tablets may be prepared by compressing in a suitable machine the active compound in a free-flowing form, e.g., a powder or granules, optionally mixed with accessory ingredients, e.g., binders, lubricants, inert diluents, surface active or dispersing agents. Molded tablets may be made by molding in a suitable machine, a mixture of the powdered active compound with any suitable carrier.

[00109] A syrup or suspension may be made by adding the active compound to a concentrated, aqueous solution of a sugar, e.g., sucrose, to which may also be added any accessory ingredients. Such accessory ingredients may include flavoring, an agent to retard crystallization of the sugar or an agent to increase the solubility of any other ingredient, e.g., as a polyhydric alcohol, for example, glycerol or sorbitol.

[00110] Formulations for rectal administration may be presented as a suppository with a conventional carrier, e.g., cocoa butter or Witepsol S55 (trademark of Dynamite Nobel Chemical, Germany), for a suppository base.

[00111] Formulations for oral administration may be presented with an enhancer. Orally-acceptable absorption enhancers include surfactants such as sodium lauryl sulfate, palmitoyl carnitine, Laureth-9, phosphatidylcholine, cyclodextrin and derivatives thereof; bile salts such as sodium deoxycholate, sodium taurocholate, sodium glycocholate, and sodium fusidate; chelating agents including EDTA, citric acid and salicylates; and fatty acids (e.g., oleic acid, lauric acid, acylcarnitines, mono- and diglycerides). Other oral absorption enhancers include benzalkonium chloride, benzethonium chloride, CHAPS (3-(3-cholamidopropyl)-dimethylammonio-1-propanesulfonate), Big-CHAPS (N, N-bis(3-D-gluconamidopropyl)-cholamide), chlorobutanol, octoxynol-9, benzyl alcohol, phenols, cresols, and alkyl alcohols. An especially preferred oral absorption enhancer for the present invention is sodium lauryl sulfate.

[00112] Alternatively, the compound may be administered in liposomes or microspheres (or microparticles). Methods for preparing liposomes and microspheres for administration to a patient are well known to those of skill in the art. U.S. Pat. No. 4,789,734, the contents of which are hereby incorporated by reference, describes methods for encapsulating biological materials in liposomes. Essentially, the material is dissolved in an aqueous solution, the appropriate phospholipids and lipids added, along with surfactants if required, and the material dialyzed or sonicated, as necessary. A review of known methods is provided by G. Gregoriadis, Chapter 14, "Liposomes," *Drug Carriers in Biology and Medicine*, pp. 287-341 (Academic Press, 1979).

[00113] Microspheres formed of polymers or proteins are well known to those skilled in the art, and can be tailored for passage through the gastrointestinal tract directly into the blood stream. Alternatively, the compound can be incorporated and the microspheres, or composite of microspheres, implanted for slow release over a period of time ranging from days to months. See, for example, U.S. Pat. Nos. 4,906,474, 4,925,673 and 3,625,214, and Jain, *TIPS* 19:155-157 (1998), the contents of which are hereby incorporated by reference.

[00114] In one embodiment, the Dear activator or inhibitor of the present invention can be formulated into a liposome, microparticle, nanoparticle, etc. which is suitably sized to lodge in capillary beds following intravenous administration. When the liposome, microparticle or nanoparticle is lodged in the capillary beds surrounding ischemic tissue, the agents can be administered locally to the site at which they can be most effective. Suitable liposomes for

targeting ischemic tissue are generally less than about 200 nanometers and are also typically unilamellar vesicles, as disclosed, for example, in U.S. Pat. No. 5,593,688 to Baldeschweiler, entitled "Liposomal targeting of ischemic tissue," the contents of which are hereby incorporated by reference.

[00115] Preferred particles are those prepared from biodegradable polymers, such as polyglycolide, polylactide and copolymers thereof. Those of skill in the art can readily determine an appropriate carrier system depending on various factors, including the desired rate of drug release and the desired dosage.

[00116] In one embodiment, the formulations are administered via catheter directly to the inside of blood vessels. The administration can occur, for example, through holes in the catheter. In those embodiments wherein the active compounds have a relatively long half life (on the order of 1 day to a week or more), the formulations can be included in biodegradable polymeric hydrogels, such as those disclosed in U.S. Pat. No. 5,410,016 to Hubbell et al. These polymeric hydrogels can be delivered to the inside of a tissue lumen and the active compounds released over time as the polymer degrades. If desirable, the polymeric hydrogels can have microparticles or liposomes which include the active compound dispersed therein, providing another mechanism for the controlled release of the active compounds.

[00117] The formulations may conveniently be presented in unit dosage form and may be prepared by any of the methods well known in the art of pharmacy. All methods include the step of bringing the active compound into association with a carrier which constitutes one or more accessory ingredients. In general, the formulations are prepared by uniformly and intimately bringing the active compound into association with a liquid carrier or a finely divided solid carrier and then, if necessary, shaping the product into desired unit dosage form.

[00118] The formulations may further include one or more optional accessory ingredient(s) utilized in the art of pharmaceutical formulations, e.g., diluents, buffers, flavoring agents, binders, surface active agents, thickeners, lubricants, suspending agents, preservatives (including antioxidants) and the like.

[00119] Compounds of the present methods may be presented for administration to the respiratory tract as a snuff or an aerosol or solution for a nebulizer, or as a microfine powder for insufflation, alone or in combination with an inert carrier such as lactose. In such a case

the particles of active compound suitably have diameters of less than 50 microns, preferably less than 10 microns, more preferably between 2 and 5 microns.

[00120] Generally for nasal administration a mildly acid pH will be preferred. Preferably the compositions of the invention have a pH of from about 3 to 5, more preferably from about 3.5 to about 3.9 and most preferably 3.7. Adjustment of the pH is achieved by addition of an appropriate acid, such as hydrochloric acid.

[00121] The preparation of a pharmacological composition that contains active ingredients dissolved or dispersed therein is well understood in the art and need not be limited based on formulation. Typically such compositions are prepared as injectables either as liquid solutions or suspensions, however, solid forms suitable for solution, or suspensions, in liquid prior to use can also be prepared. The preparation can also be emulsified.

[00122] The following is the sequence for rat Dear:

[00123] Rattus norvegicus dual endothelin 1, angiotensin II receptor (Dear), mRNA:
GeneID: 446170 Locus tag: RGD:1303105

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1  tttctaaatg attacttttc tagatacctg tttacaaaac agaagatcct ccctttgaaa
61  ccaaaactaaa ctacacttga agaataataa gtgcacaaaag gaagaccacg atgaatcagt
121 accacccatc ttcccagcat tcaagaatgt tcagcgcaca ggaggtgcac agtaagtgtt
181 cctgagagga gtggatacaa cactcaatta tctgggcatg taatgctgat ctgcggtttc
241 ctttacatca gccggcctcc ttcccgttg ggatcaagga agtgaacaga tgcagactca
301 ctctggcagg caccactgag ccagccattt actctcactg catagcaaag ttattttgtc
361 aacttgtttc caggatcctc tgcttcacac gagcagaaac acctcgtcta ggggattctg
421 atccttacct tcttctttac atttctctct ccagagaagg ttatcctcag ccaaaatcct
481 ccagtatcga caggtctgag ccgcttgacg cagggtctttg ggttcaggga atgaaagtac
541 atagagtgcg agctatggaa aaggaaataa gggaggcaca ctcacagaca tcacagaaga
601 aagggttactc tacgaagggt gagcattgag ctgggactgc tggatttcag tgggctgaac
661 gaatcaagag aagcagcatt ttaagagcaa agaaaatgct catcattctc acattaggaa
721 tctgagggtt tactctgggt aacctgtgat tctattggta tttccttaca aagtgagaac
781 aatgccactt atcacaagtt tcttgtgtga gccagtgct caagctctta gataatccaa
841 ataaatgttg ataaagagac tttatattgt tcataccaat tatcaaaaaa tacaagtaca
901 tttcatgtca gtgtggtaat aatgttttaa ataacacact tccctacagg gttaagtcta
961 tgccattatt cttccacgca gacataaagc acttcccaaa tgaagaacac cccagtagtc
1021 agaaacaaaa accatagctg atatgctaag acagggctct ctcttttgta acttcttttt
1081 tcctcaggaa gtctttgaaa gaacacagaa gccaaagaaa tcttttgggg ttttaccttt
1141 tattaatcat ctgtgcttac ttcttaaaat tctaaaacac tttcaaattt gggggactgg
1201 tgatggctca gtcagtaagg tttcatgaag atgagggctc ggatcctggc agtcttgga
1261 agtcaggcat ggcagttcta gctatagtca ctgctcactg gacagccagc caccgtagct
1321 aaaggcgtaa gctccagact cagtgaagca cgacatggca aaaacaacat ggatcagctg
1381 agggatacac ctctggcctc cacgggcaca tacgtgcagg agcatctgaa tgtacttatg
1441 tatacccaca cgaatacata cacatcctac acacatacac actctacagg aggtatcggg
1501 catgtaagat aatccagacg aatattcact tcacgccctg atggcagcaa agggatctcg
1561 tgttactttc ataagtttag tcaaagagtt ctgatgtaga aaaagctcac aagagcaaac
1621 acttttcttc tgggacactg tcacctttta aaagtactca aaagggggga aagtgccagg
1681 aaaaagatga tttatcaatt tgctttcccc cagaattata ttttaattca tcaattttac
1741 tcaaatctaa tgccagattc taactaggac tatatttaat gccactagga ctttagagtg
1801 atcatctaag aaaggagaaa gcaagactct tcctgttcaa atgaggtttc gggatcatct
1861 gtatgaagga tgtggtagtt ttttgatgct gtctttttta ctgctattta taacatgtgt
1921 atagtaattt gagaaaatat ggactatggg gcattatcta atatcacatt atttcttctc

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1981 tttgataaaa attaagctat gaagtctaata gtcaatatgt gcattatatt taaaccatca
2041 gccacacatg gctgtatgac taagtgccta agaatccaat ttttttgtgg tatctctctc
2101 tctccctctc tccgtatgtg tgtgtctttc tctgtctctg tctctctctc totttctctc
2161 tgacgaagga tgataagtag aaatgccata aaaacatata gataaatttt atatatgtgg
2221 ggctggagag atggctcagt ggttgagaac actgactggt cttcagaggt cctgaggttaa
2281 attcccagca accacatggt agctcacaac catctatatt gcatctgatg cctctctctg
2341 gtgtgtctaa agacagctac cggatatactt acatataata aataaatctt taaaaaaatt
2401 ttttataatat taaaaaaaaa tcacataatg taataaccag gagaaatagc aacaatcgat
2461 aaaattactg gtcttgaagg ggcattaaat aattagcaaa ataaaaacaa aattaatatt
2521 gttgcttagt gaatccagaa ttttgaaaac atccactata tataataaac ataccaacta
2581 actaaagtca gccttttagat aaccagggga aaactgaaga gactcggcga cttcacatga
2641 agccttactt tatccaagcg gaagaaagca gcaccttggt atgagcacac tttatgtaac
2701 agctgtacca aaaagccaca gcagtttgcc aaagtgtcaa gccatgatga gcaggacact
2761 gcttacaggc atggctatgt atctggacag cagccatgcg ggtgctgcat ccatgcaggt
2821 gagctggcgc cccttactca cctctttggg gagcaaggag atgaagtctc gctggaactg
2881 gggtcgatc acttgcatca tgtgcttcac ttgtgtgggt tcacagctat cgatgagctc
2941 atctaaggcc agcaacttct ctggtccact ccagctctac caaagaggaa ttggacacat
3001 tacaaatcca tacagaagac caccagcacc tgcattggcca tgttcgagca gtggaactac
3061 atgaaagggg accgtggaca gagaccttgt ctccagaagc caccagagcg atagcagttt
3121 ttagtttcag caagtttact cagtaccttt cccgcaaagc attaaaagtc atgactggca
3181 gaaaaataag tctgcattta tttttaatta taagacttat gctaacacca agacactggg
3241 agacacacaa tatccatctg ggttattgac tag (SEQ. ID. NO. 1)

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[00124] Translation="MSTLYVTAVPKSHSSLPKCQAMMSRLLTGMAMYLDSSHA GAASMQVSWPPLLTSLGSKEMKSRWNWGSITCIMCFTCVGSQLSMSSSKASNFSGPL QLYQRGIGHITNPYRRPPAPAWPCSSSGTT" (SEQ. ID. NO. 2)

EXAMPLE 1

[00125] The inbred Dahl/JR rat model is an established model of human essential hypertension comprised of a salt-sensitive, hypertensive strain (Dahl S) with its cognate salt-resistant, normotensive control strain (Dahl R) (52). To investigate the involvement of Dear in hypertension pathogenesis we obtained cDNAs spanning the entire amino acid coding region for both Dahl S and Dahl R receptors. Two nucleotide differences were detected resulting in two non-conservative amino acid substitutions: T²⁸¹⁴ (Dahl S)/C²⁸¹⁴ (Dahl R) nucleotide transition resulting in S44P substitution and T²⁹⁰¹ (Dahl S)/C²⁹⁰¹ (Dahl R) nucleotide transition resulting in M74T substitution (Figure 1A, 1B). The S44P substitution is located in the putative AngII binding site in the extracellular domain; while the M74T substitution is located in the putative transmembrane domain (Figure 1B). The Dahl S cDNA nucleotide sequence is identical to the previously reported Sprague Dawley rat brain Dear cDNA (1). We note that both the Dahl S and Dahl R rat strains were derived from the Sprague Dawley strain (52).

[00126] The S44P substitution spans the predicted AngII binding domain within the Dahl R Dear variant (1) (Figure 1B) suggesting the hypothesis that AngII-binding will most likely be different between Dahl S and Dahl R receptors. In order to examine this hypothesis, we first determined that there is no significant difference in Dear expression levels between Dahl

S and Dahl R rats at 12 weeks of age in both male and female rats as detected by western blot analysis comparing Dahl S and Dahl R kidney membranes (Figure 1C). To examine hormone binding, both Dahl S and Dahl R receptors were transiently expressed in Cos1 cells respectively and tested for both AngII and ET-1 binding. Dahl R *Dear* do not exhibit AngII binding, but exhibit normal ET-1 binding as shown by direct radioligand binding (Figure 2 and Table 1), and by west-western blot analysis (i.e., labeled ligand [west] binding to receptor polypeptide on western blot) of Dahl S and Dahl R rat kidney membranes and Dahl S and Dahl R *Dear* Cos1-transfectant cell membranes (Figure 2C). These data demonstrate that the Dahl S *Dear* variant is a dual receptor binding both ET-1 and AngII similar to the brain-derived clone first characterized (1), but that the Dahl R *Dear* variant responds solely to ET-1 stimulation. Two affinity binding sites for ET-1 are detected in Dahl S and Dahl R receptors (Figure 3, Table 1) and two affinity binding sites for AngII in Dahl S receptors (Figure 3, Table 1) consistent with previous characterization (1). Furthermore, when compared to the Dahl R *Dear* S44P/M74S variant, the Dahl S *Dear* S44/M74 variant exhibits 3-fold increased affinity for ET-1 (Dahl R: S44P/M74T K_H ET-1 = 12.0 ± 1.12 pM; Dahl S: S44/M74 K_H ET-1 = 4.42 ± 0.89 pM, $P < 0.001$, Table 1) – suggesting an enhanced response of the Dahl S receptor to ET-1 stimulation compared to the Dahl R receptor.

[00127] Based on its localization to the predicted AngII-binding site, it is likely that the S44P substitution accounts for the observed absent AngII binding in Dahl R *Dear*. Interestingly, this S44P substitution and resultant differential AngII binding elucidates for the first time a natural occurring mutation within a peptide-ligand binding domain predicted by the molecular recognition theory (1).

[00128] Having found functionally significant variants between Dahl S and Dahl R *Dear* genes, we then investigated the potential genetic contribution to hypertension susceptibility by performing independent QTL analysis on both male ($n = 106$) and female ($n = 102$) F2 [RxS]-intercross rats phenotyped for blood pressure by radiotelemetry after 8 and 12 weeks of high salt (8 % NaCl) challenge respectively (Table 2). The high-salt diet challenge was extended 4 weeks longer for the F2 [RxS]-intercross female rats since female BP phenotype was much lower than in male F2 [RxS]-intercross rats (average F2 [RxS]-intercross male SBP after eight weeks of high salt diet = 157.2 ± 14.2 mmHg; average F2 [RxS]-intercross female SBP after twelve weeks of high salt diet = 145.0 ± 11.4 mmHg, Table 2). Using an SSCP-based *Dear* gene-specific marker (Figure 4A), we mapped the rat *Dear* to chromosome

2 (physical position in the current assembly of the rat genome: 2q34, 176.687 Mb), 4.5 cM centromeric to the α 1-Na,K-ATPase locus, *ATP1A1*. A total chromosome-2 scan was then done with 11 informative markers that distinguish Dahl R and Dahl S strains. Marker regression and interval mapping analyses detect a single chromosomal region with suggestive linkage to mean, systolic and diastolic BP, peaking at *ATP1A1* + 2 cM (LOD = 1.70) in the F2 [RxS] male cohort (Fig. 4B, Table 2). In contrast, chromosome-2 scan analysis of F2 [RxS]-intercross females revealed two QTLs on chromosome 2, one centered at *D2Rat143* (LOD = 2.43, significant linkage) and the other centered at *Dear* – 5 cM (LOD = 3.61, highly significant linkage) (Figure 4C, Table 2). To assess pathophysiological relevance, analysis of *Dear* allele-specific contribution (Table 3) reveals that the Dahl S S44/M74 variant increases susceptibility to hypertension regardless of BP parameter – systolic, diastolic or mean arterial pressure with greatest changes in mean arterial pressure (ANOVA $P < 10^{-3}$ to 10^{-4}). Concordance of results in different blood pressure parameters provide evidence delineating the *Dear* locus as a gene for hypertension susceptibility in F2 [RxS]-intercross female rats.

[00129] To date, only *Dear* (shown here) and *ATP1A1* (38, 43) genes exhibit functionally significant variants between Dahl S and Dahl R rats with demonstrated pathogenic relevance to hypertension. These data forward said two loci as candidate genes for the *Dear* – 5 cM QTL region on chromosome 2 affecting BP in female F2 [RxS]-intercross rats based on a 4-parameter analysis framework for hypertension genes (37, 54). The causal role of *ATP1A1* in hypertension has been shown by transgenesis in both male and female Dahl S rats (38). While putative gene interactions need to be investigated for *Dear*, *ATP1A1*-Na,K,2Cl-cotransporter (*NKCC2*) gene-interaction has been detected to increase susceptibility to high blood pressure in cosegregation analysis of F2 [RxS] intercross rats (39). This epistatic nature of the *ATP1A1* effect on BP could account for the reduced statistical significance of linkage to BP detected at *ATP1A1* when analyzed as a single locus as done in this chromosome 2 scan and in previous F2-intercross and congenic studies (34, 53).

[00130] To further analyze the *Dear* locus in the context of previous genetic rat model studies which report chromosome 2 QTLs for BP which span the *Dear* locus (31, 34, 41, 51, 59), we assessed *Dear* variants on WKY, SHR, BN and LEW rat strains used in said studies by SSCP analysis. As shown in Figure 4A, the Dahl R *Dear* S44P/M74T variant is detected in Dahl R and LEW strains, while the Dahl S *Dear* S44/M74 variant is detected in SHR, WKY and BN strains. Detection of variant-specific alleles in the different strains was

corroborated by direct nucleotide sequencing of two independent *Dear* cDNA clones spanning the entire amino acid coding region (data not shown). Since SHR, WKY and BN rat strains have the S44/M74 Dahl S *Dear* allele, the *Dear* locus is *a priori* eliminated as a candidate gene for the chromosome 2 QTL for BP in F2-intercross studies derived from these strains (31, 41, 51, 59). The *Dear* locus is also eliminated as candidate gene for the reported chromosome 2 BP QTL in F2 [Dahl S x LEW]-intercross study which investigated males only (34), since the *Dear* S-variant cosegregates with high blood pressure in females.

[00131] Thus, observations from genetic, molecular and pathophysiological analyses suggest that modification in the balance of AngII and ET-1 receptor systems through variant *Dear* contributes to hypertension susceptibility in female F2 [RxS]-intercross rats. The data reiterate the importance of gender-specific factors in hypertension susceptibility and the role of *Dear* in AngII-ET-1 response-balance.

MATERIALS and METHODS

Characterization of Dahl S and Dahl R *Dear* cDNAs

[00132] Dahl S and Dahl R *Dear* cDNAs were RT-PCR from Dahl S/JRHsd and Dahl R/JRHsd rat kidney PolyA⁺ RNAs respectively (Forward primer: 5'-AAG-AAA-GCA-GCA-CCT-TGG-T-3' (SEQ. ID. NO. 3); Reverse primer: 5'-CGT-GGA-CAG-AGA-CCT-TGT-CT-3' (SEQ. ID. NO. 4)) and subsequently subcloned into the PT-vector system (Clontech, Palo Alto, CA). Primer sequences were obtained from the previously reported Sprague Dawley *Dear* cDNA (GenBank accession number AY664492). The cDNAs (432 bp) encompassing the entire *Dear* amino acid coding region was then sequenced on both strands. Six Dahl S and six Dahl R rats were sequenced showing no intra-strain sequence heterogeneity.

Detection of the *Dear* gene S44P/M74T variant by single strand conformation polymorphism (SSCP) analysis

[00133] Dahl S/jrHsd, Dahl R/jrHsd, LEW/SsNHsd, WKY/NHsd, SHR/NHsd and BN/Hsd rats were purchased from Harlan Inc. (Indianapolis, IN). SSCP analysis was performed on genomic DNA isolated from the different rat strains essentially as described (60). The SSCP

marker was based on a PCR product encompassing nucleotides 2774 - 2911 (spanning the S44P substitution) within the amino acid encoding region of the Dear cDNA (forward primer: 5'-GCT-ATG-TAT-CTG-GAC-AGC-AGC-3' (SEQ. ID. NO. 5); reverse primer: 5'-AGT-GAA-GCA-CAT-GAT-GCA-AGT-3' (SEQ. ID. NO. 6); product: 137 bp) (1). The SSCP marker was detected by 6 % non-denaturing polyacrylamide gel electrophoresis.

Receptor expression and membrane preparation

[00134] The Dahl S and Dahl R Dear cDNAs were subcloned directionally (5' to 3') into the pcDNA (+) expression vector (Invitrogen, Carlsbad, CA) and transiently expressed in Cos1 cells (ATCC). Cos1 cells were transfected with the expression vectors via lipofectin-mediated gene transfer and cell membranes were isolated 72 hr post-transfection for hormone binding. Rat kidney membranes were prepared essentially as described (42). COS-1 cell membranes were isolated as described (36). Briefly, cells were washed twice in phosphate-buffered saline and homogenized in 10-fold ice-cold buffer (0.25 M sucrose, 1 mM EDTA, 50 µg/ml aprotinin, 10 µg/ml leupeptin, 100 µM phenylmethylsulfonyl fluoride, 25 mM Imidazol/HCl, pH 7.4). The homogenate was centrifuged at 5,000g for 15 min and the pellet was discarded. The supernatant was then centrifuged at 27,500g for 30 min and the resulting pellet was washed twice in ice-cold suspension buffer (5 mM MgCl₂, 0.2 mM EDTA, 50 mM Hepes, pH 7.4). The final pellet was resuspended into the appropriate assay buffer and quickly frozen in liquid nitrogen. The membrane preparations were store at -80 °C until use. Protein concentrations of the membranes were determined by BCA protein assay kit (PIERCE).

Radioligand binding assays

[00135] Binding of [¹²⁵I]Tyr⁴-angiotensin II and [¹²⁵I]Tyr¹³-endothelin-1 to COS-1 membranes was performed by a rapid filtration method (32, 50). Briefly, [¹²⁵I]Tyr⁴-angiotensin II (0.25 ~ 6.5 nM) or [¹²⁵I]Tyr¹³-endothelin-1 (0.045 ~ 1.46 nM) was incubated with membranes (100µg) for 20 min at 37 °C in 100µl buffer A (5 mM MgCl₂, 0.2 mM EDTA, 10 mg/ml BSA, 10 mM Hepes, pH7.4). Binding reactions were terminated by the addition of 1ml ice-cold buffer A and immediately filtered through a Whatman GF/C filter (presoaked overnight at 4 °C in 10 mg/ml BSA) and subsequently washed with 15 ml ice-cold buffer A. Specific binding was determined as the difference between the total radioactivity bound to membranes and the radioactivity bound to blanks containing 1µM AngII or 1µM

ET-1. The dissociation constant (K_d) and maximum ligand-binding sites ($B_{\max}$) were determined using Hill plot analysis (55). Hill coefficient values (h) were calculated from the relationship $\ln[B/(B_{\max} - B)] = h \ln[\text{free Radioligand}] - \ln K_d$. An F test ($P < 0.05$) was used to determine whether the saturation binding curves best fitted one or two independent binding sites. The data were best fit by two affinity states determined by Scatchard plot analysis; K_H and K_L designate the K_d for high- and low-affinity states of the receptor, respectively (44). Most results are expressed as the mean $\pm$ SE (standard error) from three to five independent experiments.

Western and west-western blotting analysis

[00136] A polyclonal rabbit anti-peptide antibody raised against the synthetic peptide P₅₁LLTSLGSKE₆₀ (SEQ. ID. NO. 7) was utilized for western blot analysis (1). Plasma membranes (40 μ g protein/lane) were subjected to 12.5% SDS-PAGE and the separated proteins electro-transferred onto PVDF membranes which were incubated with blocking buffer (0.3% Tween-20, 5% non-fat milk, 137 mM NaCl, 2.7 mM KCl, 8.1 mM Na₂HPO₄, and 1.5 mM KH₂PO₄, pH 7.4) for 2 hr at room temperature, and then incubated with primary antibody (1:500) for 16 hr at 4°C. The PVDF membranes were then sequentially incubated with biotinylated goat anti-rabbit IgG followed by immunostaining with horseradish peroxidase-linked streptavidin. To confirm the interaction between Dear and ligands, we performed west-western blot analysis (62). Briefly, protein blots of kidney and COS-1 cell membranes were incubated with radioligands (0.5 μ Ci in 10 ml) in buffer A at 37 °C for 16 hr. PVDF membranes were then washed three times for 15 min with buffer A at 37 °C and exposed to X-ray film at -80 °C for 1-3 days.

Genetic crosses

[00137] Dahl S/jrHsd and Dahl R/jrHsd rat strains (Harlan, Indianapolis, Indiana) were used to develop the F2 cohort. The F2 cohort was derived from brother-to-sister mating of F1 (R female x S male) hybrids to produce the F2 male ($n = 106$, carrying exclusively Y chromosomes from the Dahl S genetic background) and F2 female ($n = 102$) segregating populations.

Phenotypic characterization of F2 cohorts

[00138] All animal procedures were performed in accordance with institutional guidelines. Animals were maintained on a LabDiet 5001 rodent chow (Harlan Teklad, Madison WI) containing 0.4 % NaCl from weaning until the high salt diet begun at 12 weeks of age. The food pellets and water were made available ad lib. Blood pressure (BP) was measured essentially as described (38) using intra-aortic abdominal radiotelemetric implants (DATASCIENCE) obtaining non-stressed blood pressure measurements taking the average over ten-seconds every 5 minutes for 24 hours (38). Systolic (SBP), diastolic (DBP) and mean arterial pressures (MAP) were obtained along with heart rate and activity. The protocol for the F2 rats was as follows: implant surgery at 10 weeks of age; only rats with no post-operative complications were used; after 12 days, baseline BP levels were obtained. High salt (8% NaCl) challenge was begun at 12 weeks of age and maintained for eight weeks for male and twelve weeks for female F2-intercross rats; a longer high-salt challenge was necessary for females to attain a similar F2-mean BP since BP in females is lower. BP values used for phenotype are the averages obtained in the final week of the salt loading from a 24-hour recording during a no-entry day ascertaining non-stress BP. We note that baseline BP means for SBP, DBP and MAP were equivalent, ± 1 mmHg range for all three BP parameters among the different *Dear* genotypes ($P > 0.5$).

Intercross linkage analysis

[00139] Genotyping was done with 10 chromosome-2 microsatellite markers informative for our Dahl [RxS] intercross and one SSCP-based *Dear* marker (described above). Marker regression and QTL analyses was performed with the Map Manager QTXb17 (MMQTXb17) program (46) using MAP as quantitative trait. MMQTXb17 generates a likelihood ratio statistic (LRS) as a measure of the significance of a possible QTL. Genetic distances were calculated using Kosambi mapping function (genetic distances are expressed in cM). Critical significance values (LRS values) for linkage were determined by a permutation test (2000 permutations at 10 cM interval) on our male and female progenies using Kosambi mapping function and a free regression model. Thus, the minimum LRS values for the F2 male cohort were for Suggestive linkage = 4.1 (LOD = 0.89); for Significant linkage = 10.6 (LOD = 2.30); for Highly Significant linkage = 18.4 (LOD = 4.00) and for the F2 female cohort were for Suggestive linkage = 3.9 (LOD = 0.85); for Significant linkage = 9.9 (LOD = 2.15); for

Highly Significant linkage = 16.6 (LOD = 3.61). LRS 4.6 delineates LOD 1-support interval. Confidence interval for a QTL location was estimated by bootstrap resampling method wherein histogram single peak delineates the QTL and peak widths define confidence interval for the QTL. Histograms which show more than one peak warn that the position for the QTL is not well defined or that there may be multiple linked QTLs (QTX Map Manager) (46).

EXAMPLE 2

[00140] We isolated the mouse *Dear* gene from a 129 SVJ mouse genomic library. Molecular characterization detects a one-exon transcription unit (Fig. 5A). The mouse receptor polypeptide contains 127 amino acids showing 78 percent homology with the rat receptor and binds solely ET-1 (data not shown) resembling the recently characterized Dahl R *Dear* S44P/M74T rat variant (2), and suggesting that observations in *Dear*^{-/-} mice are most likely not AngII-mediated. The mouse *Dear* mRNA is detected in all tissues tested with the highest level of expression in kidney and aorta (Fig. 5B).

[00141] Targeted inactivation of *Dear*^{-/-} in ES cells was done by replacement of the genomic region spanning amino acids 81–127 of *Dear* with a PGK-neomycin cassette (Fig. 5A) resulting in the deletion of the last 47 amino acids of the *Dear* polypeptide, including the putative G-protein interacting domain (1). Screening for homologous recombination was done on 196 G418-resistant colonies by Southern blot analysis (Fig. 5C). Targeting events were confirmed by polymerase chain reaction (PCR) amplification using a neomycin-specific primer and a primer flanking the integration site. Production of the expected size fragment (5.5 Kb) was indicative of a targeting event (Fig. 5D). Five ES cell clones carrying the targeted *Dear* mutation were injected into 129SVJ blastocysts and implanted into pseudopregnant foster mothers. We obtained 14 chimeric mice (representative of 2 independent targeted ES cell clones). Chimeras were bred to C57BL/6J mice and shown to germ line transmit, producing F1 progeny.

[00142] Heterozygous *Dear*-deficient (*Dear*^{+/-}) male and female mice (backcross-10 inbred C57BL/6 mouse strain) exhibit 50% less *Dear* protein in mouse kidney protein blot analysis as detected using an anti-mouse *Dear* anti-peptide specific antibody (Fig. 5F; $P < 0.05$, t-test), less body weight at 5 and 6 months of age (males: $P = 0.007$; females: $P = 0.0006$) (Fig. 5I) and decreased blood pressure in female (*Dear*^{+/-}: 134 ± 4.0 mmHg vs *Dear*^{+/-}: 112.3 ± 6.1 ; $P < 0.01$) but not in male mice while heart rate remains equivalent (Fig.

5G-H). Gender-specific blood pressure effects are concordant with observations in a recent study of rat genetic hypertension wherein *Dear* variants cosegregated with hypertension in female but not in male F2-intercross rats (2).

[00143] To assess potential embryonic lethality of the gene-targeting event, we analyzed progeny from F1-*Dear*^{+/-} male and female cross which were genotyped for the presence/absence of the targeted *Dear* allele. Sixty-eight pups were produced from 17 litters showing the following genotype distribution: 29 wild type (+/+), 39 heterozygous (+/-), 0 null (-/-). The absence of null genotypes in the F2 progeny demonstrates that *Dear* null mutation is embryonic lethal.

[00144] In order to investigate embryonic lethality in *Dear*^{-/-} embryos, we analyzed embryos from timed-pregnancies derived from *Dear*^{+/-} mice at different stages of development to determine the exact developmental stage in which lethality occurs. We produced 129 embryos (from E9.5 to E12.5) detecting 33 (-/-), 67 (+/-) and 29 wildtype (+/+) genotypes (Fig. 5D). This conforms to the expected segregation ratio 1 (+/+) : 2 (+/-) : 1 (-/-) for a standard (+/-) x (+/-) intercross. Analysis of the embryos revealed that lethality occurs around E12.5.

[00145] Anatomic analysis of E9.5-E12.5 embryos reveals absent yolk-sac collecting vessels associated with homozygous *Dear*^{-/-}-deficiency (Fig. 6A-F); heterozygous *Dear*^{+/-} deficient embryos exhibit normal yolk sac vascularization (data not shown). All embryos with absent yolk-sac collecting vessels are *Dear*^{-/-} by genotype; heterozygous *Dear*^{+/-} deficient embryos are not distinguishable from *Dear*^{+/+} embryos (data not shown). Hemorrhagic, resorbed embryos were detected as early as E10.5 but mostly at E12.5 (Fig. 6D). Although smaller and strikingly paler than *Dear*^{+/+} and *Dear*^{+/-} embryos, *Dear*^{-/-} embryos exhibit two size phenotypes: a dysmorphic phenotype detected at E10.5-E12.5 (Fig. 6A-C) that is relatively larger than a second, hypoplastic phenotype (Fig. 6E-F). In order to determine whether genetic variation influences the null phenotype, speed congenics were done onto C57BL/6j genetic background and backcross-10 null mice were generated and analyzed confirming embryonic range of lethality, absent yolk-sac collecting vessels and both embryo morphology phenotypes in *Dear*^{-/-} embryos (Fig. 6A-F).

[00146] At E10.5 and E11.5, blood-filled pumping hearts were detected in larger dysmorphic *Dear*^{-/-} mice (Fig. 6B, 6C), but not apparent in hypoplastic *Dear*^{-/-} mice (Fig. 6E,

F). *Dear*^{-/-} E10.5 embryos lack the vascular network formation marked by prominent blood-filled dorsal aortae (Fig. 6G) and blood vessels in the cranial region which are normal features characteristic of E9.5 *Dear*^{+/+} embryo (Fig. 6G left panel). Furthermore, E10.5 *Dear*^{-/-} embryos exhibit disorganized, blood-filled pools in the cranial region without apparent connection to a blood-filled heart (Fig. 6G) observed to pump (data not shown) despite lack of vascular networking. In contrast to E11.5 *Dear*^{+/+} embryo, E11.5 dysmorphic-type *Dear*^{-/-} embryo exhibits minimal and altered vascular networks in both cranial and caudal regions, dilated heart albeit blood-filled, and altered brain development (Fig. 6H). Furthermore, while both *Dear*^{-/-} and *Dear*^{+/+} E11.5 hearts pump, observation of cardiac pumping reveals single chamber filling and contraction in *Dear*^{-/-} embryos, in contrast to distinct filling and pumping of ventricles in E11.5 *Dear*^{+/+} embryo (data not shown). In E10.5 and E11.5 hypoplastic *Dear*^{-/-} embryos, minimal cardiovascular development is detected (Fig. 6E-F). Altered brain and cardiac development is confirmed in the analysis of cleared, fixed E11.5 embryos revealing poor delineation of brain regions particularly the telencephalon and cardiac chamber formation (Fig. 6I).

[00147] In summary, analysis of dysmorphic *Dear*^{-/-} embryos at E10.5 and E11.5 detects blood-filled hearts (Fig. 6G-H) which contracted, despite aberrant vascular formation typified by disorganized, blood-filled pools in the cranial region without apparent connection to a blood-filled heart (Fig. 6G), or minimal vascular networks in both cranial and caudal regions, and a dilated blood-filled heart (Fig. 6H). This contrasts the prominent vascular network marked by blood-filled dorsal aorta and blood vessels in the cranial region which are characteristic features of E9.5 *Dear*^{+/+} embryo (Fig. 6G). Furthermore, analysis of fixed E11.5 embryos reveals abnormal brain and cardiac development in *Dear*^{-/-} embryos (Fig. 6I).

[00148] Histological analysis of Masson-trichrome stained E10.5-E11.5 embryo sections confirm minimal to absent collecting vessels in the yolk sac in *Dear*^{-/-} embryos (Fig. 7A) compared with *Dear*^{+/+} (Fig. 7B) at E10.5. The yolk-sac plexus of smaller vessels are present, with fewer nucleated red blood cells (Fig. 7A). A few are enlarged (Fig. 7A). Blood islands are present but the number of nucleated red blood cells is decreased in *Dear*^{-/-} embryos (Fig. 7A) compared with *Dear*^{+/+} embryos (Fig. 7B). At E12.5, comparative histological analysis reveals amorphous cellular areas with a lack of apparent organogenesis in dysmorphic-type *Dear*^{-/-} embryos (Fig. 7C) compared with *Dear*^{+/+} (Fig. 7D). High magnification reveals large areas of nucleated red blood cells in the ventral midportion that are not contained in blood

vessels or in recognizable liver tissue (Fig. 7C). The heart is thin-walled, enlarged and with poor delineation of chambers in *Dear*^{-/-} embryos (data not shown) corroborating anatomical observations (Fig. 6). Blood vessels with few nucleated red blood cells are rudimentary, thin-walled and sparse in *Dear*^{-/-} (Fig. 7C) compared with *Dear*^{+/+} (Fig. 7D) embryos most evident in the cranial region. Rudimentary, thin-walled blood vessels are detected in the perineural regions with sparse nucleated rbc in *Dear*^{-/-} (Fig. 7E), in contrast to *Dear*^{+/+} embryos which exhibit perineural blood vessels filled with nucleated rbc and with perivascular sheaths (Fig. 7D, F), thus corroborating the observed vascular network deficiency evident in anatomical analyses (Fig. 6). Concordant with sparse perineural vessels, only a few penetrating capillaries are evident in *Dear*^{-/-} embryo neuroepithelium (Fig. 7G) in contrast to *Dear*^{+/+} embryo (Fig. 7H). Scattered nucleated rbc are detected in the neuroepithelium (Fig. 7G) suggesting possible vascular leakiness and/or failure of vasculogenesis. Immunohistochemical analyses comparing E12.5 *Dear*^{+/+} and *Dear*^{-/-} embryos do not detect upregulation of VEGF, VEGF-receptor 2 flk-1, or angiopoietin-1 and -2 expression (data not shown).

[00149] To further analyze vascular deficits, immunohistochemical staining for smooth muscle cell (smc) α -actin reveals scattered expression in E12.5 *Dear*^{-/-} embryos and intense staining in the embryo-placenta vascular connection (Fig. 9A-F). Perineural blood vessels exhibit α -actin immunostaining in *Dear*^{-/-} embryos but have minimal angiogenic-branching in contrast to *Dear*^{+/+} embryos wherein angiogenic sprouting is evident (Fig. 9A-F). Closer histological analysis reveals sporadic blood islands incompletely circumscribed by α -actin stained single-cell vascular wall in *Dear*^{-/-} embryos (Fig. 9A-F).

[00150] To investigate mouse *Dear* temporal and spatial expression patterns, we analyzed *Dear* expression in E9.5-E12.5 wild type embryos using an anti-mouse *Dear* specific anti-peptide antibody validated to detect *Dear* polypeptide (Fig. 10). At E9.5 days, we detect *Dear* expression predominantly in the heart, yolk sac mesodermal layer and endothelium, fetal vascular endothelium in the placenta, dorsal aorta, and ependymal layer of the neural tube (Fig. 10A). These expression patterns persist at E12.5 days, wherein we detect increased expression in some hemangioblasts in yolk sac blood islands (Fig. 10B), as well as more prominent expression in the ependymal layer of the neuroepithelium and in perineural blood vessel walls (Fig. 10B). Observed temporal and spatial expression patterns are concordant with vascular, cardiac and neuroepithelial phenotypes observed in *Dear*^{-/-} deficient mice.

[00151] In contrast to minimal blood islands in the yolk sac, we detect scattered blood islands in *Dear*^{-/-} embryos but markedly underdeveloped dorsal aorta and peripheral vasculature, suggesting deficiencies in primary vascularization despite the presence of blood islands (Fig. 8A-F). Analysis of cardiac development in adjacent littermates reveals that *Dear*^{-/-} hearts have poor cardiac chamber formation and endocardial cushion formation (Fig. 8A-F), consistent with incomplete cardiac looping observed on analysis of whole embryos (Fig. 6).

[00152] The *Dear*^{-/-} mutant vascular and cardiac phenotypes in the C57BL/6J genetic background (BC10) is similar to that observed in *VEGF*^{+/-} deficient embryos (18, 19), but quite distinct from that observed in previously reported ET-1, ET_A and ET_B receptor null embryos (10-12, 24), as well as AngII, AT1a, AT1b, and AT2 receptor null mutants (14-17). The similarity to *VEGF*^{+/-} deficient mouse vascular phenotype (18, 19) suggests that both VEGF and *Dear*-mediated signaling are necessary for angiogenesis and vascular network development, as well as modulate blood island formation. The fact that both *VEGF* and *Dear* null mutations are embryonic lethal, along with other similar vascular-phenotype null mutants such as transforming growth factor- β 1 (25), suggest that multiple pathways are involved in vascular network formation – all necessary but none sufficient. The slightly later but overlapping range of embryonic lethality indicates that *Dear*-mediated pathways are downstream to VEGF-mediated pathways. The association of vascular network deficiency and arrest of cardiac development in both *VEGF*^{+/-} and *Dear*^{-/-} deficiency suggests that vascular-derived signaling plays a role in the progression of the complex development of the heart into a multi-chambered pump. The finding that *Dear*^{-/-} deficiency results in embryonic lethal vascular network abnormalities, while *ET-1*^{-/-} inactivation does not interfere with vascular networking (10) implies the existence of an alternative ET-1 source that is produced independently of the well known Pre-pro-ET-1 pathway (26) or alternatively, the existence of an [ET-1]-like ligand that activates *Dear* and underlies *Dear*-mediated angiogenic roles.

METHODS

Northern blot analysis

[00153] Total RNA was extracted with TRIzol (Invitrogen, Life Technologies Inc.,) from the different tissues analyzed. PolyA⁺ RNA was subsequently isolated from total RNA using

the Dynabeads mRNA purification kit (DynaL Biotech) as per manufacturer's specifications. PolyA⁺ RNA (3 µg) was run on a 1% formaldehyde-denaturing agarose gel, transferred to Zeta-Probe blotting membrane (Bio-Rad) and UV cross-linked prior to hybridization. Hybridization was done in a buffer containing 5xSSC, 20mM Na₂HPO₄, 7% SDS, 1X Denhardt's, 100ug/ml denatured Calf thymus DNA at 50°C for 24h. A γ-³²P-end labeled anti-sense mouse *Dear* oligonucleotide (5'-AGT-GAT-AGA-GCC-CCA-GTT-CCA-GCG-AGA-CTT-CAT-CTC-CTT-GC-3' (SEQ. ID. NO. 8)) was used as probe. Membranes were washed sequentially with 3XSSC, 5% SDS at 50°C two times for 30 minutes each, and once with 1XSSC, 1% SDS at 50°C for 30 min. Autoradiography was carried out at -80°C with intensifying screen.

Characterization of 129SVJ mouse *Dear* gene

[00154] One million independent recombinants from a λFIXII 129SVJ mouse genomic library were screened with the full-length 3274 bp rat *Dear* cDNA¹ as probe. Six independent genomic clones were identified and plaque-purified after a fourth round of screening. One of them, λ191, was characterized further by restriction digestion and subsequent southern blot analysis. A single 8 kb BamHI/BamHI restriction fragment (that hybridized to the 3274 bp rat *Dear* cDNA probe) was subcloned into psp73 plasmid vector and sequenced.

Targeted disruption of *Dear* in mice and production of chimeric mice

[00155] All animal procedures were performed in accordance with institutional guidelines. A targeting vector was constructed by replacing a 300-bp piece containing the 3'- end of *Dear* with the PGKNeo-cassette (Fig. 5) effectively deleting amino acids 81-127 of *Dear*. The targeting vector was electroporated into 129SVJ ES cells and G418 resistant cell clones were isolated. Genomic DNA was obtained from each ES cell clone, restricted with *SphI* and subjected to Southern blot analysis. A 1.5 Kb fragment of *Dear* was used as probe (Fig. 5). The presence of an 8 Kb endogenous band and a 5.2 Kb band was indicative of homologous recombination (Fig. 5). Homologous recombination was further verified by PCR analysis using an upstream primer (P1: 5'-TGTGAGGCTAGAAGGCTGC-3' (SEQ. ID. NO. 9)) located 171 bp upstream from the 5'-end of the targeting vector and a reverse primer (P2: 5'-GAGCAAGGTGAGATGACAGG-3' (SEQ. ID. NO. 10)) located in the PGKNeo cassette (Fig. 5). Amplification of a 5.5 Kb fragment that hybridized to the same probe used in the Southern blot analysis (Fig. 5) was indicative of homologous recombination. Five positive ES

cell clones were then microinjected into 129SVJ blastocysts generating 14 chimeric mice that were used to establish the *Dear* knockout line. Speed-congenic backcross breeding to inbreed onto C57BL/6 genetic background was done for more than ten generations, $\geq$ BC10, providing all *Dear*^{+/-} and *Dear*^{-/-} mice for analyses (> 99.95 % congenic line in C57BL/6 background).

Characterization of mouse *Dear* cDNA and expression studies

[00156] Mouse *Dear* cDNA was obtained by RT-PCR from C57BL/6 mouse kidney PolyA⁺ RNA (forward primer, 5'-CACACAAAGCCTTACTTTATCC-3' (SEQ. ID. NO. 13); reverse primer, 5'-AAAGCCAGCCTTTAGATAACC-3' (SEQ. ID. NO. 14)), subcloned into the PT-vector system (Clontech, Palo Alto, CA) and then sequenced (GenBank accession no. DQ009865). RNA blot analysis was done as described (1) using PolyA⁺ RNA (3 μ g), γ -³²P-end labeled anti-sense mouse *Dear* oligonucleotide (5'-AGTGATAGAGCCCCAGTTCCAGCGAGACTTCATCTCCTTGC-3' (SEQ. ID. NO. 15)) as probe. Receptor expression studies, ¹²⁵I-ET-1-1 and ¹²⁵I-AngII binding to membranes were done as described (2).

Genotyping of mouse embryos

[00157] Genotyping was done by PCR analysis of genomic DNA isolated from extraembryonic membranes. Primers flanking the *SacI* site localized within the amino acid coding region of *Dear* (upstream primer: 5'-AACTTCTCTGGTCCGCTCC-3' (SEQ. ID. NO. 11); downstream primer: 5'-ACTTGCTGAACTAAAACCTGC-3' (SEQ. ID. NO. 12)) were used to detect the wild type allele (PCR product = 153 bp indicative of the presence of the wild type allele) and primers P1 and P2 (described above) to detect the mutated allele (PCR product = 5.5 Kb indicative of the presence of the mutated allele).

Analysis of heterozygous *Dear*^{+/-} phenotype

[00158] We analyzed backcross BC10[C57BL/6] *Dear*^{+/-} mice for *Dear* protein levels by Western blot analysis using equal amounts of protein (40 μ g) from mouse kidney membranes and rabbit IgG anti-mouse *Dear* anti-peptide specific antibody (1:500 dilution) developed against mouse *Dear* specific synthetic peptide: L₁₆SKCNHNEQDTA₂₇ (SEQ. ID. NO. 16) to detect *Dear*-specific polypeptide. We measured blood pressure in 6 month old mice by tail-

cuff sphygmomanometer (Visitech BP 2000, Visitech CA) under light anesthesia ascertaining equivalent physiologic state by limiting BP measurements to periods with heart rate ranging from 300-500 beats per minute. We obtained three sets of 10 consecutive readings per mouse and took the average of at least 20 readings within the prescribed normal heart rate range.

Histology

[00159] Embryos were collected at embryonic E9.5 – E12.5 days from timed-pregnant mice (counting noon of the day a vaginal plug is detected as E0.5); genotypes were determined by PCR analysis of extraembryonic membrane tissue DNA. Embryos were analyzed and photographed within their yolk sacs, then fixed in 4% freshly prepared PBS-buffered paraformaldehyde. Histology processing and Masson-trichrome staining were done following established procedures. Digital stereophotomicroscopy and bright-field photomicroscopy were done using a Nikon stereomicroscope and Zeis Axioskop microscope respectively. Immunohistochemistry was done essentially as described (27).

EXAMPLE 3

Blood pressure measurements

[00160] Male and female cohorts of Dear KO and wild type (N10 backcross generation) were used to measured BP. Twelve (+/-) and 11 (+/+) female mice and 14 (+/-) and 14 (+/+) male mice were studied. Testing was done at 6 months of age.

[00161] Mice were maintained on regular rodent chow and on a 12-hour light/dark cycle. Mice were transported and allowed to settle in the procedure room 1 hour before measurements were taken. Systolic BP along with heart rate was measured by a programmable tail-cuff sphygmomanometer (Visitech BP 2000, Visitech, NC). Mice were lightly anesthetized with intraperitoneal ketamine (80 mg/kg) and xylazine (18 mg/kg) and placed on the heated platform after a 2 minute interval. Three sets of 10 consecutive readings each were taken per mouse. Data is presented as average of at least 20 readings per mouse spanning the heart rate range of 300-500 bpm.

Results

[00162] As shown in Figure 10A, SBP did not differ between WT and KO male mice (WT, 137.2 ± 5.1 ; KO, 138.6 ± 3.7 ; $t = 0.05$, $P > 0.8$) at 6 months of age. In contrast, SBP is significantly lower in KO female mice when compared with WT female mice (WT, 134.9 ± 4.0 ; KO, 112.3 ± 6.1 ; $t = 3.03$, $P < 0.01$). Mean heart rates did not differ between contrasting groups (Figure 10B) affirming the SBP differences observed between WT and KO female mice. Thus, heterozygosis at the *Dear* locus shows gender-specific effects on BP affecting only females. This result is consistent with recent data suggesting a female-specific effect of *Dear* variants in salt-sensitive hypertension in the Dahl rat model (2).

EXAMPLE 4

[00163] We next investigated the role of *Dear*-inhibition in two established rodent tumor models. First, comparing heterozygous *Dear*^{+/-} deficient mice and wild type *Dear*^{+/+} littermates, we detect significant reduction in tumor mass (Fig. 11A-B) and tumor volume (Fig. 11C-D) in B16-F10 melanoma cell-induced tumor model (74) in heterozygous *Dear*^{+/-} deficient-female (t-test, $P < 0.02$) mice but not in male mice. Secondly, because effects were seen only in female *Dear*^{+/-} mice, we next tested whether *Dear*-inhibition would reduce tumor growth in ¹³⁷Cs-radiation induced breast cancer model (70) in female rats with tumor latency less than 3 months. Using two independent inhibition methods, anti-rat *Dear* anti-peptide specific antibody begun 4 weeks after irradiation (Fig. 11C) and anti-rat *Dear* DNA vaccine begun two weeks after irradiation (Fig. 11D), we detect significant reductions in tumor growth during a 6-week observation period. In contrast to respective control groups, both anti-*Dear* treatments prevented tumor growth with significant reductions in %-change in tumor volume detected from 4-6 weeks after tumor appearance (ab-Rx: $P < 0.05 - 0.01$; DNA-v: $P < 0.02 - 0.001$). Furthermore, we detect significant tumor regression with 68 % reduction in tumor volume in anti-*Dear* DNA-vaccinated rats (Fig. 11D, $P < 0.01$). Inhibition of tumor growth is associated with decrease in malignancy-potential based on tumor pattern, nuclear grade and vascular invasion in both anti-*Dear* antibody and DNA vaccine treated rats compared with age-matched, non-treated control rats (Fig. 11E). Furthermore, decrease in the number of chaotic and mosaic vessels was also detected as a result of anti-*Dear* treatment.

METHODS

Tumor studies and Dear-specific inhibition

[00164] We developed B16-F10 (ATCC) melanoma cell-induced subcutaneous tumor model essentially as described (74) in 10-week old *Dear*^{+/-} and littermate *Dear*^{+/+} male and female mice (*n* = 5 per group). Thirteen days after tumor induction, we excised tumors and measured tumor weight and volume. We induced rat mammary gland tumors in 48 Sprague Dawley rats (*n* = 12 per group) essentially as described (70) at 40 days of age via ¹²⁷Cs-radiation. Only rats with tumor latency less than 3 months were used for study (*n* = 4 for anti-*Dear* anti-peptide antibody; *n* = 3 for control antibody; *n* = 3 for anti-*Dear* DNA-vaccine; *n* = 3 for control pCDNA). We began antibody treatments 6 weeks after irradiation at 12 weeks of age. We used affinity-purified rabbit IgG anti-*Dear* anti-peptide antibody raised against the synthetic peptide P₅₁LLTSLGSKE₆₀ (1) (SEQ. ID. NO. 7). As control, we used rabbit IgG (sc-2027, Santa Cruz Biologicals, Santa Cruz CA). Test and control antibodies were injected thrice weekly intraperitoneally (6 µg/injection) until the end of the study at 6 weeks post tumor appearance. In parallel, we injected test and mock-DNA vaccines – using anti-*Dear* (pCDNA-*Dear*) DNA-vaccine and control expression vector (pCDNA, Invitrogen, Carlsbad, CA) mock-vaccine – two weeks after irradiation at 8 weeks of age, and thereafter bi-weekly until 6 weeks from tumor appearance (500 µg per dose, intramuscularly). Tumor volume was measured using the formula $(4/3\pi r_1^2 \times r_2)$ where *r*₁ is the smaller, and *r*₂ the larger radius as described (71). We used t-test, two-way repeated measures ANOVA and Tukey's post test for multiple pairwise comparisons for statistical analysis as appropriate.

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All references described herein are incorporated herein by reference in their entirety.

Table 1. Ligand affinities for Dear S44P/M74T and S44/M74 variants.

[¹²⁵I]Tyr⁴-Angiotensin II				
<i>Variant</i>	<i>B_{max}</i>	<i>K_H</i> AngII (nM)	<i>K_L</i> AngII (nM)	<i>h</i>
S44P/M74T	no binding	---	---	---
S44/M74	23.6 ± 0.92	0.23 ± 0.08	2.65 ± 0.11	2.63 ± 0.25

[¹²⁵I]Tyr¹³-Endothelin 1				
<i>Variant</i>	<i>B_{max}</i>	<i>K_H</i> ET-1 (pM)	<i>K_L</i> ET-1 (pM)	<i>h</i>
S44P/M74T	20.21 ± 1.59	12.0 ± 1.12	836 ± 38.1	1.45 ± 0.09
S44/M74	26.25 ± 1.29	4.42 ± 0.89	450 ± 12.4	1.41 ± 0.12

Values are mean ± s.e.m.; *B_{max}*, maximum ligand binding sites in pmol/mg membrane protein; *K_H*, dissociation constant for high affinity binding site; *K_L*, dissociation constant for low affinity binding site; *h*, Hill coefficient. * *P* < 0.01 (t-test).

Table 2. Chromosome-2 analysis of F2 [RxS] male and female cohorts.

		F2[RxS]males			F2[RxS]females		
MAP (mean $\pm$ sd)		134.3 $\pm$ 13.1			122.6 $\pm$ 10.4		
Locus Marker		LRS	%	P	LRS	%	P
(*Distance: males/females)							
<i>D2Rat124</i>	[0.0 / 0.0]	1.8	2	0.40800	1.2	1	0.55024
<i>D2Rat196</i>	[9.1 / 7.2]	0.7	1	0.71099	1.1	1	0.57694
<i>D2Rat19</i>	[14.1 / 13.5]	0.9	1	0.62681	2.5	2	0.29225
<i>D2Rat21</i>	[8.4 / 6.1]	1.3	1	0.52159	3.4	3	0.17980
<i>D2Rat143</i>	[12.3 / 14.9]	1.6	1	0.45032	11.4	11	0.00332
<i>D2Rat161</i>	[25.2 / 10.8]	0.2	0	0.91259	8.8	8	0.01247
<i>D2Rat34</i>	[25.8 / 12.4]	4.3	4	0.11848	11.2	10	0.00376
<i>Dear</i>	[14.8 / 14.6]	6.1	6	0.04816	15.2	14	0.00050
<i>D2Mgh11/ATP1A1</i>	[2.9 / 6.1]	7.7	7	0.02155	9.6	9	0.00840
<i>D2Rat169</i>	[7.8 / 4.5]	6.2	6	0.04520	5.4	5	0.06632
<i>D2Rat59</i>	[10.1 / 8.8]	2.7	3	0.26394	1.8	2	0.41202

SBP (mean $\pm$ sd)		157.2 $\pm$ 14.2			145.0 $\pm$ 11.4		
Locus Marker		LRS	%	P	LRS	%	P
<i>D2Rat143</i>		1.3	1	0.50959	11.9	11	0.00255
<i>Dear</i>		7.0	6	0.03082	13.1	12	0.00145
<i>D2Mgh11/ATP1A1</i>		8.4	8	0.01491	8.3	8	0.01609

DBP (mean $\pm$ sd)		113.5 $\pm$ 11.8			102.4 $\pm$ 9.7		
Locus Marker		LRS	%	P	LRS	%	P
<i>D2Rat143</i>		1.5	1	0.47431	9.8	9	0.00763
<i>Dear</i>		5.2	5	0.07525	14.9	14	0.00059
<i>D2Mgh11/ATP1A1</i>		7.1	6	0.02875	8.8	8	0.01204

* Genetic distance in cM between markers, males, females; MAP, mean arterial pressure; SBP, systolic blood pressure; DBP, diastolic BP; LRS, likelihood ratio statistic for the association of the trait with loci; %, the amount of the total trait variance which would be explained by a QTL at these loci, as a percent; P, probability value for the association. Statistical values presented were derived from regression analysis based on a free regression model using the MapManager QTXb17 program (19). The localization of *Dear* and *ATP1A1* genes are highlighted.

Table 3. Analysis of S-allele effects on blood pressure of *Dear* locus in F2 [RxS] intercross rats

	BP (mmHg, mean $\pm$ sd) per Genotype			ANO VA	Tukey Test <i>P</i>			S-allele
FEMALES	SS	SR	RR	<i>P</i>	SS vs RR	SS vs SR	SR vs RR	effect
MAP	130 $\pm$ 13.1	122 $\pm$ 9.1	119 $\pm$ 8.3	6.2 $\times 10^{-4}$	4.8 $\times 10^{-4}$	0.01	n.s.	4
SBP	152 $\pm$ 14.2	145 $\pm$ 10.0	141 $\pm$ 9.7	1.7 $\times 10^{-3}$	1.0 $\times 10^{-3}$	0.02	n.s.	4
DBP	109 $\pm$ 12.0	102 $\pm$ 8.7	99 $\pm$ 7.6	7.3 $\times 10^{-4}$	5.5 $\times 10^{-4}$	0.01	n.s.	4
MALES								
MAP	139 $\pm$ 13.6	133 $\pm$ 13.4	131 $\pm$ 10.0	0.052	n.a.	n.a.	n.a.	
SBP	162 $\pm$ 14.4	156 $\pm$ 14.7	152 $\pm$ 10.9	0.034	0.04	n.s.	n.s.	4
DBP	117 $\pm$ 12.6	113 $\pm$ 12.0	110 $\pm$ 9.2	0.085	n.a.	n.a.	n.a.	

Legend: MAP, mean arterial blood pressure; SBP, systolic blood pressure; DBP, diastolic blood pressure; ANOVA, analysis of variance; Tukey Test, all pairwise multiple comparison procedure; n.s., not significant; n.a., not applicable.

We claim:

1. A method for determining an individual's susceptibility to hypertension comprising:
 - (a) obtaining a biological sample from a patient; and
 - (b) detecting the presence or absence of at least one mutation or polymorphism in the Dual Endothelin-1/Angiotensin II Receptor (Dear) in said tissue sample as compared to a control sample,
 - (c) determining whether the mutation or polymorphism increases the expression of Dual Endothelin-1/Angiotensin II Receptor (Dear), enhances the affinity of ET-1 binding to Dual Endothelin-1/Angiotensin II Receptor (Dear), enhances the affinity of VEGF-signal peptide (VEGFsp) binding to Dual Endothelin-1/Angiotensin II Receptor (Dear), or increases Dear-activation when Dear is stimulated with a ligand, wherein the presence of at least one of the mutations or polymorphisms indicates that the individual is susceptible to hypertension.
2. A method for diagnosing hypertension comprising:
 - (a) obtaining a biological sample from a patient; and
 - (b) detecting the presence or absence of at least one mutation or polymorphism in the Dual Endothelin-1/Angiotensin II Receptor (Dear) in said tissue sample as compared to a control sample;
 - (c) determining whether the mutation or polymorphism increases the expression of Dual Endothelin-1/Angiotensin II Receptor (Dear), enhances the affinity of ET-1 binding to Dual Endothelin-1/Angiotensin II Receptor (Dear), enhances the affinity of VEGF-signal peptide (VEGFsp) binding to Dual Endothelin-1/Angiotensin II Receptor (Dear), or increases Dear-activation when Dear is stimulated with a ligand, wherein the presence of at least one of the mutations or polymorphisms indicates that the individual has hypertension.

3. The method of claim 1 or 2, further comprising performing a polymerase chain reaction (PCR) to amplify the DEAR coding sequence.
4. The method of claim 1, 2, or 3 wherein the DEAR coding sequence is a human DEAR coding sequence and has at least 75% homology or identity to SEQ ID NO. 1.
5. The method of claim 1 or 2, further comprising:
 - (a) isolating nucleic acid from the biological sample; and
 - (b) contacting the nucleic acid with at least one nucleic acid probe under selective hybridization conditions, wherein said probe preferentially hybridizes with a nucleic acid sequence comprising a Dear mutation or polymorphism, wherein the binding of the probe to the isolated nucleic acid indicates that the individual is susceptible to or currently has hypertension.
6. A method for inhibiting angiogenesis in an individual comprising administering to said patient an effective amount of a Dual Endothelin-1/Angiotensin II Receptor (Dear) inhibitor.
7. The method of claim 6, wherein the Dear inhibitor is selected from the group consisting of an antibody or antibody fragment that blocks binding of ET-1, AngII, or VEGF-signal peptide to DEAR, a small molecule inhibitor, competitive inhibitor, sirna or aptamer.
8. The method of claim 7, wherein the antibody or antibody fragment is a humanized antibody or antibody fragment.
9. The method of claim 6, wherein the angiogenesis is associated with a disease or disorder selected from the group consisting of, immune and non-immune inflammation, chronic articular rheumatism, psoriasis, diabetic retinopathy, neovascular glaucoma, restenosis, macular degeneration, capillary proliferation in atherosclerotic plaques, osteoporosis, cancer, solid tumors, solid tumor metastases, angiofibromas, retrolental fibroplasia, hemangiomas, and Kaposi sarcoma.

10. The method of claim 12, wherein the cancer is selected from the group consisting of gastrointestinal cancer, prostate cancer, ovarian cancer, breast cancer, head and neck cancer, lung cancer, non-small cell lung cancer, cancer of the nervous system, kidney cancer, retina cancer, skin cancer, liver cancer, pancreatic cancer, genital-urinary cancer and bladder cancer.
11. A method for enhancing angiogenesis at a clinically relevant site in an individual comprising administering to said patient an effective amount of a Dual Endothelin-1/Angiotensin II Receptor (Dear) activator.
12. The method of claim 11, wherein said clinically relevant site is selected from the group consisting of a wound, ulcer, diabetic ulcer, and a heart with coronary artery disease.

Figure 1.

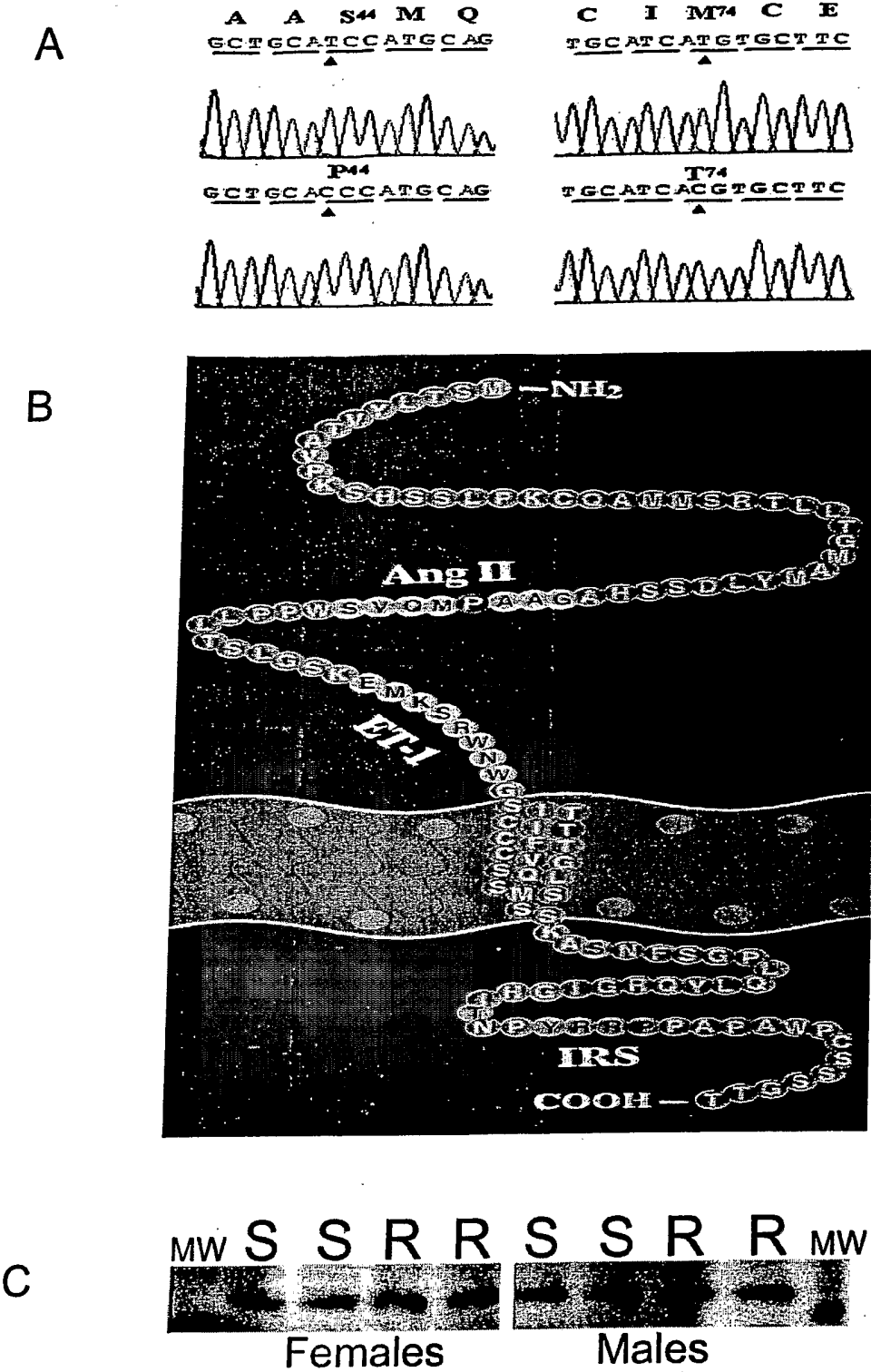


Figure 2.

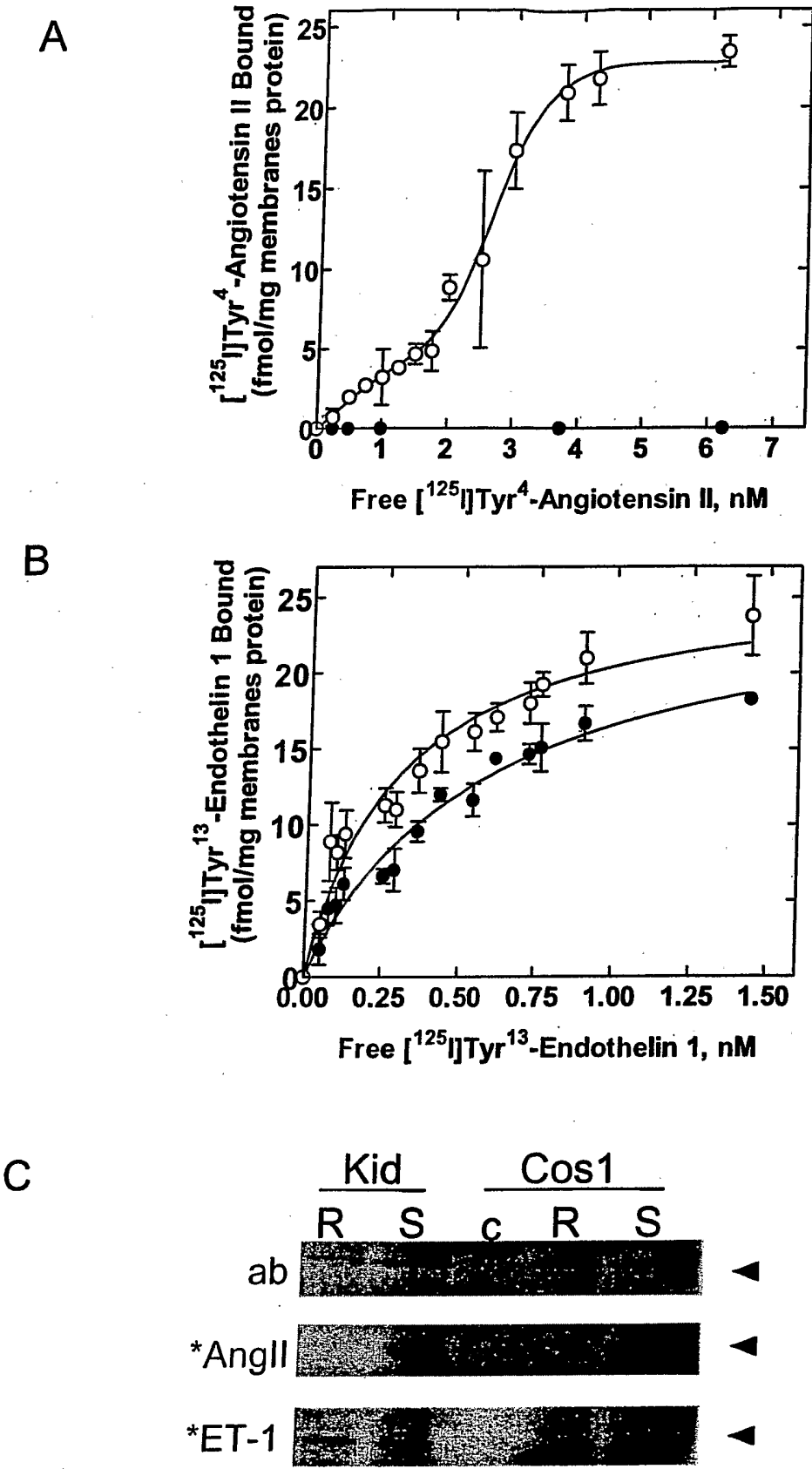
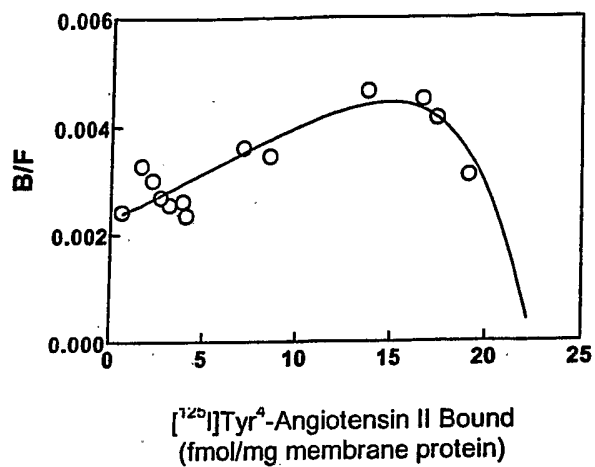
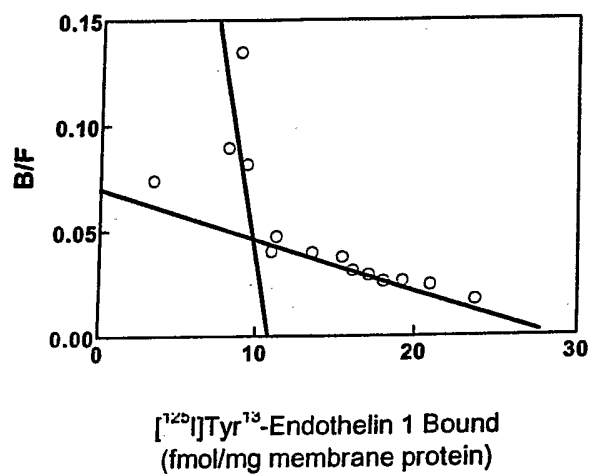


Figure 3.

A



B



C

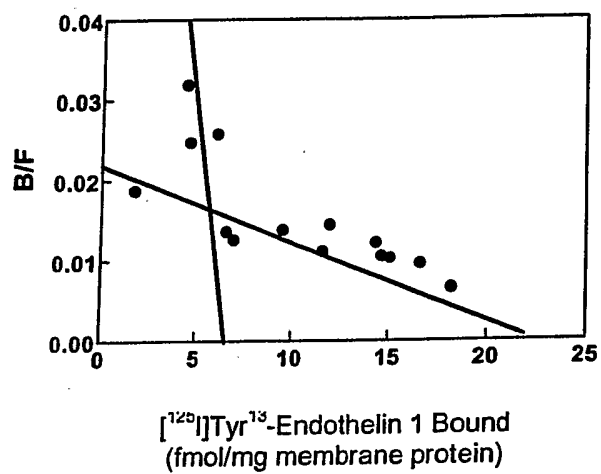


Figure 3D

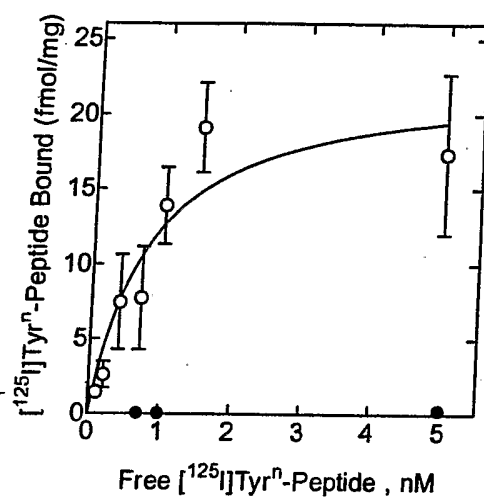
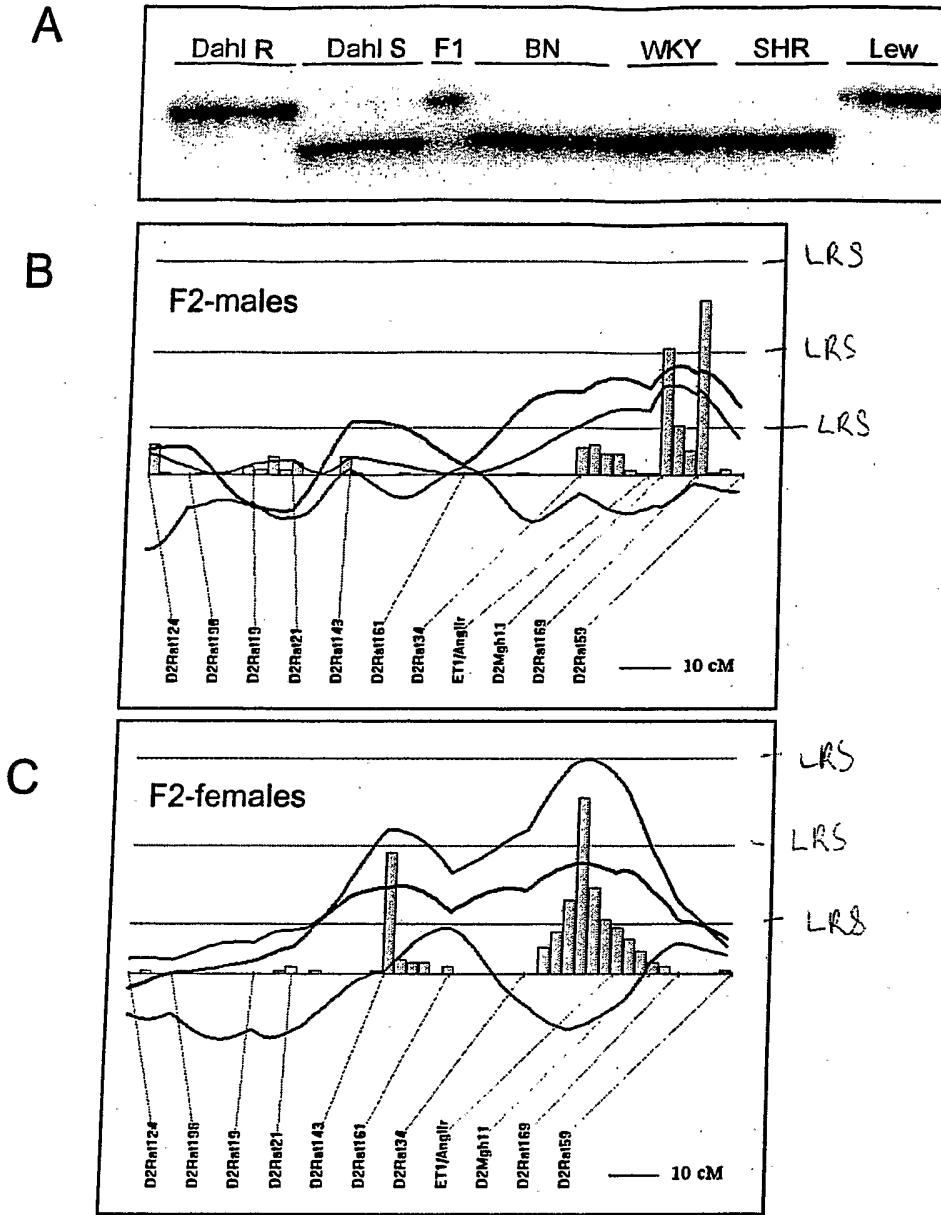


Figure 4.



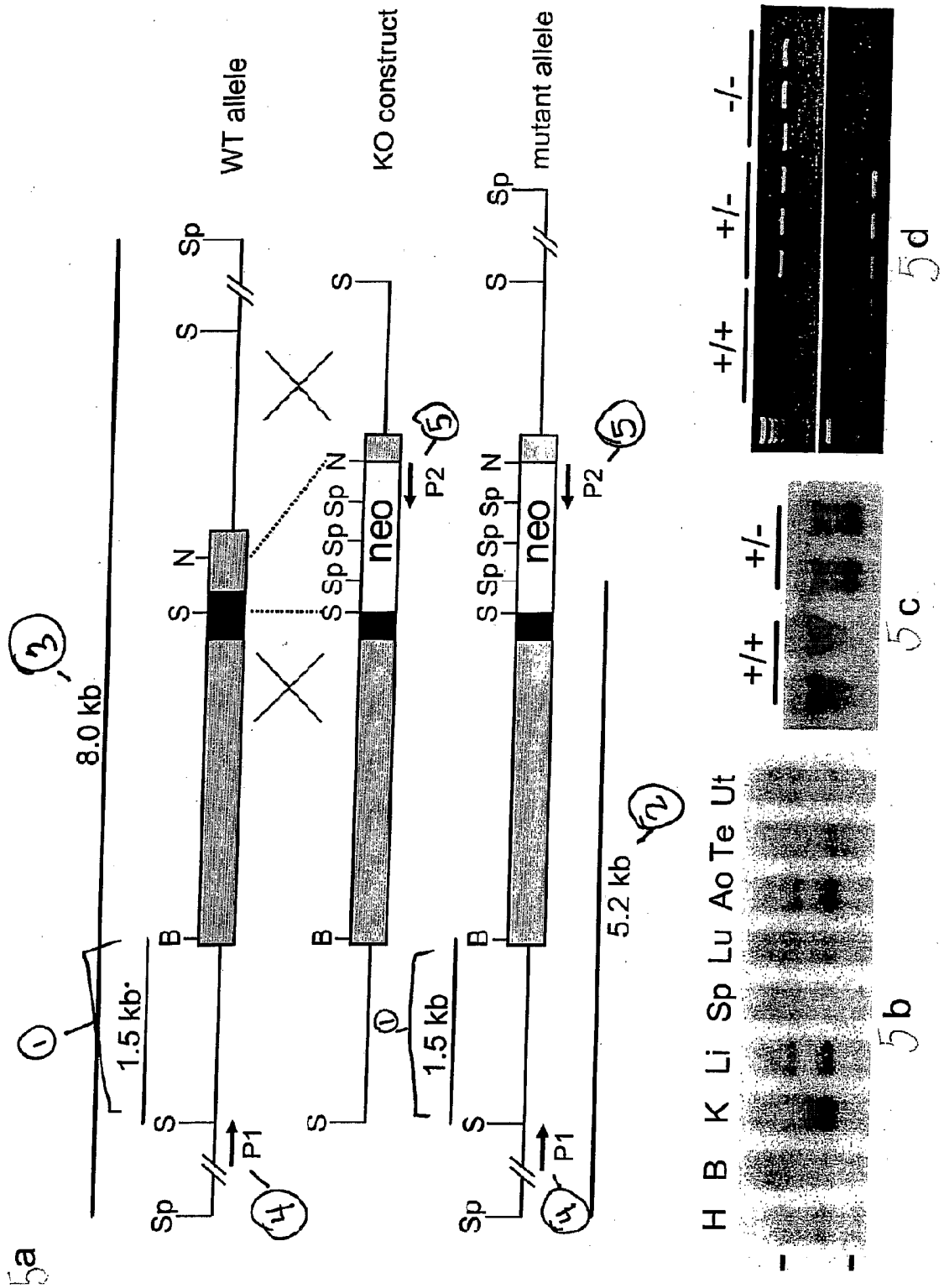


Figure 5

Figure 5e

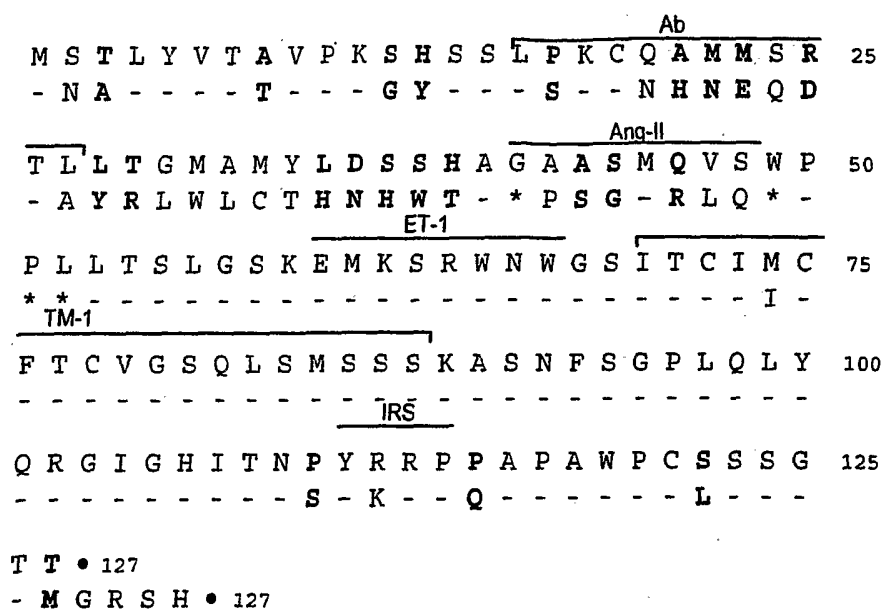


Figure 5f

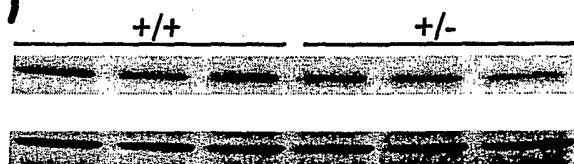
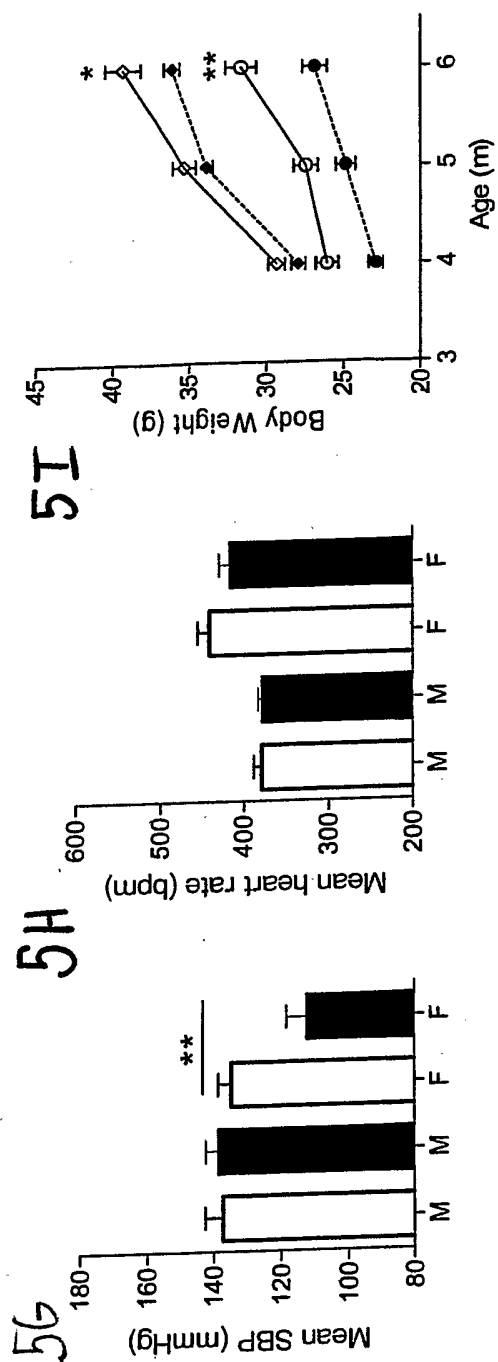


Figure 5g-5I



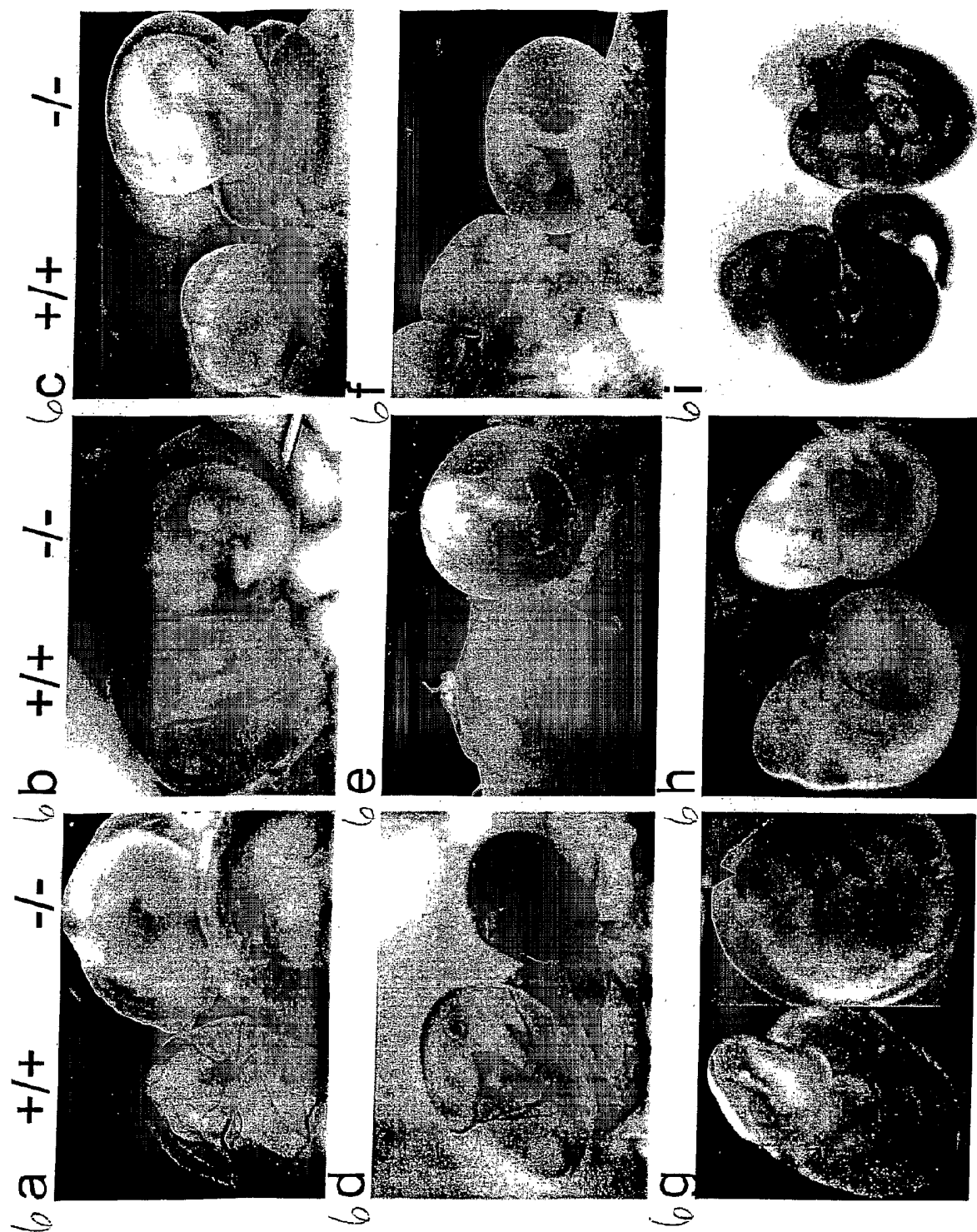


Figure 6

Figure 7

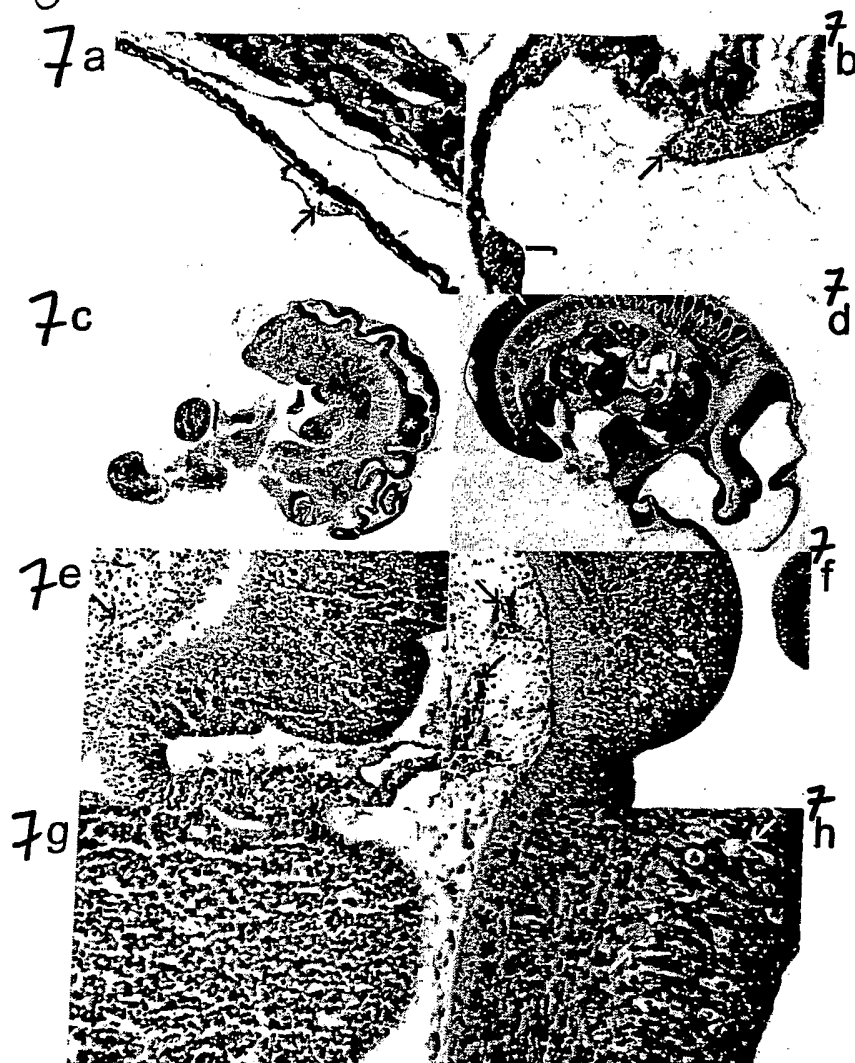
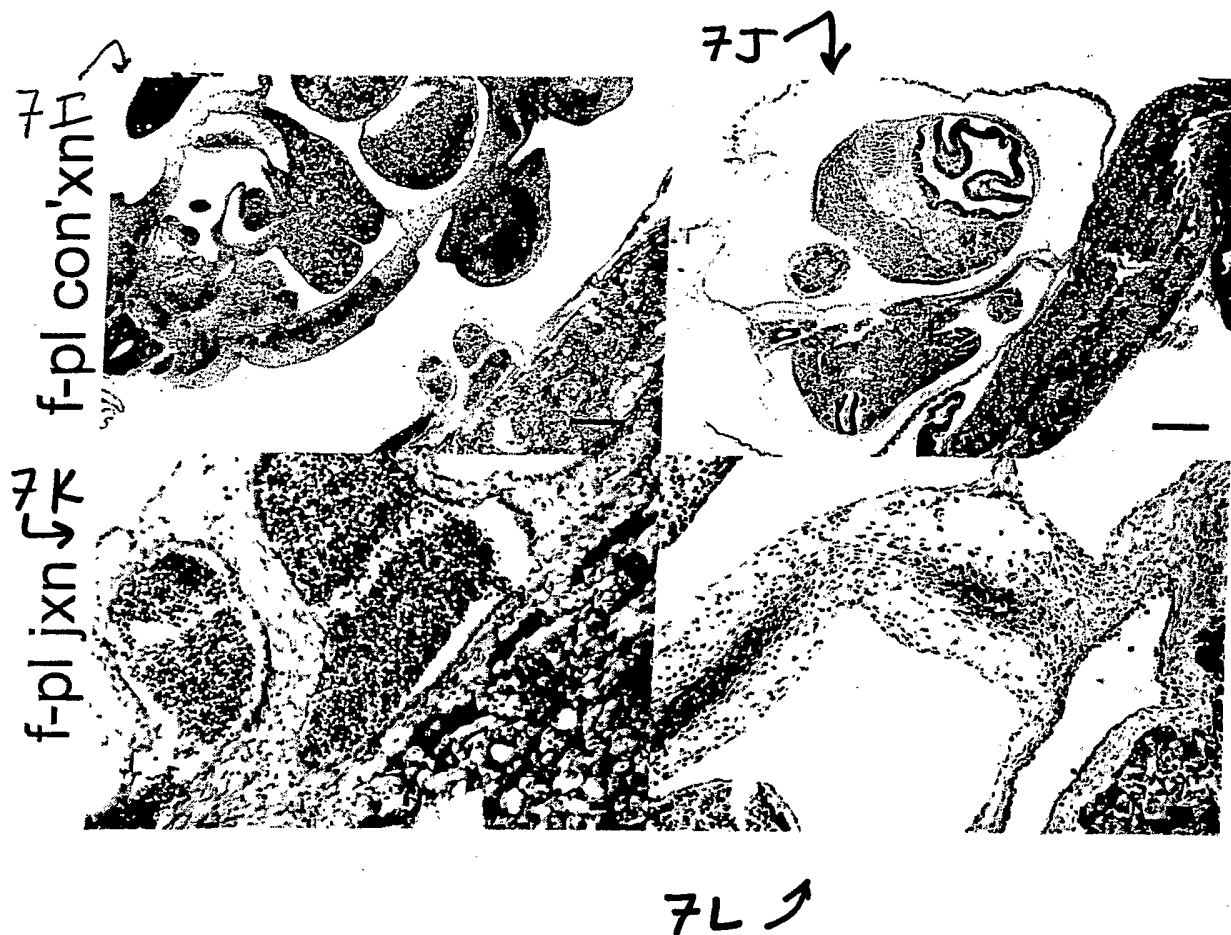


Fig. 7 cont.



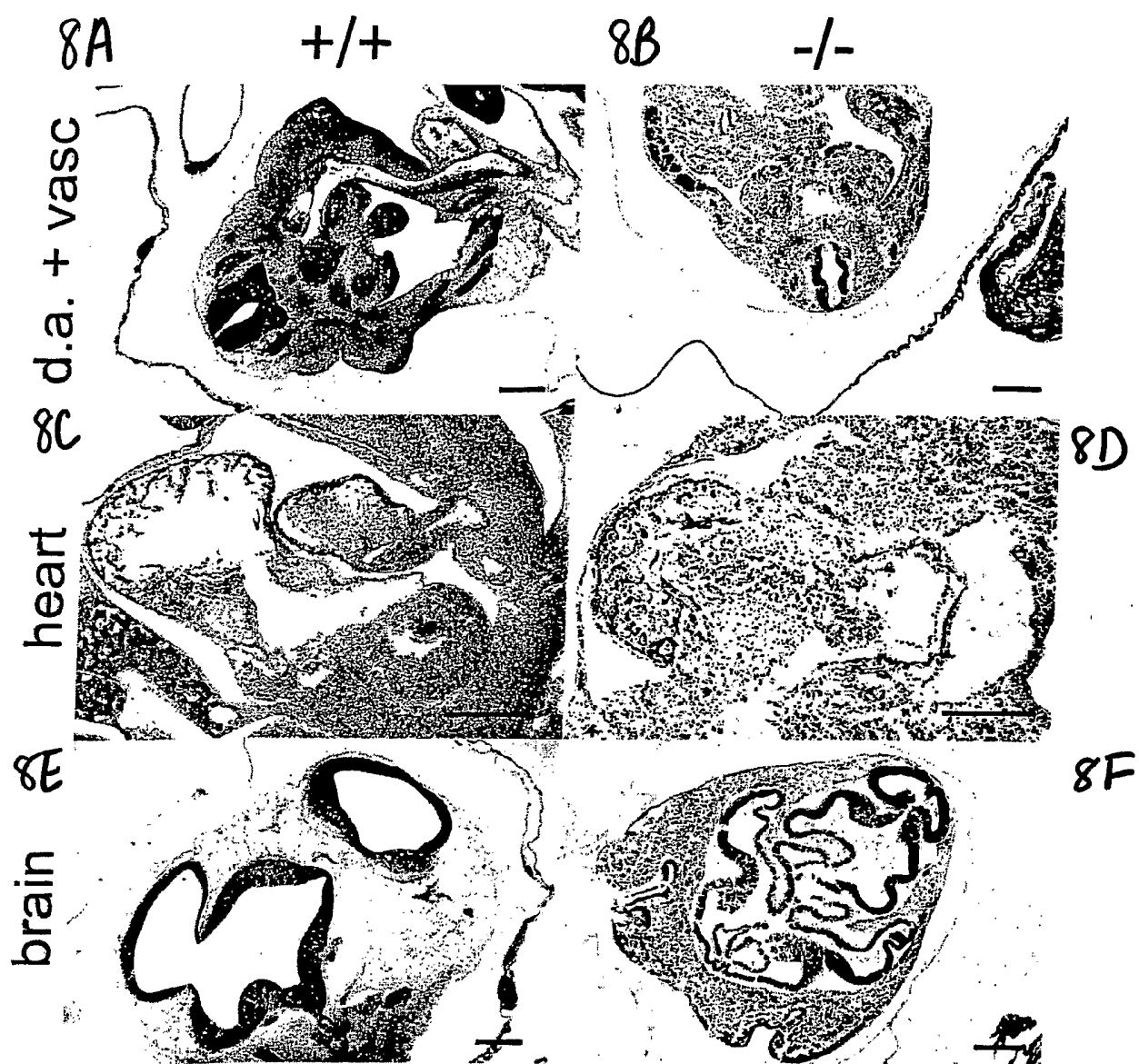


Figure 8

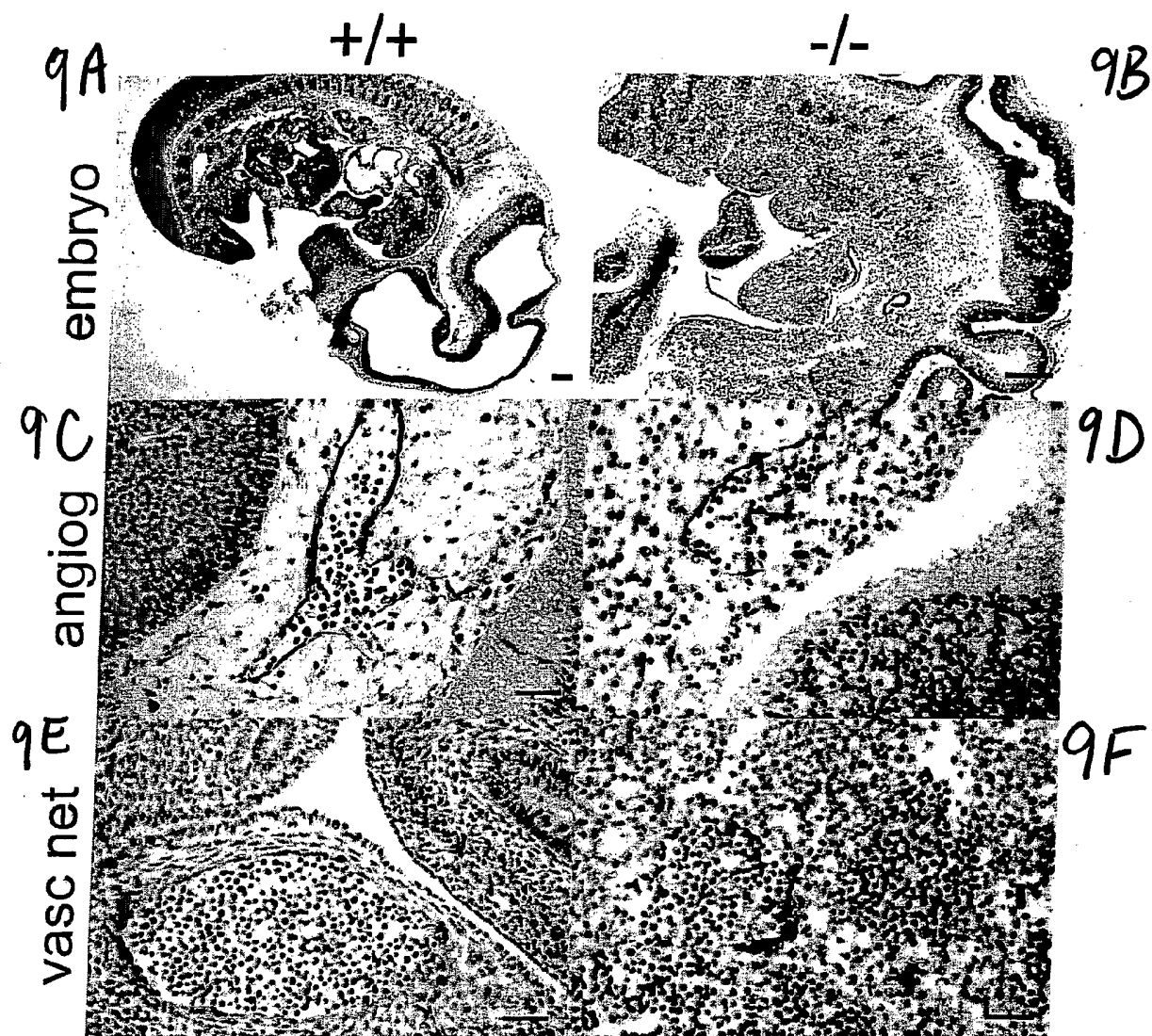


Figure 9

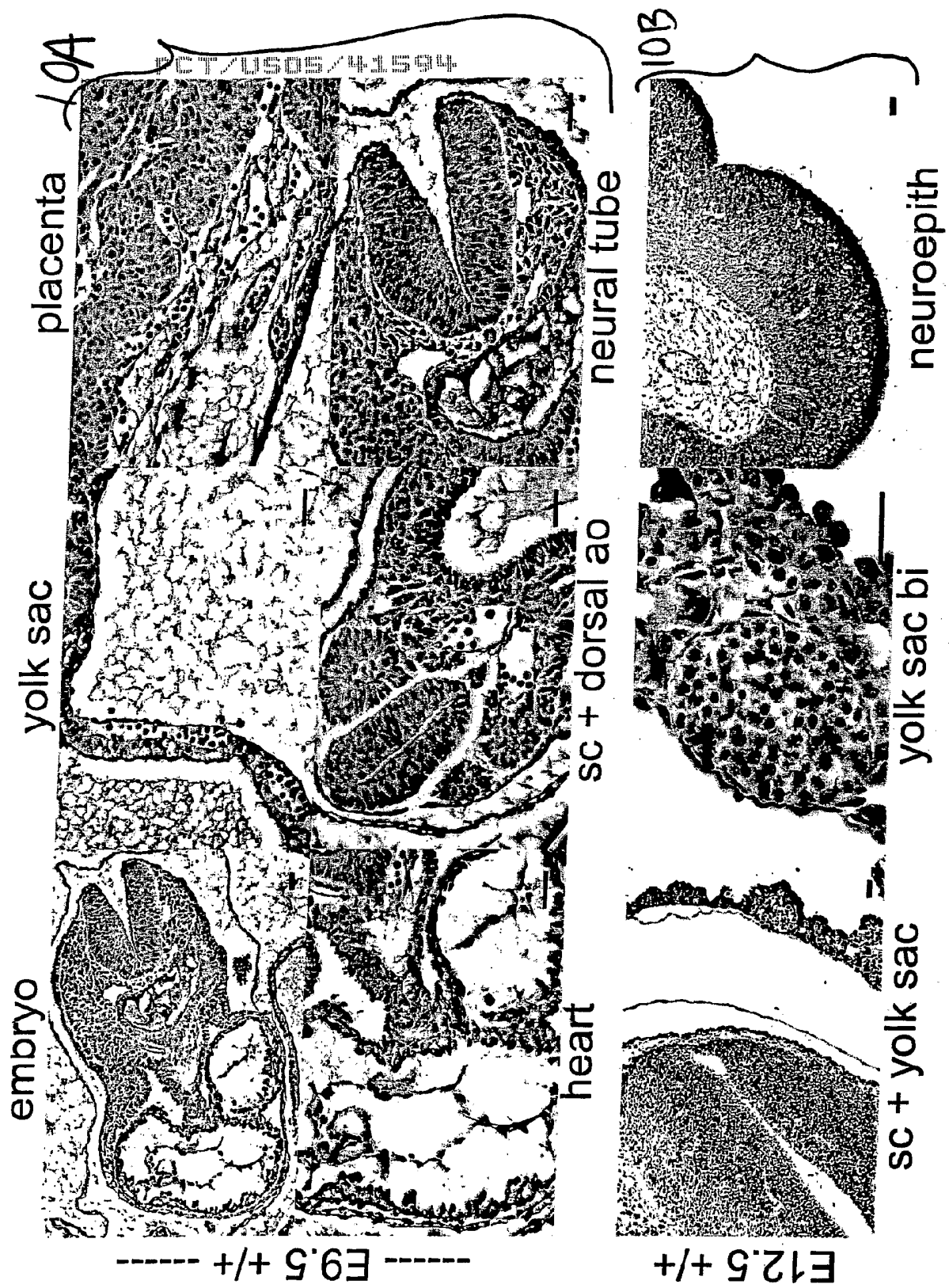
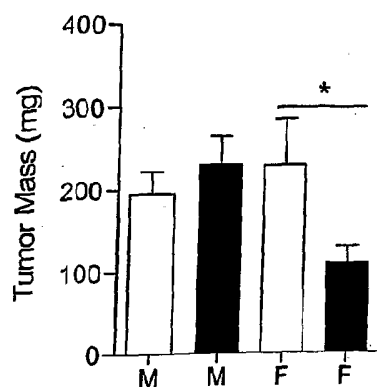
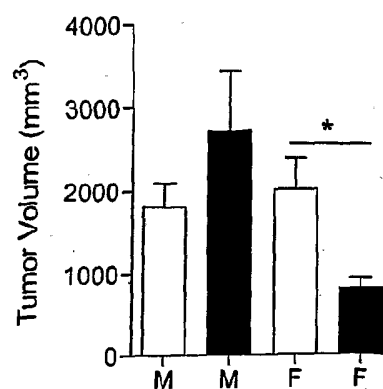


Figure 10

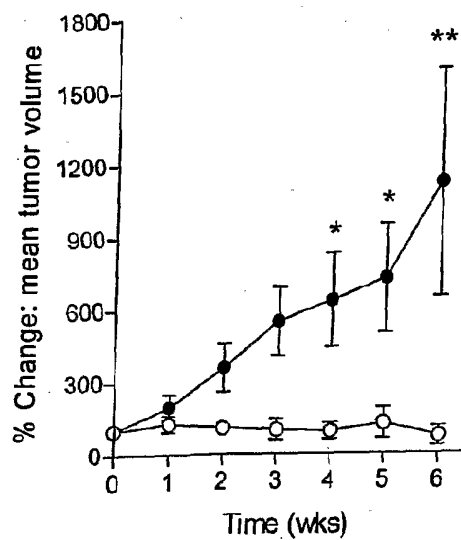
11a



11b



11c



11d

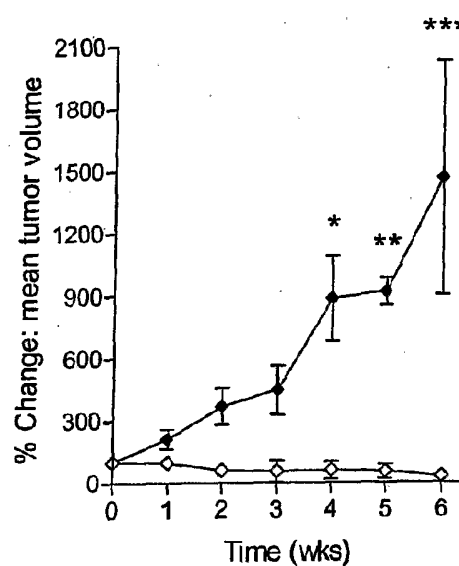


Figure 11

