A NOVEL PEPTIDE INVOLVED IN ENERGY HOMEOSTASIS

[0001] The benefit of the 5 August 2005 filing date of United States provisional patent application serial number 60/705,940 is claimed under applicable treaties and conventions in all countries. In the United States, the benefit of the August 5, 2005 filing date of provisional application serial number 60/705,940 is claimed under 35 U.S.C. §119(e).

TECHNICAL FIELD

[0002] This invention pertains to a novel gene and resulting protein, named "suppressed with insulin resistance 1" (Swirl) which was found to be involved in the association of obesity with insulin resistance and lipidemia, and changes in energy homeostasis.

BACKGROUND ART

[0003] Obesity is an increasingly prevalent global disease and has reached epidemic proportions. Current estimates suggest that at least 50% of the Western population is either overweight or obese. Obesity, particularly abdominal obesity, combined with other conditions such as insulin resistance, dyslipidemia, hepatic steatosis, and hypertension is known as the Metabolic, or Insulin Resistance, Syndrome. The central pathophysiological features of dyslipidemia associated with insulin resistance and type 2 diabetes are increased plasma triglycerides (TG) in very low density lipoproteins (VLDL), and reduced high density lipoprotein (HDL) cholesterol. Commonly, increased circulating TGs are hydrolyzed into free fatty acids (FFA) and are taken up by peripheral tissues including the liver and can lead to hepatic steatosis, or non-alcoholic fatty liver. Studies of several mutant mouse models of

obesity and metabolic disorders suggest that the link between insulin resistance and dysregulated TG is complex and involves both peripheral and central factors.

[0004] Insulin resistance refers to reduced insulin-stimulated glucose uptake in skeletal muscle and fat, and an impaired suppression of liver glucose output (2). Hyperglycemia and hyperlipidemia are both side effects of, and causative agents in, the pathophysiology of type 2 diabetes. Glucotoxicity and lipotoxicity further promote insulin resistance and type 2 diabetes due to suppression of insulin action and secretion from the β-cell. Hyperinsulinemia is initially successful in suppressing liver glucose output, however the deleterious effects of increased insulin offset the gains associated with maintaining normal blood glucose levels (2). Hyperinsulinemia is thought to be a factor in a cluster of metabolic abnormalities, including hypertension, non-alcoholic fatty liver disease (NAFLD), and coronary heart disease (2). NAFLD disease is commonly associated with insulin resistance, and requires two transcription factors: sterol regulatory element binding protein-1c (SREBP1c) and peroxisome proliferator receptor-γ (PPARγ) (3-6). Absence of SREBP1c or PPARγ signaling in liver inhibits the development of liver steatosis that occurs in obese insulin resistant mice (5-7).

[0005] Defining a common mechanism explaining insulin resistance has been difficult because of the complexity of the insulin receptor (IR) signaling system, and the realization that it is not one, but many factors that contribute to the development of this disorder. The tyrosine phosphorylation of two adaptor proteins, IRS1 and IRS2, is a critical early step in the stimulation of glucose uptake by insulin (8-11). IRS1 and IRS2 have no intrinsic enyzmatic activity, and are thought to function as part of a molecular scaffold that facilitates the formation of complexes of proteins with kinase, phosphatase or ubiquitin ligase function (12). Stimulation of phosphoinositide 3' kinase (PI3K) by association with the IRS is a critical step in insulin-stimulated glucose uptake. Activation of the p110 catalytic subunit of PI3K activates the lipid kinase domain, which phosphorylates phosphatidylinositol-4,5-bisphosphate. Activation of PI3K is necessary for full stimulation of glucose uptake by insulin, although other pathways might also be involved (12).

[0006] A metabolic state conducive to the development of insulin resistance is thought to result from an imbalance of caloric intake with oxidative metabolism (13,14). Studies suggest that reduced mitochondrial function in muscle is a factor in the development of insulin resistance associated with obesity (14,15). Stimulation of energy expenditure and

suppression of appetite both result in improved glucose metabolism in mouse models of obesity and type 2 diabetes. A well-characterized example of this is the adipocytokine leptin. Leptin acts in the hypothalamus and hindbrain to suppress appetite and, through stimulation of the autonomic nervous system, increases oxidative metabolism in skeletal muscle (16-20). However, leptin can also improve hepatic insulin sensitivity independently of marked effects on food intake or body weight (17).

[0007] Infusion of fatty acids (FAs) is associated with a rapid reduction in insulin sensitivity in muscle within 4-6 h (21-23). The exact mechanism by which FAs reduce insulin-stimulated glucose uptake remains a matter of debate. Recent data indicate that FAs interfere with the IR signal transduction pathways that stimulate glucose uptake (21,22,24). One hypothesis is that an increase in the intracellular concentration of FAs and diacyl-glycerol leads to the activation of a serine kinase, protein-kinase C θ (PKCθ) (25). Phosphorylation of IRS1 on Ser^{307} by PKCθ inhibits the phosphorylation of IRS-1 by the IR, leading to reduced activation of PI3K and a reduction in the stimulation of glucose uptake by insulin.

[0008] *Abnormal activity of secreted polypeptides as a link between obesity and insulin resistance.* Determining mechanisms linking obesity with insulin resistance is important for developing new glucose lowering therapies. Recent research investigating insulin resistance has focused on adipocytes. Obesity is associated with aberrant regulation and function of a regulatory network of polypeptides secreted from adipocytes (adipocytokines). Adipocytokines such as leptin, adiponectin, and resistin regulate hepatic glucose production, glucose disposal in muscle, and the proliferation and storage of lipid in adipocytes (26). Leptin regulates energy homeostasis through effects on neurons located in the hypothalamus and hindbrain that regulate ingestive behavior, autonomic nervous activity, and neuroendocrine system that govern metabolism (thyroid, adrenals) (16). Leptin resistance or reduced serum adiponectin associated with obesity are factors that contribute to insulin resistance, through diminished insulin-sensitizing actions and by increasing risk for developing steatosis (intracellular fatty acid accumulation) (27,28). Non-adipose tissues also secrete peptides that affect energy metabolism and insulin sensitivity, such as musclin from muscle (29) and angiopoietin-related growth factor from liver (30). These factors may also be targets for the treatment of the metabolic syndrome.

[0009] *Melanocortin receptor knockouts for investigating the link between obesity and insulin resistance:* Two melanocortin receptors expressed in areas of the central nervous system are involved in energy homeostasis. Targeted deletion of the neuronal melanocortin-4 receptor (MC4R) gene in mice (Mc4r-/- or Mc4rKO mice) causes obesity and hyperinsulinemia, and is also associated with increased hepatic lipogenic gene expression and hepatic steatosis. Mice deficient for another neuronal melanocortin receptor (Mc3r-/- or Mc3rKO mice) develop a similar degree of obesity to Mc4r-/- mice when fed a high fat diet, but do not exhibit the same level of insulin resistance, hyperlipidemia and increased hepatic steatosis. Studies using Mc3rKO and Mc4rKO strains have shown that both exhibit an exaggerated diet-induced obesity, however the deterioration of insulin sensitivity in Mc4rKO is more rapid and severe (31,32). Figs. 1A-1E illustrate some of the known differences in wild-type mice (C57BL/6J) and the two knockout mice in terms of body mass as a function of either a low fat diet or high fat diet. (31,32) Severe insulin resistance in mice and humans is associated with hepatomegaly and steatosis with increased hepatic lipogenesis (33). Mc4rKO develop hepatic insulin resistance and hepatomegaly in the obese state, and on a high fat diet (HFD) exhibit a marked deterioration of glucose homeostasis associated with severe glucose and insulin intolerance. Figs. 2A-2E show the differences in hepatomegaly and steatosis in the two mouse strains, and also differences in expression of genes involved in lipid metabolism. (4,17,57) On the other hand, Mc3rKO matched to Mc4rKO for fat mass (FM) exhibit a very modest impairment of glucose homeostasis.

[0010] *Sequences of cDNA Similar to SWIR1.* A sequence and putative open reading frame of a cDNA encoding a putative protein homologous to SWIR1 have previously been published by several consortiums involved in large-scale sequencing of cDNAs. See R.L. Stausberg *et al.*, "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences," Proc. Natl. Acad. Sci. U.S.A., vol. 99, pp. 16899-16903 (2002) (Genbank accession number: BC021944, cDNA with complete coding sequence); and H.F. Clark *et al.*, "The secreted protein discovery initiative (SPDI), a large-scale effort to identify novel human secreted and transmembrane proteins: a bioinformatics assessment," Genome Res., vol. 13, pp. 2265-2270 (Genbank accession number: NM_198573, cDNA with complete coding sequence). A protein with similar homology for the first 37 amino acid residues of SEQ ID NO:2 has been identified. However, the nucleotide and amino acid sequence of this described protein may be incorrect, due to a single nucleotide error in the

sequencing of the cDNA. No previous function has been published for the protein described here.

DISCLOSURE OF INVENTION

[0011] We have discovered a novel secreted peptide (Swir1) based on an investigation using two transgenic murine models of obesity. Using microarray gene expression analysis and validation by RealTime quantitative PCR, the expression of an mRNA (genbank accession number: AK009710) encoding a putative 76 amino acid, secreted protein was found to be reduced 10-fold in severely insulin resistant and glucose intolerant Mc4rKO and Leptin-deficient (*Lep^{ob}/Lep^{ob}*) mice. In contrast, in obese Mc3rKO mice, which are moderately glucose intolerant but exhibit a normal response to insulin, a modest 30-40% reduction was seen in the expression of the Swir1 protein. In C57BL/6J mice a negative correlation was found in the hepatic expression of *Swir1* mRNA with fasting glucose levels. The expression of Swir1 in the hypothalamus also declined with obesity and insulin resistance. We also confirmed that the mRNA encoded a secreted protein. Based on the negative effect of diet-induced obesity and insulin resistance on *Swir1* mRNA expression in liver and brain, the gene encoding the protein was designated "*Swir1*" ("suppressed with insulin resistance 1"). A recombinant adenovirus was used to increase the expression of Swir1in mouse models of obesity. Over-expression of Swir1 by adenovirus injection significantly and reproducibly reduced fasting insulin, triglyceride and cholesterol levels. Additionally, the expression of a key gene involved in lipogenesis (fatty acid synthase) and FAS protein levels were reduced by *Swir1* adenoviral treatment in Lep^{ob}/Lep^{ob} mice.

[0012] A transgenic FVB/NJ strain of mouse was created which over expressed the Swir1 protein, using *Swir1* DNA (SEQ ID NO:1) controlled by the human β-actin promoter which is expressed in all tissues. Female FVB/NJ mice over expressing Swir1 had a significant reduction in fat mass, and a higher metabolic rate determined by measuring oxygen consumption (VO2) using indirect calorimetry (Oxymax, Columbus Instruments, Columbus, Ohio). The increase in metabolic rate observed in the transgenic mice had been predicted based on the results from experiments using mice injected with the recombinant adenovirus expressing Swir1. Mice infected with recombinant adenovirus expressing Swir1 lost more weight during an overnight fast, suggesting an impaired ability to reduce metabolic

rate to compensate during fasting. FVB/NJ Swirl transgenic mice exhibited the same exaggerated weight loss during a fast, associated with a higher metabolic rate. A component of Swirl's anti-diabetic actions may therefore involve stimulation of pathways involved in oxidative metabolism. That is, Swirl may improve the metabolic profile of obese, insulin-resistant individuals partially through normalizing the balance of caloric (kJ) consumption with calorie expenditure through effects on physical activity, basal metabolic rate, or a combination of both.

[0013] Full-length Swirl peptide, or peptide fragments, derivatives, homologues, analogues, or mimetics thereof, delivered by oral intake, injection, subcutaneous patch, or intranasal routes, could be used as therapeutic or diagnostic agents for hypercholesterolemia, hypertriglyceridemia, insulin resistance, obesity, diabetes, and/or disorders of energy imbalance.

[0014] Antibodies (AB1 (SEQ ID NO:8) and AB2 (SEQ ID NO:9)) were raised against peptide fragments derived from the open reading frame predicted for BC021944, and shown in Fig. 5. These antibodies were used to verify the presence of Swirl-immunoreactivity in human serum and in rat brain, strongly supporting the conclusion that the open reading frame predicted for BC021944 encodes a small secreted peptide. Swirl-immunoreactivity was detected in human plasma. (data not shown) In rat brain, neurons with Swirl immunoreactivity have been identified in the arcuate nucleus of the hypothalamus. The significance of this observation is that neurons in the arcuate nucleus of the hypothalamus have been implicated in the regulation of energy expenditure, through effects on both facultative thermogenesis and physical activity, and on glucose homeostasis [Cone RD. Anatomy and regulation of the central melanocortin system. Nat Neurosci. 2005 May;8(5):571-8; Coppari R, Ichinose M, Lee CE, Pullen AE, Kenny CD, McGovern RA, Tang V, Liu SM, Ludwig T, Chua SC Jr, Lowell BB, Elmquist JK. The hypothalamic arcuate nucleus: a key site for mediating leptin's effects on glucose homeostasis and locomotor activity. Cell Metab. 2005 Jan;1(1):63-72.] The increased energy expenditure and physical activity of the FVB/NJ Swirl transgenic mice may therefore involve action in the central nervous system, and more specifically through actions based on regulating activity of neurons in the arcuate nucleus of the hypothalamus.

Brief Description of the Drawings

[0015] Fig. 1A illustrates the differences in body mass in 6-month-old, female mice after 12 weeks feeding either a low-fat diet (LF) or a high-fat diet (HF) among three different strains, wild-type (WT), Mc3r -/- deficient mice (Mc3rKO), and Mc4r -/- deficient mice (Mc4rKO). (Significant effect of diet is indicated by "*" ($p<0.001$) or "#" ($p<0.05$); significant effects within diet indicated by letters, with groups significantly different ($p<0.05$) given different letters; significance based on 2-way AVOVA.)

[0016] Fig. 1B illustrates the differences in body weight gain as a percent of starting weight in 6-month-old, female mice after 12 weeks feeding either a low-fat diet (LF) or a high-fat diet (HF) among three different strains, wild-type (WT), Mc3r -/- deficient mice (Mc3rKO), and Mc4r -/- deficient mice (Mc4rKO). (Significant effect of diet is indicated by "*" ($p<0.001$) or "#" ($p<0.05$); significant effects within diet indicated by letters, with groups significantly different ($p<0.05$) given different letters; significance based on 2-way AVOVA.)

[0017] Fig. 1C illustrates the differences in percent body fat in 6-month-old, female mice after 12 weeks feeding either a low-fat diet (LF) or a high-fat diet (HF) among three different strains, wild-type (WT), Mc3r -/- deficient mice (Mc3rKO), and Mc4r -/- deficient mice (Mc4rKO). (Significant effect of diet is indicated by "*" ($p<0.001$) or "#" ($p<0.05$); significant effects within diet indicated by letters, with groups significantly different ($p<0.05$) given different letters; significance based on 2-way AVOVA.)

[0018] Fig. 1D illustrates the differences in fat mass in 6-month-old, female mice after 12 weeks feeding either a low-fat diet (LF) or a high-fat diet (HF) among three different strains, wild-type (WT), Mc3r -/- deficient mice (Mc3rKO), and Mc4r -/- deficient mice (Mc4rKO). (Significant effect of diet is indicated by "*" ($p<0.001$) or "#" ($p<0.05$); significant effects within diet indicated by letters, with groups significantly different ($p<0.05$) given different letters; significance based on 2-way AVOVA.)

[0019] Fig. 1E illustrates the differences in fat-free mass in 6-month-old, female mice after 12 weeks feeding either a low-fat diet (LF) or a high-fat diet (HF) among three different strains, wild-type (WT), Mc3r -/- deficient mice (Mc3rKO), and Mc4r -/- deficient mice (Mc4rKO). (Significant effect of diet is indicated by "*" ($p<0.001$) or "#" ($p<0.05$); significant effects within diet indicated by letters, with groups significantly different ($p<0.05$) given different letters; significance based on 2-way AVOVA.)

[0020] Fig. 2A illustrates a comparison of liver histology, as shown in liver cross-sections stained with hemotoxylin and eosin, from female mice fed a high fat diet among three mice strains, wild-type (WT), Mc3r -/- deficient mice (Mc3rKO), and Mc4r -/- deficient mice (Mc4rKO).

[0021] Fig. 2B illustrates the differences in liver weight as a function of adiposity (percent body fat) in mice fed both low and high fat diets among three mice strains, wild-type (WT), Mc3r -/- deficient mice (Mc3rKO), and Mc4r -/- deficient mice (Mc4rKO).

[0022] Fig. 2C illustrates the differences in mean liver weight (n=5-6/group) of male and female mice fed a moderate high fat diet among three mice strains, wild-type (WT), Mc3r -/- deficient mice (Mc3rKO), and Mc4r -/- deficient mice (Mc4rKO). ("*" indicates $p<0.05$ versus WT and Mc3rK0 mice).

[0023] Fig. 2D illustrates the differences in expression of stearoyl-CoA desaturase 1 (SCD1) in liver of mice fed a high fat diet among three mice strains, wild-type (WT), Mc3r -/- deficient mice (Mc3rKO), and Mc4r -/- deficient mice (Mc4rKO). Data is expressed as arbitrary units (a.u.). ("*" indicates $p<0.05$ versus WT and Mc3rK0 mice.)

[0024] Fig. 2E illustrates the differences in expression of apolipoprotein A4 (ApoA4) in liver of mice fed a high fat diet in three mice strains, wild-type (WT), Mc3r -/- deficient mice (Mc3rKO), and Mc4r -/- deficient mice (Mc4rKO). ("*" indicates $p<0.05$ versus WT and Mc3rK0 mice; "#" indicates $p<0.05$ versus WT mice, within gender.)

[0025] Fig. 3A illustrates the amount of hepatic AK009710 mRNA expression (given as a percent of WT expression) in wild-type (WT) mice and in obese Mc3r -/- deficient mice (Mc3rKO).

[0026] Fig. 3B illustrates the amount of hepatic AK009710 mRNA expression (given as a percent of WT expression) in wild-type mice (WT), Mc4r -/- deficient mice (Mc4rKO), and leptin-deficient Lep^{ob}/Lep^{ob} mice (two models of obesity).

[0027] Fig. 3C illustrates the amount of hepatic AK009710 mRNA expression (given as a percent of expression with saline) in leptin-deficient Lep^{ob}/Lep^{ob} mice injected 4 times over 2 days with either saline or leptin (0.5 mg/g).

[0028] Fig. 4 illustrates the mRNA sequence of the *Swirl* gene (BC021944; SEQ ID NO:1), with the open reading frame encoding the Swirl protein underlined, and showing its putative amino acid translation product Swirl (SEQ ID NO:2).

[0029] Fig. 5 illustrates the alignment of the putative Swir1 protein sequences for mouse (SEQ ID NO:2), human (SEQ ID NO:14), rat (SEQ ID NO:12), dog (SEQ ID NO:15), pig (SEQ ID NO:16), cow(SEQ ID NO:17), sheep (SEQ ID NO:18), and chimpanzee (SEQ ID NO:13), showing the regions of the putative secreted polypeptide used to generate polyclonal antibodies (pAB1 ((SEQ ID NO:8) and pAB2(SEQ ID NO:9)).

[0030] Fig. 6A illustrates the results of a Northern blot analysis using a radioactive-labeled portion of the AK009710 DNA sequence encoding Swir1 protein on human tissue samples (Lanes 1-8 represents RNA from heart, brain, placenta, lung, liver, skeletal muscle, kidney and pancreas, respectively).

[0031] Fig. 6B illustrates the relative intensity of *Swir1* mRNA bands from a Northern blot analysis using the full-length mouse AK009710 DNA probe on mouse tissue samples.

[0032] Fig. 6C illustrates the results of a Western blot analysis for FLAG immunoreactivity in media (M) and cell lysates (Pel) from HEK293 human-kidney derived cells transfected with pCMV-Swir1:FLAG, pCMV-GFP, or in media from HEK293 cells infected with adenoviral vector expressing Swir1:Flag fusion protein [no transfected DNA (lanes 1,2); transfected with a pCMV-Swir1:FLAG construct (lanes 3,4); transfected with pCMV-Swir1 (lanes 5,6); or transfected with pCMV-GFP (lanes 7,8); infected with Ad5Swir1:FLAG (lane 9); infected with Ad5Swir1 (lane 10); or infected with Ad5GFP (lane 11)]. To visualize Swir1 protein, a fusion protein was created with a C-terminal FLAG-epitiope tag.

[0033] Fig. 6D illustrates the results of a Western blot analysis for Swir1 protein in various tissues (liver, muscle, and brain) from Mc4r-/- mice injected with Ad5-Swir1:FLAG 4 days prior to the assay, along with controls, both positive (HEK293 cells infected with Ad5- Swir1:FLAG) and negative (Liver from non injected Mc4r-/- mice).

[0034] Fig. 7A illustrates the results of a Western blot analysis using lysate from HEK293 cells infected with recombinant Ad5Swir1 (native protein) or Ad5Swir1:FLAG (C-terminal FLAG-tagged fusion protein) after incubation with a polyclonal antibody (pAB1) against the N-terminus of Swir1 (as shown in Fig. 5).

[0035] Fig. 7B illustrates the results of a Western blot analysis using lysate from HEK293 cells infected with recombinant Ad5Swir1 (native protein) or Ad5Swir1:FLAG (C-

terminal FLAG-tagged fusion protein) after incubation with a polyclonal antibody (pAB2, SEQ ID No:9) against the C-terminus of Swirl (as shown in Fig. 5).

[0036] Fig. 7C illustrates the treatment protocol used to administer Ad5Swirl or Ad5-GFP into the tail vein of various strains of mice to test the effects of Swirl treatment on mice metabolism (results presented in Table 1).

[0037] Fig. 8A illustrates the expression level of fatty acid synthase (Fasn) mRNA in liver from obese leptin-deficient (Lep^{ob}/Lep^{ob}) mice eight days after injection with either Ad5-Swirl or Ad5-GFP. Data expressed in arbitrary units (AU) (n=6-8/group; "*" $p<0.05$).

[0038] Fig. 8B illustrates the expression level of stearoyl-CoA desaturase (Scd1) protein in liver from obese leptin-deficient (Lep^{ob}/Lep^{ob}) mice eight days after injection with either Ad5-Swirl or Ad5-GFP. Data expressed in arbitrary units (AU) (n=6-8/group; "*" $p<0.05$).

[0039] Fig. 8C illustrates the expression level of acetyl CoA carboxylase (Acc) mRNA in liver from obese leptin-deficient (Lep^{ob}/Lep^{ob}) mice eight days after injection with either Ad5-Swirl or Ad5-GFP. Data expressed in arbitrary units (AU) (n=6-8/group; "*" $p<0.05$).

[0040] Fig. 8D illustrates the expression level of a gene involved in insulin resistance (a suppressor of cytokine signaling) in liver from obese leptin-deficient (Lep^{ob}/Lep^{ob}) mice eight days after injection with either Ad5-Swirl or Ad5-GFP. Data expressed in arbitrary units (AU) (n=6-8/group; "*" $p<0.05$).

[0041] Fig. 9A illustrates the construction of the transgene (BAP-Swirl) used to generate transgenic mouse strains that over express Swirl.

[0042] Fig. 9B illustrates the amount of Swirl expression in livers from transgenic mice pups (produced using the transgene of Fig. 9A) from FVB/NJ founders at 5 weeks.

[0043] Fig. 9C illustrates the level of fasting triglycerides (TG) from serum of transgenic mice pups (produced using the transgene of Fig. 9A) from FVB/NJ founders at 9 weeks.

[0044] Fig. 9D illustrates the body composition as measured by percent body fat (%body fat; left graph) and fat mass (showing both free fat mass (FFM) and fat mass (FM); right graph) in transgenic mice pups (produced using the transgene of Fig. 9A) from FVB/NJ founders at 5 and 9 weeks as compared with control.

[0045] Fig. 9E illustrates change in fat mass (showing both free fat mass (FFM) and fat mass (FM)) of transgenic mice pups (produced using the transgene of Fig. 9A) from FVB/NJ founders after 7 days on a 60% high fat diet.

[0046] Fig. 10 illustrates the results from a PCR screen for integration of BAP-Swirl into the genome of C57BL/6J pups (from injection of BAP-Swirl into C57BL/6J oocytes) showing six pups out of 23 with integration of the transgene into the genome.

[0047] Fig. 11A illustrates the increase in Erk phosphorylation in 3T3-L1 adipocytes 15 minutes after the application of the secreted portion of protein Swirl (Swirl$^{34-76}$; SEQ ID NO:10).

[0048] Fig. 11B illustrates the increase in Erk phosphorylation in HepG2 hepatocytes 15 minutes after the application of the secreted protein Swirl (Swirl$^{34-76}$; SEQ ID NO:10).

[0049] Fig. 12A illustrates the association between hypothalamic *Swirl* mRNA expression and body weight in six-month-old mice from three strains (C57BL/6J(WT), Mc3rKO (Mc3r), or Mc4rKO (Mc4r) fed for three months on one of two diets (LF = 10% kJ/fat; HF = 60% kJ/fat).

[0050] Fig. 12B illustrates the association between hypothalamic *Swirl* mRNA expression and HOMA-IR [(fasting insulin x glucose)/ 22.5] in six-month-old mice from three strains (C57BL/6J(WT), Mc3rKO (Mc3r), or Mc4rKO (Mc4r) fed for three months on one of two diets (LF = 10% kJ/fat; HF = 60% kJ/fat).

[0051] Fig. 12C illustrates the association between HOMA-IR [(fasting insulin x glucose)/ 22.5] and hypothalamic Socs3 (suppressor of cytokine signaling 3) mRNA expression in six-month-old mice from three strains (C57BL/6J(WT), Mc3rKO (Mc3r), and Mc4rKO (Mc4r) fed for three months on one of two diets (LF = 10% kJ/fat; HF = 60% kJ/fat).

[0052] Fig. 13A illustrates the physical activity (measured in beam breaks/10 min) in wild-type (WT) and BAP-Swirl transgenic mice (FVB.Tg) over 3 days.

[0053] Fig. 13B illustrates the physical activity (measured in average number beam breaks/10 min for the period) in dark and light periods in wild-type (WT) and BAP-Swirl transgenic mice (FVB.Tg) over a 24 hr period.

[0054] Fig. 13C illustrates whole body fat oxidation (RER) in dark and light periods in wild-type (WT) and BAP-Swirl transgenic mice (FVB.Tg) over a 24 hr period.

[0055] Fig. 13D illustrates the metabolic rate (measured as VO2 (ml/h x 10^3)) in dark and light periods in wild-type (WT) and BAP-Swir1 transgenic mice (FVB.Tg) over a 24 hr period.

[0056] Fig. 13E illustrates the metabolic rate as a function of free fat mass (measured as VO2 (ml/h/gFFM x 10^3)) in dark and light periods in wild-type (WT) and BAP-Swir1 transgenic mice (FVB.Tg) over a 24 hr period.

[0057] Fig. 13F illustrates the metabolic rate as a function of body weight (measured as VO2 (ml/h/gBW x 10^3)) in dark and light periods in wild-type (WT) and BAP-Swir1 transgenic mice (FVB.Tg) over a 24 hr period.

MODES FOR CARRYING OUT THE INVENTION

[0058] The present invention discloses a novel secreted protein (Swir1) and identifies some of its functions. The sequence of this protein were found to be highly conserved across several mammalian species, and the sequences are shown in SEQ ID NOS:2 and 12-18. In addition the nucleic acids that encode this protein were used to make mice that over expressed the Swir1 protein, either by infection with a recombinant adenovirus expressing Swir1 or by making a transgenic strain using *Swir1* DNA controlled by an actin promoter.

[0059] In one embodiment, the Swir1 protein, fragment, derivative or analogs are used therapeutically to prevent a pathophysiology associated with increased body mass, e.g., obesity, hyperglycemia, hyperinsulinemia, insulin resistance, hyperlipidemia, and non-insulin dependent type 2 diabetes mellitus.

[0060] In another embodiment, the purified Swir1 protein, fragment, derivative or analog is isolated from various mammals, or made synthetically, or made using cell cultures that express the protein, fragments, derivatives or analogs using nucleic acids encoding at least twenty amino acids from the open reading frame in SEQ ID NO:1, and as shown in Fig. 4.

[0061] In another embodiment, antibodies are made to the Swir1 protein, its fragments, derivatives or analogs. These antibodies can be used in a kit to identify the Swir1 protein from various samples, including body fluids.

[0062] In another embodiment, transgenic animals are made that over express the Swir1 protein by linking the *Swir1* sequence to an active promoter, e.g., an actin promoter.

In another embodiment, a transformation vector comprising at least the open reading frame of SEQ ID NO:1 (the portion underlined in Fig. 4) are made.

Example 1

Discovery of Swir1 Protein and Its Function

[0063] Microarrays analyzing hepatic gene expression in lean and obese Mc3rKO mice were performed using arrays printed from libraries of 16,463-18,400 70-mer oligonucleotides (Mouse Array-Ready Oligo Set Version 2.0, Qiagen Operon, Alameda, CA) (34-36). The microarray data indicated increased expression of genes involved in lipid metabolism (apoliproteins) and oxidative stress secondary to obesity. Interestingly, the expression of only three genes was reduced in liver of Mc3rKO mice irrespective of age, gender, and adiposity. Two of the genes encoded proteins with known function: neuraminidase 3 (**neu3**), encoding an enzyme that cleaves sialic acid from glycoproteins and glycolipids, and solute carrier family 21 (**slc21a1**) which encodes an organic anion transporter. The third gene (AK009710) was novel and had no assigned function in the databases.

[0064] Quantitative RealTime PCR confirmed the microarray data showing a tendency for a modest reduction in the expression of AK009710 in liver of Mc3rKO (Fig. 3A). Intriguingly, a more dramatic reduction in the expression of AK009710 was observed in liver of severely insulin resistant Mc4rKO and leptin-deficient (Lep^{ob}/Lep^{ob}) mice (Fig. 3B). In addition, short-term treatment with leptin (4 injections of 0.5 mg/g leptin over 2 days) significantly increased Swir1 in the liver of Lep^{ob}/Lep^{ob} mice. (Fig. 3C). Expression of AK009710 in 6-wk-old, lean Mc4rKO is normal (data not shown), indicating that the decline in liver expression of Mc4rKO is secondary to the age-related onset of obesity, insulin resistance, and hepatic steatosis (32). Moreover, AK009710 expression correlated negatively with fasting glucose in diet-induced obese C57BL/6J mice ($n=13$, $R^2=0.67$, $P<0.001$) (data not shown).

[0065] Overall, these results indicate the identification of a small secreted protein whose expression in liver declines with insulin sensitivity and hepatic steatosis. Based on the observation that the decline in AK009710 expression in liver correlates with the severity of hepatic steatosis and insulin resistance, and that this decline is reversed by an insulin sensitizor, the name "suppressed with insulin resistance 1" (Swir1) was chosen.

[0066] Oligonucleotide primers targeted to AK009710 mRNA were utilized to measure AK009710 gene expression in liver cDNA from various mouse models of obesity and insulin resistance. Sequences of primers were: sense 5′-cctgagggtgctgtctgtcatg-3′ (SEQ ID NO:3), antisense 5′-cagtagcagcaagaagcctacg-3′ (SEQ ID NO:4), probe 5′-6FAM-ctctcatcgccatcgtctgca-BHQ-3′ (SEQ ID NO:5). In agreement with the initial microarray result, AK009710 mRNA was down regulated in the liver of Mc3r-/- mice compared to WT mice (by 55%, $p<0.05$; Fig. 3A). Next was examined the AK009710 liver mRNA expression in two other models of obesity: Mc4r-/- mice and leptin-deficient Lep^{ob}/Lep^{ob} mice. AK009710 mRNA was expressed at approximately 10-fold lower levels in both of these models compared to wild-type mice (WT) (Fig. 3B). When all animals were grouped together negative relationships between AK009710 mRNA expression and glucose and insulin values were observed (Data not shown). AK009710 gene expression was not altered in the liver of young and aged WT mice fed ad libitum, fasted for 16 h, or fasted for 24 h and re-fed for 4 h. (data not shown) AK009710 is not thought to be altered by nutritional status.

[0067] In order to determine whether AK009710 mRNA might be regulated secondary to the development of insulin resistance, AK009710 mRNA was measured in the liver of young, normoinsulinemic and older hyperinsulinemic Mc4r-/- mice. AK009710 mRNA was observed to be similar to the wild-type mice in young Mc4r-/- mice (average age ~7 weeks), whereas it was significantly reduced in older (~16 weeks) Mc4r-/- mice. (data not shown). Furthermore, AK009710 mRNA was also measured in a small number (n=4) of human-derived hepatocytes from diabetic and non-diabetic subjects. Although the expression tended to be lower in the diabetic samples, the difference was not statistically significant (data not shown).

[0068] Thus, while obesity of Mc3r-/- and Mc4r-/- mice is similar, insulin resistance and elevated serum lipids (triglyceride, cholesterol) are known to be far more severe for Mc4r-/- mice. The reduction in AK009710 gene expression in the liver correlated with the known severity of insulin resistance and hyperlipidemia in Mc4r-/- mice.

Example 2

Sequence and Bioinformatics Analysis

[0069] AK009710 is a mouse tongue cDNA clone 1247 bp in length and belongs to the Unigene cluster Mm.34074, 2310040A07Rik: RIKEN cDNA 2310040A07 gene. It

hypothetically could encode a 534 amino acid protein immediately from the 5' end of the sequence. Given that this putative protein did not start with a methionine residue, it was listed as a truncated product. BLAST analysis of AK009710 for homologous EST or cDNA sequences on the NCBI database revealed a significant match with NM198573, a human transcript discovered by a large-scale Secreted Protein Discovery Initiative encoding a hypothetical protein of 87 aa (UNQ470/GAAI470) (37). The match with human sequence - NM_198573 was 85% identity across 392 nucleotides, $p=5e^{-83}$. The human sequence encoded an 87 amino acid protein in one exon. Translation of AK009710 in six frames revealed an open reading frame encoding a 76 amino acid protein (SEQ ID NO:2). An alignment between this putative mouse protein and the human protein encoded by NM_198573 (GAAI470, or UNQ470) revealed strong homology over the first 37 residues. UNQ470/GAAI470 maps to chromosome 9p13.2. and is adjacent to the ciliary neurotrophic factor receptor (CNTFR) gene.

[0070] The sequence of AK009710 was verified using cDNA isolated from mouse liver. Moreover, an 868 bp cDNA cloned from mouse liver by the National Institutes of Health Mammalian Gene Collection (MGC) Program, with the accession number BC021944, recently posted on the NCBI database agreed with our sequencing data. (Fig. 4, SEQ ID NO:1) BLAST analysis revealed that the predicted 76 aa sequence for mouse (SEQ ID NO:2) is highly conserved in several mammalian species (Fig. 5; SEQ ID NO:12 (rat), SEQ ID NO:13 (chimpanzee); SEQ ID NO:14 (human); SEQ ID NO:15 (dog); SEQ ID NO:16 (pig); SEQ ID NO:17 (cow); SEQ ID NO:18 (sheep)). In Fig. 5, pAB1 (SEQ ID NO: 8) and pAB2 (SEQ ID NO:9) refer to the regions of the putative secreted polypeptide used to generate polyclonal antibodies. The predicted signal sequence is underlined. In addition peptides were synthesized corresponding to amino acids 34 through 76 ($Swirl^{34-76}$; SEQ ID NO:10), and to amino acids 39 through 76 ($Swirl^{39-76}$; SEQ ID NO:11) of SEQ ID NO:2, the mouse protein.

[0071] Further analysis of the putative mouse sequence from AK009710 and the human GAAI470 sequence revealed a single nucleotide gap in the human sequence on GenBank. Therefore a mouse AK009710 PCR product was cloned and sequenced in both directions to confirm which sequence, either the mouse or the human, was correct. The sequence-verified AK009710 mouse clone revealed a 76 amino acid translation product (SEQ

ID NO:2) (Fig. 4). A publicly available Origene clone of human GAAI470 was analyzed and shown not to contain the nucleotide gap, indicating a sequencing error in the NM_198573 sequence on GenBank. Alignment of AK009710 sequence from different species, including human, revealed a 100% homology between rat, human, mouse and chimp sequences at the protein level (Fig. 5).

[0072] Bioinformatics analysis revealed that this protein is highly likely to be a secreted peptide (87% probability, SignalP 3.0) with the most likely cleavage site between positions 33 and 34. The human sequence contains 1 possible serine site, and 1 possible threonine phosphorylation sites, all 3′ to the predicted cleavage point, as well as 6 possible glycosylation sites, also all 3′ to the cleavage site.

Example 3

Tissue Distribution of Swirl

[0073] In order to examine the tissue distribution of AK009710 mRNA a Northern blot was performed using the 210 nt sequence containing the 76 amino acid protein SWIR1 and a human Multiple Tissue Northern blot (BD Biosciences, Palo Alto, California). As can be seen in Fig. 6A, a single band of ~1.35 kb was detected in humans in brain and liver samples only, with highest levels detected in the liver. However, as seen in Fig. 6B, Swirl was found in mice in the liver, brain, and muscle.

Example 4

Confirmation that Swirl is a Secreted Polypeptide

[0074] Bioinformatics analysis predicted the presence of a putative signal sequence suggesting that AK009710 is a secreted peptide. To test this, the coding sequence of the 76 amino acid protein was amplified from mouse liver cDNA by PCR using primers with Not1 (5′-ggggcggccgcaccatgggggcagccatctcccaa-3′ (SEQ ID NO:6)) and Xho1 (5′-gggctcgagggccagagcccttcagggctgcag-3′ (SEQ ID NO:7)) restriction enzyme sites attached. The product was ligated into a pCMV-Tag1 vector with a FLAG epitope at the C-terminal end (pCMV-Swirl:FLAG), then transiently transfected into HEK human kidney-derived cells. This product was also used to create two adenoviral constructs – one with Swirl attached to a FLAG epitope (Ad-Swirl:FLAG), and another without the FLAG epitope (Ad-Swirl).

[0075] HEK293 cells were transfected with pCMV-Swir1 or pCMV-Swir1:FLAG. Media was collected after 16 h, immunoprecipitated, and then run on a 20% polyacrylamide gel to be visualized by an anti-FLAG antibody. These experiments were repeated using recombinant adenovirus (Ad5) expressing native or FLAG-tagged Swir1.

[0076] When HEK293 cells were untransfected (lanes 1, 2), or transfected with empty vector (lanes 5, 6), or vector containing GFP (lanes 7, 8), no FLAG-immunoreactive bands were visualized (Fig. 6C). However, when the pCMV-Swir1:FLAG construct was transfected into HEK293 cells (lanes 3, 4), FLAG-positive immunoreactivity was detected in both the media and the cell pellet, indicating that at least some of the transfected Swir1 product was being actively secreted by the cells into the media. Similar results were observed in the media of HEK293 cells infected with Ad-Swir1:FLAG (Fig. 8, lane 9). Lanes 10 and 11 show no FLAG immunoreactivity in media of cells infected with adenovirus containing Swir1 without the FLAG epitope, or with GFP, respectively. Thus the presence of FLAG immunoreactivity in cultured media of HEK-293 cells transfected with an expression vector expressing an epitope-tagged fusion protein (pCMV-Swir1FLAG) confirmed that an undefined portion of the 76 aa protein is secreted.

[0077] Most adenovirus injected in the tail vein infects liver (38). To test whether tail vein injection of adenovirus leads to increased expression of *Swir1* mRNA in the liver, as well as other tissues, three Mc4r-/- mice were injected with Ad5-Swir1:FLAG adenovirus and the tissues collected after four days. Analysis by Western blot revealed the presence of FLAG immunoreactivity in the liver, muscle, and brain tissue indicating the presence of Swir1 in these tissues. (Fig. 6D) The distribution of Swir1FLAG immunoreactivity in tissues of mice infected with Ad5-Swir1FLAG is consistent with a polypeptide secreted into the circulatory system from liver. Both of these tests indicated that Swir1 is a secreted protein.

Example 5

Treatment of Obese Insulin Resistant Mice with Ad5-Swir1: Mc4rKO

[0078] Recombinant adenoviral vector-mediated expression has been used to investigate regulation of liver metabolism and insulin sensitivity (39-41). Three recombinant adenovirus vectors were constructed expressing the 76 aa protein (Ad5-Swir1), a C-terminal FLAG-tagged fusion protein (Ad5-Swir1:FLAG), or green fluorescent protein for the negative control (Ad5-GFP). Expression of protein following tail vein injection was

confirmed using anti-FLAG antibody (Fig. 6D and data not shown). Synthesis of Swirl was confirmed in HEK293 cells transfected with Ad5-Swirl using polyclonal antibodies (pAB1 (SEQ ID NO:8) & pAB2 (SEQ ID NO:9) in Fig. 5) against N- and C-terminal regions of the putative secreted protein (Fig. 7A, B).

[0079] To investigate whether Swirl is involved in glucose metabolism, Ad5-SWIR1 or Ad5-GFP ($5x10^8$ pfu) was injected into the tail vein of 20-week-old male and female Mc4r-/- (n=3 of each sex per group). Both groups of animals were matched for body weight, glucose levels and glucose tolerance before Ad5-Swirl or Ad5-GFP injections. An intraperitoneal glucose tolerance test (IPGTT) was performed one week prior to injection of Ad5-Swirl or Ad5-GFP, and all mice were observed to be glucose intolerant. IPGTT were performed on mice after an overnight fast, with a single intraperitoneal injection of 1g/kg glucose, and blood glucose measured with a blood glucose meter and test strips (Glucometer Elite, Bayer Corp., Elkhart, Indiana) from the tail blood of the animals at several intervals, as described by W. Fan *et al.*, "The Central Melanocortin System Can Directly Regulate Serum Insulin Levels," Endocrinology, vol. 141, pp. 9 3072-3079 (2000).

[0080] Mice were injected with $5x10^8$pfu of Ad5-Swirl or Ad5-GFP in 100 µl of diluent (DMEM) into the tail vein. Animals were observed and weighed daily throughout the 4-day experiment. On day 4 animals were given another IPGTT (0.4 mg glucose/g body weight).

[0081] Four days after injection of Ad5-Swirl, the mice demonstrated improved glucose tolerance as measured using IPGTT (data not shown). There was no change in body weight, blood glucose, or cholesterol levels throughout the experiment. There was a trend for a decrease in insulin and serum triglyceride levels (Table 1).

Table 1. Characteristics of Mc4r-/- mice 4 days post adenoviral infusion.

Group	Body Weight (g)	Glucose (mg/dL)	Insulin (ng/mL)	Cholesterol (mg/dL)	Triglycerides (ng/mL)
Ad5-Swirl	50.4 ± 1.8	184 ± 10	5.9 ± 1.5	91 ± 7	26 ± 4
Ad5-GFP	49.5 ± 2.2	169 ± 16	10.4 ± 2.0	82 ± 6	38 ± 6

Example 6

Treatment of Obese Insulin Resistant Mice with Ad5-Swir1: B6 Ay/a

[0082] A second adenoviral experiment was performed whereby Ad5-Swir1 or Ad5-GFP was injected into the tail vein of male C57BL6 Ay/a mice (n=9 per group) that had been maintained on a very high fat diet for ~3 months. Mice were given 1 week to recover from the injections, and then an IPGTT was performed. The mice were then given another week to recover, and an insulin tolerance test (ITT) was performed.

[0083] No differences in body weight (40.3 ± 1.3 g for the Ad5-Swir1 mice; 41.4 ± 1.2 g for the Ad5-GFP mice), fasting insulin (0.97 ± 0.2 ng/mL for the Ad5-Swir1 mice; 1.13 ± 0.2 ng/mL for the Ad5-GFP mice), or fasting glucose levels (126 ± 7 mg/dL for the Ad5-Swir1 mice; 139 ± 8 mg/dL for the Ad5-GFP mice) were observed at 20 days after injection. IPGTT 7 days after injection revealed a very modest improvement in glucose tolerance in the Ad5-Swir1 group at the 30-minute ($p=0.06$) and 45-minute ($p=0.15$) time points. Changes in blood glucose levels 14 days after injection were significantly different between groups, being significantly reduced in the Ad5-Swir1 group (data not shown). An ITT 14 days post-infection revealed no significant difference in insulin sensitivity at any time point; however Ki (calculated as glucose at 30 minutes post insulin injection subtracted from baseline glucose, divided by 30) was significantly different.

[0084] The lower fasting blood glucose levels observed in these mice 14 days after infection was not apparent at 21 days after infection. In agreement with the first adenoviral experiment in Mc4r-/- mice, there was a trend for a decrease in serum triglycerides in the Ad5-Swir1 group (Table 2).

Table 2. Infection with Ad5-Swir is associated with evidence of improved metabolic profile in mouse models of obesity and insulin resistance.

* $P<0.05$ compared to Ad5-GFP treated controls (within strain), n=5-8/group.

Strain	Treat-ment	BW pre-injection	BW post-injection	Liver wgt (g)	Liver wgt as a % BW	Liver lipid content (mg/g)	Total liver lipid (mg)	Serum TG (mg/dL)	Serum TC (mg/dL)	HOMA-IR
OBOB	GFP	64.0 ± 1.9	64.8 ± 2.0	4.7 ± 0.2	7.4 ± 0.3	142 ± 8	654 ± 25	63 ± 6	173 ± 6	308 ± 114
	Swir1	65.0 ± 2.2	64.6 ± 2.0	4.3 ± 0.2	6.7 ± 0.3	128 ± 7	552 ± 50	38 ± 4*	146 ± 8 *	157 ± 18
KK-A^y	GFP	48.0 ± 1.9	46.7 ± 1.7	2.1 ± 0.2	4.7 ± 0.3	57 ± 10	117 ± 24	435 ± 53	214 ± 13	98 ± 19
	Swir1	46.6 ± 1.2	45.3 ± 0.8	1.8 ± 0.1	4.3 ± 0.1	33 ± 2*	58 ± 5 *	315 ± 16*	172 ± 9	62 ± 11
Ay/a	GFP	45.2 ± 2.5	44.6 ± 2.1	2.2 ± 0.2	5.1 ± 0.2	119 ± 11	282 ± 39	71 ± 18	79 ± 3	40 ± 6
	Swir1	44.8 ± 1.4	44.5 ± 1.1	1.8 ± 0.2	4.2 ± 0.3*	81 ± 20	145 ± 41*	53 ± 4	72 ± 2	28 ± 4

Example 7

Treatment of Obese Insulin Resistant Mice with Ad5-Swirl: Agouti (KK-A^y) mice (Genetically Obese and Hyperlipidemic Mice)

[0085] To more specifically address the effect of adenoviral infusion on measures of blood lipids, the adenoviral constructs were further purified to remove any contaminating viral particles and cellular debris. Another adenoviral experiment was then conducted whereby Ad5-SWIR1 or Ad5-GFPAd5-GFP was injected into the tail vein of genetically obese and hyperlipidemic KK-A^y mice (n=6 female per group). Mice were given an IPGTT 5 days post virus injection, and then sacrificed 2 days later after an overnight fast.

[0086] IPGTT revealed that glucose tolerance was not significantly improved by Ad5-SWIR1 treatment compared to Ad5-GFP treatment. Statistically significant reductions in circulating triglycerides (by 28%, p=0.04) and cholesterol (by 20%, p=0.02) were observed in the Ad5-SWIR1 group compared to Ad5-GFP controls (Table 1). Liver weight of Ad5-SWIR1 mice tended to be lower than liver weight of Ad5-GFP controls (Table 2). Body weight, and serum glucose and insulin levels were not significantly different between Ad5-SWIR1 and Ad5-GFP controls (Table 2).

Table 3. Characteristics of KK-A^y mice treated with Ad5-Swirl or Ad5-GFP for 8 days.

Treatment	Body Weight (g)	Liver weight (g)	Liver as % of body weight	Glucose (mg/dL)	Insulin (ng/mL)
Ad5-SWIR1	41.9 ± 0.9	1.8 ± 0.1	4.3 ± 0.1	239 ± 19	4.3 ± 0.7
Ad5-GFP	44.1 ± 1.5	2.1 ± 0.2	4.6 ± 0.2	246 ± 41	5.1 ± 0.9

[0087] *Swirl* mRNA was elevated approximately 4-fold in the liver of KK-A^y Ad5-Swirl-treated mice compared to Ad5-GFP-treated mice (data not shown).

Example 8

Treatment of Obese Insulin Resistant Mice with Ad5-Swirl: Lep^{ob}/Lep^{ob} Mice

[0088] To confirm the lipid-lowering effect of adenoviral-mediated Swirl overexpression, another experiment was performed in which Ad5-Swirl or Ad5-GFP was injected into the tail vein of Lep^{ob}/Lep^{ob} (OBOB) mice (n=7-8 male per group), another mouse model of hyperlipidemia, steatosis and insulin resistance. The injected mice were not

given an IPGTT, but were monitored for body weight changes, and then sacrificed 7 days post injection after an overnight fast.

[0089] Ad5-GFP-treated mice gained approximately 1 g of body weight over the 7-day period. However, Ad5-Swirl treatment blocked weight gain in these obese Lep^{ob}/Lep^{ob} mice (data not shown). Mean body weight was not statistically different between groups, and food intake was not measured. Similar phenotypic changes to that observed in KK-A^y mice (See Example 7 above) were also observed. Serum triglycerides were reduced by 40% in the Ad5-Swirl group (Ad5-GFP 63 ± 6 mg/dL (Ad5-GFP); 38 ± 4 mg/dL (Ad5-Swirl), p=0.006; Table 2). A 15% reduction in serum cholesterol levels was also observed (173 ± 6 mg/dL (Ad5-GFP); 146 ± 8 mg/dL (Ad5-Swirl), p=0.02; Table 2). A trend for a reduction in liver weight was observed that was not significant when expressed as a percentage of body weight (p=0.12). Trends for reduced fasting blood glucose and insulin levels in the Ad5-Swirl group did not reach statistical significance.

[0090] Purification of the adenoviral constructs and use of larger sample populations in the experiments using KK-A^y mice and Lep^{ob}/Lep^{ob} (*OBOB*) mice demonstrated that overexpression of Swirl for 7-8 days lead to reduced circulating triglyceride and cholesterol levels compared to control mice. (Table 2) Trends for these effects were observed in previous experiments using unpurified adenovirus with observations at later time points. Swirl gene expression in the liver was elevated in Ad5-Swirl-treated group in these experiments, whereas no increase was detectable in previous experiments at later time points. Without wishing to be bound by this theory, it is believed that increased gene expression of Swirl leads to increased circulating levels of the Swirl protein.

Example 9

Summary of Results of Treatment of Obese Insulin Resistant Mice with Ad5-Swirl

[0091] In summary, $5x10^9$ pfu of Ad5-Swirl or Ad5-GFP was administered into the tail vein of KK-A^y, B6 *Ay/a*, or *OBOB* mice purchased from the Jackson Laboratory (Bar Harbor, Maine). The treatment protocol, shown in Fig. 7C, was based on the pilot experiments demonstrating peak expression of Ad5-Swirl:FLAG during this period (data not shown). Animal and food weight were recorded daily. Ad5-Swirl infection was well tolerated in mouse strains used for these experiments. There were no marked differences in the body weight (Table 2) of mice infected with Ad5-Swirl compared to controls infected

with Ad5-GFP over the treatment period. A 4-5 fold increase in *Swirl* mRNA was observed in mice infected with Ad5-Swirl, compared to Ad5-GFP treated controls (data not shown).

[0092] Liver weight and lipid content were consistently reduced in mice infected with Ad5-Swirl. In KK-A^y and *OBOB* mice, significant reductions (≈ 40%) in fasting triglyceride and total cholesterol were observed. A smaller decline was observed in *Ay/a* mice. Meta-analysis of data from several experiments using obese *OBOB*, KK-A^y and *Ay/a* mice indicated a 40% reduction of HOMA-IR [(fasting insulin x glucose)/ 22.5] in *OBOB*, KK-A^y and *Ay/a* mice (Table 4). In *Ay/a* mice, fasting insulin levels were significantly reduced with Ad5-Swirl (2.6 ± 0.4 vs. 3.9 ± 0.3 ng/ml, P<0.05), with no difference in blood glucose (175 ± 12 vs. 162 ± 11 mg/dL).

Table 4. Meta-analysis of HOMA-IR, calculated by mutiplying fasting insulin and glucose, from *OBOB*, KK-A^y and *Ay/a* mice infected with Ad5-GFP or Ad5-Swirl.
Data are expressed as % ± SEM of control group.

Ad5-GFP	Ad5-Swirl	Student's *t* -test
100 ± 12%	62 ± 4%	P<0.005

Example 10

Overexpression of Swirl Effects on Genes Involved in Lipid Biosynthesis

[0093] Reversal of hepatic steatosis by adipocytokines is at least partially attributable to the suppression of hepatic lipogenesis and stimulation of fatty acid oxidation (42,43). To investigate the mechanism by which Swirl reduced hepatic lipid content, the expression of genes involved in lipogenesis was measured by quantitative RT-PCR (Figs. 8A-8D). There was a coordinate 40-50% reduction in the expression of several genes involved in lipogenesis in the liver of *OBOB* and KK-A^y mice infected with Ad5-Swirl. Swirl may therefore reduce hepatic lipid content, at least in part, by inhibiting hepatic lipogenesis.

[0094] A significant decrease in fatty acid synthase (Fasn) mRNA in the Ad5-Swirl-treated group was observed compared to the Ad5-GFP controls (Fig. 8A, p=0.02), as well as a decrease in protein levels (data not shown). Fasn mRNA and protein levels were measured using quantitative RealTime PCR and western blot, as described in D.C. Albarado *et al.*, "Impaired Coordination of Nutrient Intake and Substrate Oxidation in Melanocortin-4 Receptor Knockout Mice," Endocrinology, vol. 145, pp. 243-252 (2004). Gene expression of

the fatty acid translocase CD36 was also significantly elevated in the Ad5-Swirl group (p=0.02, not shown). Fig. 8A illustrates the expression level of fatty acid synthase (Fasn) mRNA in liver from obese leptin-deficient (Lep^{ob}/Lep^{ob}) mice eight days after injection with either Ad5-Swirl or Ad5-GFP. Data expressed in arbitrary units (AU) (n=6-8/group; "*" $p<0.05$). Swirl overexpression caused a decrease in Fasn. Fig. 8B illustrates the expression level of stearoyl-CoA desaturase (Scd1) protein in liver from obese leptin-deficient (Lep^{ob}/Lep^{ob}) mice eight days after injection with either Ad5-Swirl or Ad5-GFP. Data expressed in arbitrary units (AU) (n=6-8/group; "*" $p<0.05$). Again, Swirl overexpression caused a decrease in Scd1. Fig. 8C illustrates the expression level of acetyl CoA carboxylase (Acc) mRNA in liver from obese leptin-deficient (Lep^{ob}/Lep^{ob}) mice eight days after injection with either Ad5-Swirl or Ad5-GFP. Data expressed in arbitrary units (AU) (n=6-8/group; "*" $p<0.05$). Again, the mice with Swirl showed lower levels of liver Acc. Fig. 8D illustrates the expression level of a gene involved in insulin resistance (suppressor of cytokine signaling 3 or Socs3) in liver from obese leptin-deficient (Lep^{ob}/Lep^{ob}) mice eight days after injection with either Ad5-Swirl or Ad5-GFP. Data expressed in arbitrary units (AU) (n=6-8/group; "*" $p<0.05$). The presence of Swirl again decreased the gene express of Socs3.

Example 11

Transgenic Over Expression of Swirl (BAP-Swirl)

[0095] Transgenic strains over expressing Swirl were generated using a construct (BAP-Swirl) containing the human β-actin promoter, a synthetic exon 1 and intron, and the open reading frame encoding the 76 aa Swirl protein (Fig. 9A; see Fig. 4, the open reading frame is underlined). Eight founders were obtained (2 FVB/NJ, 6 C57BL/6J). One of the FVB strains [FVB/NJ.Tg-(BAP-Swirl)AAB20], hereafter referred to as **FVB.Tg**, exhibited an increase in hepatic Swirl expression at 5-6 wk of age (Fig. 9B). Fig. 10 illustrates the results of PCR screening of the pups in the first round of injection of BAP-Swirl into C57BL/6J oocytes, showing six pups (6, 8, 14, 19, 21, and 22) with integration of the transgene into the genome.

[0096] At 5-6 wk of age, reductions in serum TG and TC were already evident in FVB.Tg (Table 5, Fig. 9C). Body weight (Table 5) and FM (Fig. 9D) of FVB.Tg transgenics was reduced relative to WT littermate. Weight gain of FVB.Tg mice was also reduced on HFD (60% kJ/fat), indicating protection from diet-induced obesity (Fig. 9E). Reduced body

weight and fat content was still observed after 1 month on HFD, associated with a tendency for reduced fasting insulin levels of BAP-Swirl transgenics compared to WT controls (180 ± 60 vs. 310 ± 40 pg/ml, 2-tailed Student's *t*-test P=0.085).

Table 3. Data from the first 3 litters of FVB.Tg mice.
All mice are female aged approximately 4.5 weeks, n=3-5 per group.
* P<0.05 compared to control group.

	Body weight (g)	Liver weight (g)	Liver as % of body weight	Glucose (mg/dL)	Triglyceride (mg/dL)	Cholesterol (mg/dL)
FVB WT	20.5 ± 1.1	0.88 ± 0.01	4.3 ± 0.4	151 ± 14	105 ± 3	219 ± 7
FVB.Tg	17.8 ± 0.1*	0.69 ± 0.01*	3.9 ± 0.2	105 ± 6 *	82 ± 6 *	198 ± 4 *

[0097] As shown above, it was observed that over expression of Swirl impaired the metabolic adaptation to fasting, perhaps indicating increased energy expenditure. To determine whether Swirl increases energy expenditure, VO2 and RER was measured using indirect calorimetry (15,46,50). The Pennington Biomedical Research Center has a 16 chamber comprehensive laboratory animal monitoring system (CLAMS) housed in a temperature controlled incubator. The CLAMS simultaneously measures oxygen consumption (VO2), respiratory exchange ratio (RER, an indicator of whole animal substrate oxidation), physical activity in the X and Z axis, and food intake. Mice were placed in the CLAMS system, and the parameters indicated recorded for 72 h. Mice were fed ad libitum for 48 h, with a fast for the final 24 h. The results for FVB.Tg are shown in Figs. 13A-13F. Increased weight loss was observed after an overnight fast in obese KK-A^y, in obese B6 Ay/a mice expressing Ad5Swirl (% weight loss after overnight fast for Ad5-Swirl vs Ad5-GFP: 5.5 ± 0.4% vs. 3.5±0.4%, P<0.01), and in 9-wk-old lean FVB.Tg (13.6 ± 1.1% vs. 10.0 ± 0.7%, P<0.05). After 1 month of high fat feeding, measurement of energy metabolism in the transgenic mice by indirect calorimetry indicated significantly increased oxygen consumption (VO2 in ml/h: BAP-Swirl Tg 4551 ± 240, WT FVB 3807 ± 145, P<0.05) and physical activity during lights off (X beam breaks per hour: BAP-Swirl Tg 1431 ±181; WT FVB 2678 ± 327, P<0.01), as compared to the controls. Increased energy expenditure may thus be a factor in the amelioration of diet-induced obesity and insulin resistance by Swirl.

Example 12

Swir1 Effects Adipocytes

[0098] An experiment was conducted to test the use of a recombinant or synthetic form of the short secreted polypeptide Swir1$^{34-76}$(SEQ ID NO:10). The response of adipocytes and hepatocytes (two potential sites of Swir1 action) to synthetic Swir1$^{34-76}$ was analyzed for changes in extracellular regulated kinase (ERK). ERK1/2 and p38α are important in the regulation of lipolysis and thermogenesis in adipocytes.

[0099] Application of 1 μg/ml Swir1$^{34-76}$ was associated with a robust increase in the phosphorylation of Erk1 in fully differentiated 3T3-L1 adipocytes (Fig. 11A) and in HepG2 cells (Fig. 11B). These results indicated that functional receptors for Swir1$^{34-76}$ are active in adipocytes and hepatocytes, and that the synthetic peptide is biologically active. In addition, a shorter, second peptide was synthesized using amino acids 39 through 76 of SEQ ID NO:2, and called "Swir1$^{39-76}$"(SEQ ID NO:11). Similar results using adipocytes and hepatocytes were observed with this peptide. The loss of four amino acids did not appear to affect Swir1 function.

Example 13

Swir1 Function in Hypothalamus

[0100] Hypothalamic Swir1 may be involved in the regulation of energy homeostasis. Preliminary analysis using pAB1 (SEQ ID NO:8) demonstrated the presence of Swir1-immunoreactivity in neurons located in the arcuate nucleus of the hypothalamus (data not shown). It was predicted that a negative correlation would exist between hypothalamic Swir1 expression and obesity and insulin resistance. In other words, reduced synthesis of Swir1 in liver and hypothalamus in situations of obesity may be a factor contributing to obesity and insulin resistance.

[0101] *Swir1* mRNA expression was measured by quantitative RT-PCR in mediobasal hypothalamic blocks from control (low fat diet) and diet-induced obese C57BL/6J, Mc3rKO and Mc4rKO mice (Figs. 12A-12B). As predicted, Swir1 mRNA abundance in the hypothalamus was reduced in the obese state (Fig. 12A). Swir1 expression was also low in mice with elevated HOMA-IR values, an indicator of insulin resistance (Fig. 12B).

[0102] In contrast, *Socs3* mRNA expression was elevated in situations of obesity and insulin resistance (Fig. 11C). This data indicated that reduced synthesis of Swirl in situations of obesity is not limited to the liver. Reduced Swirl activity in the hypothalamus would also contribute to the development of obesity and insulin resistance.

[0103] In summary, an expression vector was constructed using a partial cDNA sequence encoding the predicted 76 residues of Swirl (between nucleotides 207 and 437 of BC021944; SEQ ID NO:2), with an epitope-tag inserted onto the carboxyterminal end to allow visualization of the protein on Western blot using a commercially available antibody to the tag. Using this construct, it was verified that the reported sequences encoded a secreted protein. This expression vector and an expression vector encoding the native protein without an epitope label were then used to construct a recombinant adenovirus (Ad5-Swirl) for use in mouse studies. Injections of $5x10^8$ pfu of the adenovirus into the tail vein resulted primarily in an infection of the liver, and to a lesser extent, the spleen. Using the adenovirus expressing the epitope-tagged Swirl, it was demonstrated that 5 days after injection of the virus, there was wide spread distribution of Swirl protein in liver, brain, and skeletal muscle. Using this adenovirus expressing the native form of Swirl, a new function (reduction of fasting serum triglyceride and cholesterol) was shown for the secreted protein. A reduction in liver *Swirl* mRNA expression was observed in obese mice with hyperlipidemia, with the magnitude of the reduction correlating with the increase of total cholesterol and triglyceride. Using the adenovirus expressing the native form of Swirl, it was shown that increasing the expression of the mRNA encoding the Swirl protein in mouse models of obesity with high cholesterol and triglycerides was effective at reducing both cholesterol and triglycerides toward normal levels. The effects of Ad5- Swirl infection to reduce triglyceride and total cholesterol were reproducible, being observed in three different mouse strains (Lep^{ob}/Lep^{ob}, KK-A^y, and C57BL/6J). In some mice, an improvement in insulin sensitivity was observed in a trend of lower fasting insulin and glucose and an improvement in glucose tolerance test results. The latter observations indicate that Swirl may be effective at improving insulin sensitivity in an obese, insulin-resistant patient.

[0104] The data strongly suggest that full-length Swirl peptide (SEQ.ID.NO. 2), or peptide derivatives, homologues, analogues, or mimetics thereof, delivered by oral intake, injection, subcutaneous patch, or intranasal routes, could be used as therapeutic or diagnostic

agents for hypercholesterolemia, hypertriglyceridemia, insulin resistance, obesity, diabetes, and/or energy imbalance. By methods known in the art, substitutions within the native coding sequence can be made to make derivatives of Swirl with increased stability and/or biological potency. Moreover, the Swirl peptide can be used to identify its cell receptor which can then be used as as-yet-unidentified receptor(s) for Swirl is (are) a potential drug target(s) for the development of therapies aimed at reducing total cholesterol, triglycerides, insulin resistance, obesity, diabetes and/or energy imbalance.

[0105] A novel secreted protein, Swirl, that is an important factor in the etiology of insulin resistance and hepatic steatosis in the obese state has been identified by Microarray analysis of gene expression in mouse models of moderate- to severe-diabesity. Swirl significantly reduces HOMA-IR, an index of fasting insulin and glucose, and serum lipids in mouse models of type 2 diabetes, and significantly reduces hepatic lipids indicating a reversal of hepatic steatosis. Transgenic over expression of Swirl is associated with a lean phenotype. Swirl may act in a manner similar to leptin and adiponectin, improving metabolic profile in the obese insulin state by stimulating energy expenditure and increasing oxidative metabolism.

Example 14

Swirl Treatment Will Reverse Hepatic Insulin Resistance

[0106] Preliminary data from Ad5-Swirl and BAP-Swirl transgenics (shown above) indicated improved insulin action and lipid metabolism. In FVB.Tg mice, increased oxidative metabolism is a likely factor explaining these effects. It may not be possible to dissect the anti-diabetc actions of Swirl from those secondary to reductions of FM. Preliminary data using recombinant adenovirus indicate that Swirl reduces hyperinsulinemia and hyperlipidemia independently of effects on obesity. Further experiments using recombinant adenovirus and synthetic peptide may therefore provide important information regarding 'direct' effects of Swirl on liver metabolism and insulin sensitivity.

[0107] Experiments will be conducted to determine whether the reversal of hepatic steatosis with Ad-Swirl treatment is associated with improved insulin sensitivity in liver and skeletal muscle by measuring insulin receptor signaling. These will include analysis of insulin receptor substrates 1 and 2 phosphorylation, which are distal to the insulin receptor tyrosine kinase. Activity of protein kinase B (PKB)/Akt, a serine/threonine kinase involved

in regulating glucose transport that is downstream of phosphatidyl-3' kinase (44,45), will also be measured as an indicator of insulin receptor activation. Pilot data showing significantly greater weight loss of mice infected with Ad5-Swirl suggested increased basal metabolic rate. Whether Ad5-Swirl increases whole body metabolic rate during postprandial and fasting states will be determined using indirect calorimetry. Oxidative metabolism in tissue lysates from liver, skeletal muscle and brown adipose tissue will also be determined.

[0108] The basic protocol for adenovirus treatment is shown in Fig. 7C. Briefly, all mice will have $5x10^9$ pfu of Ad5-SWIR1 or Ad5-GFP injected into the tail vein (n=12/group, 24 total). Mice shall be allowed 4 d to recover before use in the following experiments. A liver sample taken at termination will be used to estimate infection by measuring *Swir1* mRNA by RealTime PCR and Northern blot analysis. In preliminary experiments, a 4-fold increase in *Swir1* mRNA was observed 4-7d post infection. Swirl protein shall also be measured either by Western blot, or through the use of assays (RIA / ELISA) currently under development. Mice shall be weighed on the day of adenovirus injection, and pre- and post-fasting. If possible, body composition shall be determined using nuclear magnetic resonance (NMR) (15,32,46). Mice shall be acclimated to housing in wire-mesh caging that allows for measurement of food intake and spillage, as previously described (15).

[0109] If the sexual dimorphic phenotype of the FVB.Tg is reproducible and observed in BAP-Swirl transgenics on the C57BL/6J background, the Ad5 experiments will be modified to investigate the response of males and females. Most of the experiments investigating the response of obese insulin resistant mice to Ad5-Swirl treatment used males; it may be that females will exhibit a different response, perhaps exhibiting weight loss in addition to improved insulin sensitivity. This would not be unprecedented, for example sexual dimorphism has been observed in the response of male and female rats to the anorectic actions of insulin and leptin (47,48).

[0110] *Determine Whether Reversal of Hepatic Steatosis Is Associated With Increased Insulin Sensitivity.* This experiment will involve KK-A^y and *Ay/a* mice, with two groups of twelve within genotype (Ad5-Swirl, Ad5-GFP controls) (24 KK-A^y, 24 *Ay/a*). On day 5 after an overnight fast, six of the Ad5-SWIR1 and Ad5-GFP groups shall be administered a single intraperitoneal of insulin (1 U/kg), with the remaining six receiving saline. Mice shall be euthanized either 10 or 20 minutes (n=3/group) post injection, and tissue samples collected (liver, quadriceps muscle) and snap frozen on liquid nitrogen. IRS

phosphorylation, PKB activity, and FoxO1 phosphorylation shall be measured as previously described (15,49). This experiment shall be repeated two more times with only 8 mice per group to do insulin and glucose tolerance tests.

[0111] It is predicted that the anti-steatotic effect of Ad5-Swirl will increase insulin-stimulated activity of the insulin receptor tyrosine kinase cascade in liver. Ad5-Swirl may also improve insulin signaling in muscle and/or adipose tissue. The initial studies investigating glucose clearance resulted in mixed results (data not shown), perhaps due to sub-optimal experimental design [i.e., small numbers of mice (n=4-5); performed at variable times (up two two weeks) after adenovirus injection]. It is predicted that Ad5-Swirl will improve glucose clearance in response to glucose/insulin injections.

[0112] *Determine Whether Swirl Increases Whole Body Energy Expenditure and Oxidtive Metabolism.* To determine whether hepatic expression of Swirl increases energy expenditure, VO2 and RER of obese Ay/a and lean and diet-induced obese C57BL/6J mice infected with Ad5-Swirl or Ad5-GFP (n=8/group) shall be measured using indirect calorimetry (15,46,50). The Pennington Biomedical Research Center has a 16 chamber comprehensive laboratory animal monitoring system (CLAMS) housed in a temperature controlled incubator. The CLAMS simultaneously measures oxygen consumption (VO2), respiratory exchange ratio (RER, an indicator of whole animal substrate oxidation), physical activity in the X and Z axis, and food intake. Mice shall be placed in the CLAMS system 96 h after adenovirus injection, and the parameters indicated recorded for 72 h. Mice shall be allowed to feed ad libitum for 48 h, with a fast for final 24 h. In a separate experiments, fatty acid oxidation (C^{14}-palmitate) and mitochondrial enzyme function (citrate synthase activity, cytochrome c oxidase) will be measured in liver, gastrocnemius, and brown adipose tissue collected from *Ay/a* and C57BL/6J mice infected with Ad5-Swirl or Ad5-GFP (n=8/group). A portion of liver shall be collected and snap frozen for measurement of mRNA and protein expression of transcription factors (i.e., SREBP1c, PPARγ) and enzyme involved in lipogenesis (32).

[0113] The increased weight loss of mice infected with Ad5-Swirl indicated increased basal metabolic rate, a finding corroborated by fasting weight loss and indirect calorimetry data from BAP-Swirl transgenics. (See Figs. 13A-F) It is predicted that infection with Ad5-Swirl will increase VO2, although this may only be evident during the fasting phase. An increase in mitochondrial oxidative enzyme activity in liver only would be

consistent with Swirl acting as an autocrine/paracrine factor. Increased mitochondrial oxidative enzyme activity in skeletal muscle and brown adipose tissue would suggest an endocrine function, either acting through the autonomic nervous system or through receptors expressed in muscle and/or brown adipose tissue. If Ad5-Swirl is markedly increasing energy expenditure (as observed in FVB.Tg) but is not affecting body weight, then a compensatory increase in food intake would be predicted. A reduction in the expression of genes involved in lipogenesis, as observed in *OBOB* mice treated with Ad5-Swirl, is also predicted. (Fig. 8A-8D).

Example 15

Transgenic Expression of Swirl Prevents Obesity and Insulin Resistance

[0114] Transgenic mice over expressing leptin (51,52) and adiponectin (53,54) have demonstrated the anti-diabetic action of over expression of either protein. It is expected that over expression of Swirl will have outcomes comparable to that observed with over expression of adiponectin and leptin; i.e. improved insulin sensitivity and glucose tolerance, and lower fasting lipids in situations of diet- and genetically induced obesity. It is also predicted that Swirl will increases energy expenditure by increasing oxidative metabolism in liver, skeletal muscle, and/or brown adipose tissue. A comprehensive analysis of the physiology of Swirl action is important for future experiments that focus on the mechanism(s) by which this polypeptide regulates energy metabolism and insulin signaling.

[0115] *Transgenics:* A sequence encoding the 76 aa protein has been ligated into a synthetic transgene controlled by the human β-actin promoter (BAP) (Fig. 9A). Swirl is a secreted polypeptide (Fig. 4), and thus tissue-selectivity is not important for these transgenic studies. Promoters specific for tissues have not been used where the endogenous gene is abundantly expressed, because suppression of the endogenous gene may limit efficacy of over expression (53,54). A comprehensive analysis of mRNA expression shall be completed using quantitative RT-PCR (qRT-PCR) as previously described (31,32,46) and Northern blot analysis. Protein levels shall be measured by Western blot using the two polyclonal antibodies against the N- and C-terminus of Swir $^{34\text{-}76}$ (pAB1 (SEQ ID NO:8), pAB2 (SEQ ID NO:9)) (Fig. 5). This may require using immunoprecitipitation to detect protein. Alternatively, if antibodies in hand or in development are useful for developing sensitive and quantitative assays, then these shall be used. Transgene copy number shall be determined by

Southern blot analysis. A sub-aim of this experiment is therefore a more comprehensive analysis of *Swirl* mRNA expression in mouse tissues (liver, hypothalamus, forebrain, hindbrain, skeletal and cardiac muscle, retroperitoneal and inquinal adipose depots, stomach, intestine, pancreas, kidney). Major organs (heart, kidney, gut, liver) shall be weighed and inspected histologically for major morphological changes.

[0116] We have shown that Swirl is one of a small group of secreted polypeptides (leptin, adiponectin) that, when over expressed, improves metabolic profile (i.e. increased insulin sensitivity, reduced hepatic lipogenesis) in mouse models of obesity and insulin resistance. The over expression of Swirl has leptin-like effects on energy metabolism, protecting against diet-induced obesity and insulin resistance. Administering Swirl can reverse insulin resistance and dyslipidemia associated with diet- and genetically-induced obesity, and can prevent or delay onset of type 2 diabetes.

Miscellaneous

[0117] The term "Swirl" used herein and in the claims refers to the protein Swirl (SEQ ID NO:2), its functional peptides (e.g., $Swirl^{34-76}$), derivatives and analogs. The terms "derivatives" and "analogs" are understood to be proteins that are similar in structure to Swirl and that exhibit a qualitatively similar effect to the unmodified Swirl. The term "functional peptide" refers to a piece of the Swirl protein that still binds to the Swirl receptor or is able to activate changes inside body cells, e.g., adipocytes or hepatocytes.

[0118] The administration of Swirl, its functional peptides, its analogs and derivatives in accordance with the present invention may be used to reverse insulin resistance and dyslipidemia, and to prevent or delay onset of obesity. These compounds can also be used as therapeutic or diagnostic agents for hypercholesterolemia, hypertriglyceridemia, insulin resistance, obesity, and diabetes.

[0119] The term "therapeutically effective amount" as used herein refers to an amount of Swirl protein, a fragment, or a derivative or analog sufficient either increase body energy expenditure, decrease serum triglyceride, decrease serum cholesterol, decrease hyperlipidemia, decrease insulin resistance, or delays or reduces the onset of type 2 diabetes in insulin resistant patients to a statistically significant degree ($p<0.05$). The dosage ranges for the administration of Swirl protein are those that produce the desired effect. Generally, the dosage will vary with the age, weight, condition, and sex of the patient. A person of

ordinary skill in the art, given the teachings of the present specification, may readily determine suitable dosage ranges. The dosage can be adjusted by the individual physician in the event of any contraindications. In any event, the effectiveness of treatment can be determined by monitoring either the body metabolism, body weight, or the serum glucose, triglyceride, or cholesterol levels by methods well known to those in the field. Moreover, Swirl can be applied in pharmaceutically acceptable carriers known in the art.

[0120] This method of treatment may be used in mammals generally, including human and non-human mammals. Peptides in accordance with the present invention may be administered to a patient by any suitable means, including oral, intravenous, parenteral, subcutaneous, intrapulmonary, and intranasal administration.

[0121] Parenteral infusions include intramuscular, intravenous, intraarterial, or intraperitoneal administration. The peptides may also be administered transdermally, for example in the form of a slow-release subcutaneous implant, or orally in the form of capsules, powders, or granules. It may also be administered by inhalation.

[0122] Pharmaceutically acceptable carrier preparations for parenteral administration include sterile, aqueous or non-aqueous solutions, suspensions, and emulsions. Examples of non-aqueous solvents are propylene glycol, polyethylene glycol, vegetable oils such as olive oil, and injectable organic esters such as ethyl oleate. Aqueous carriers include water, alcoholic/aqueous solutions, emulsions or suspensions, including saline and buffered media. Parenteral vehicles include sodium chloride solution, Ringer's dextrose, dextrose and sodium chloride, lactated Ringer's, or fixed oils. The peptides may be mixed with excipients that are pharmaceutically acceptable and are compatible with the active ingredient. Suitable excipients include water, saline, dextrose, glycerol and ethanol, or combinations thereof. Intravenous vehicles include fluid and nutrient replenishers, electrolyte replenishers, such as those based on Ringer's dextrose, and the like. Preservatives and other additives may also be present such as, for example, antimicrobials, anti-oxidants, chelating agents, inert gases, and the like.

[0123] The form may vary depending upon the route of administration. For example, compositions for injection may be provided in the form of an ampule, each containing a unit dose amount, or in the form of a container containing multiple doses.

[0124] The compound may be formulated into therapeutic compositions as pharmaceutically acceptable salts. These salts include acid addition salts formed with

inorganic acids, for example hydrochloric or phosphoric acid, or organic acids such as acetic, oxalic, or tartaric acid, and the like. Salts also include those formed from inorganic bases such as, for example, sodium, potassium, ammonium, calcium or ferric hydroxides, and organic bases such as isopropylamine, trimethylamine, histidine, procaine and the like. The compositions may be administered intravenously, subcutaneously, or intramuscularly.

[0125] Controlled delivery may be achieved by admixing the peptide with appropriate macromolecules, for example, polyesters, polyamino acids, polyvinyl pyrrolidone, ethylenevinylacetate, methylcellulose, carboxymethylcellulose, prolamine sulfate, or lactide/glycolide copolymers. The rate of release of the active compound may be controlled by altering the concentration of the macromolecule.

[0126] Another method for controlling the duration of action comprises incorporating the peptides into particles of a polymeric substance such as a polyester, peptide, hydrogel, polylactide/glycolide copolymer, or ethylenevinylacetate copolymers. Alternatively, a peptide may be encapsulated in microcapsules prepared, for example, by coacervation techniques or by interfacial polymerization, for example, by the use of hydroxymethylcellulose or gelatin-microcapsules or poly(methylmethacrylate) microcapsules, respectively, or in a colloid drug delivery system. Colloidal dispersion systems include macromolecule complexes, nano-capsules, microspheres, beads, and lipid-based systems including oil-in-water emulsions, micelles, mixed micelles, and liposomes.

[0127] In addition, all or portions of the nucleic acid sequence (SEQ ID NO:1) (e.g., the open reading frame underlined in Fig. 4) can be used to make plasmids or vectors to incorporate the *Swirl* gene into organisms to increase the production of the Swirl protein. It will be understood by those skilled in the art that the nucleic acid sequence of SEQ ID NO:1 is not the only sequence that can be used to produce the Swirl protein. Also contemplated are those nucleic acid sequences that encode identical proteins but that, because of the degeneracy of the genetic code, possess different nucleotide sequences. The genetic code may be found in numerous references concerning genetics or biology, including, for example, Figure 9.1 on page 214 of B. Lewin, *Genes VI* (Oxford University Press, New York, 1997). Figure 9.3 on page 216 of Lewin directly illustrates the degeneracy of the genetic code. For example, the codon for asparagine may be AAT or AAC.

[0128] The invention also encompasses nucleotide sequences encoding Swirl proteins having one or more silent amino acid changes in portions of the molecule not

involved with receptor binding or protein secretion. For example, alterations in the nucleotide sequence that result in the production of a chemically equivalent amino acid at a given site are contemplated; thus, a codon for the amino acid alanine, a hydrophobic amino acid, may be substituted by a codon encoding another hydrophobic residue, such as glycine, or may be substituted with a more hydrophobic residue such as valine, leucine, or isoleucine. Similarly, changes that result in the substitution of one negatively-charged residue for another, such as aspartic acid for glutamic acid, or one positively-charged residue for another, such as lysine for arginine, can also be expected to produce a biologically equivalent product. See, e.g., Fig. 1.8 on page 10 of Lewin (1997), showing the nature of the side chains of the "standard" 20 amino acids encoded by the genetic code. (Note also a typographical error in that published figure, namely that the abbreviation for glutamine should be "Gln.")

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[0129] The complete disclosures of all references cited in this specification are hereby incorporated by reference. In the event of an otherwise irreconcilable conflict, however, the present specification shall control.

SEQUENCE LISTING

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Lys Pro Ser His Glu Gly Ser Tyr Leu Leu Gln Pro
65 70 75

What is claimed:

1. A purified Swir1 peptide, and fragment, homologs, analogs and derivatives thereof, wherein the peptide has the following characteristics:

    a. it is a substantially homogenous preparation; and

    b. it has at least 70% homology to any one of the sequences set forth in SEQ ID NOS: 2, 10, 11, 12-18; wherein

    c. the peptide modulates energy metabolism, lipid metabolism, and/or insulin action.

2. A peptide of Claim 1, wherein the peptide is a mammalian peptide.

3. A peptide of Claim 1, wherein the peptide is a murine peptide.

4. A peptide of Claim 1, wherein the peptide is a human peptide.

5. A peptide of Claim 1, wherein the peptide is a synthetic peptide.

6. A peptide of Claim 1, wherein said homology to any one of the sequences set forth in SEQ ID NOS: 2, 10, 11, 12-18 is greater than 85%.

7. A peptide of Claim 6, wherein the homology is greater than 95%.

8. A pharmaceutical composition comprising any one of the Swirl peptides of claims 1-7, and a pharmaceutical acceptable carrier.

9. A therapeutically effective amount of a pharmaceutical composition for use in treating a pathophysiology relating to homeostasis of body mass, comprising a Swirl peptide, or fragments, homologs, analogs and derivatives thereof.

10. A therapeutically effective amount of a pharmaceutical composition for use in preventing a pathophysiology relating to homeostasis of body mass, comprising a Swirl peptide, or fragments, homologs, analogs and derivatives thereof.

11. A therapeutically effective amount of a pharmaceutical composition for use of any one of claims 9 or 10, wherein the Swirl peptide has at least 70% homology to any one of the sequences set forth in SEQ ID NOS: 2 and 10-18.

12. A therapeutically effective amount of a pharmaceutical composition for use of any one of claims 9 or 10, wherein the pathophysiology is obesity.

13. A therapeutically effective amount of a pharmaceutical composition for use of any one of claims 9 or 10, additionally comprising a compound selected from the group consisting of leptin and adiponectin.

14. A therapeutically effective amount of a pharmaceutical composition for use of any one of claims 9 or 10, wherein the pathophysiology is one related to obesity comprising any one of hyperglycemica, hyperinsulinemia, insulin resistance,

hyperlipidemia, Type II diabetes mellitus, and non-insulin dependent diabetes mellitus.

15. A therapeutically effective amount of a pharmaceutical composition for use of any one of claims 9 or 10, wherein the treatment comprises intraperitoneal administration.

16. A vector comprising a least 200 nucleic acids of the open reading frame of the nucleic acid sequence of SEQ ID NO:1.

17. A cultured cell that produces a Swirl peptide according to any one of claims 1-7.

18. The cell of claim 17, wherein the cell is selected from the group consisting of bacteria, yeast, mammalian cells, plant cells, and insect cells.

19. A method for preparing a Swirl peptide comprising:
    a. culturing a cell containing a nucleic acid corresponding to at least the open reading frame of SEQ ID NO:1 under conditions that provide for expression of the peptide; and
    b. recovering the expressed peptide.

20. A pharmaceutical composition comprising at least the open reading frame of SEQ ID NO:1, wherein the nucleic acid encodes a Swirl peptide, and a pharmaceutical acceptable carrier.

21. An antibody, and fragments, derivatives, homologs and analogs thereof, which immunospecifically binds to the peptide of any one of claims 1-7.

22. An antibody of claim 21 labeled with a detectable label.

23. An antibody of claim 21, wherein said antibody is generated using any one of the peptides of SEQ ID NOS: 2 and 8 – 18, and fragments, derivatives, homologs, and analogs of said peptide.

24. An antibody or fragment of claim 21, wherein the antibody is a polyclonal antibody.

25. An antibody or fragment of claim 21, wherein the antibody is a monoclonal antibody.

26. A kit comprising in one or more containers a Swirl peptide according to any one of claims 1-7, a portion of the nucleic acid sequence of SEQ ID NO:1, or an antibody that recognizes a Swirl protein according to any one of claims 21-25.

27. A recombinant non-human animal containing a nucleic acid, wherein the nucleic acid is an isolated nucleic acid comprising a nucleotide sequence encoding any one of the Swirl related peptides of SEQ ID NOS:2 and 8-18, and fragments, derivatives, homologs, and analogs thereof of those peptides.

28. A pharmaceutical composition for use to ameliorate or decrease insulin resistance in a subject, comprising a therapeutically effective amount of a Swirl peptide with a sequence as given in SEQ ID NOS:2 and 8-18, and fragments, derivatives, homologs, and analogs thereof of those peptides.

29. A pharmaceutical composition for use to ameliorate or treat symptoms of diabetes in a subject, comprising a therapeutically effective amount of a Swirl peptide with a sequence as given in SEQ ID NOS:2 and 8-18, and fragments, derivatives, homologs, and analogs thereof of those peptides.

30. A pharmaceutical composition for use to prevent or delay the onset of obesity in a subject, comprising a therapeutically effective amount of a Swirl peptide with a sequence as given in SEQ ID NOS:2 and 8-18, and fragments, derivatives, homologs, and analogs thereof of those peptides.

31. A pharmaceutical composition for use to ameliorate or decrease hyperlipidemia in a subject, comprising a therapeutically effective amount of a Swirl peptide with a sequence as given in SEQ ID NOS:2 and 8-18, and fragments, derivatives, homologs, and analogs thereof of those peptides.

32. A pharmaceutical composition for use to decrease total cholesterol in the serum in a subject, comprising a therapeutically effective amount of a Swirl peptide with a sequence as given in SEQ ID NOS:2 and 8-18, and fragments, derivatives, homologs, and analogs thereof of those peptides.

33. A pharmaceutical composition for use to decrease serum triglycerides in a subject, comprising a therapeutically effective amount of a Swirl peptide with a sequence as given in SEQ ID NOS:2 and 8-18, and fragments, derivatives, homologs, and analogs thereof of those peptides.

34. A pharmaceutical composition for use of any one of claims 28 - 33, additionally comprising a compound selected from the group consisting of leptin and adiponectin.

35. A non-human transgenic animal having cells that carry a exogenous promoter and a cDNA corresponding to at least the open reading frame of SEQ ID NO:1 wherein said cells constituitively over express a Swirl peptide with a sequence as given in SEQ ID NOS:2 and 8-18, and fragments, derivatives, homologs, and analogs thereof of those peptides.

36. The transgenic animal of claim 35, wherein said exogenous promoter is an actin promoter.

37. The transgenic animal of claim 35, wherein said non-human animal is a mouse.

38. A transformation vector comprising at least the open reading frame of a nucleic acid sequence as recited in SEQ ID NO:1.

39. A host cell comprising at least the open reading frame of the nucleic acid sequence as recited in SEQ ID NO:1.

40. A nucleic acid construct comprising at least the open reading frame of the nucleic acid sequence as recited in SEQ ID NO:1, wherein said sequence is operably linked to a promoter that is functional in mammals.

41. A nucleic acid construct as recited in claim 40, wherein said promoter is an actin promoter.

42. An animal transformed with a nucleic acid construct as recited in Claim 40.

43. A purified Swirl peptide, and fragment, homologs, analogs and derivatives thereof, wherein the peptide has the following characteristics:

    a. it is a substantially homogenous preparation; and

    b. it has at least 70% homology to any one of the sequences set forth in SEQ ID NOS: 10, 11; wherein

    c. the peptide modulates energy metabolism, lipid metabolism, and/or insulin action.

44. A peptide of Claim 43, wherein the peptide is a mammalian peptide.

45. A peptide of Claim 43, wherein the peptide is a murine peptide.

46. A peptide of Claim 43, wherein the peptide is a human peptide.

47. A peptide of Claim 43, wherein the peptide is a synthetic peptide.

48. A peptide of Claim 43, wherein said homology to any one of the sequences set forth in SEQ ID NOS: 10, 11 is greater than 85%.

49. A peptide of Claim 48, wherein the homology is greater than 95%.

50. A pharmaceutical composition comprising any one of the Swirl peptides of claims 43-49, and a pharmaceutical acceptable carrier.

51. A vector comprising a least 200 nucleic acids of the open reading frame of the nucleic acid sequence of SEQ ID NO:10.

52. A vector comprising a least 200 nucleic acids of the open reading frame of the nucleic acid sequence of SEQ ID NO:11.

53. A cultured cell that produces a Swirl peptide according to any one of claims 43-49.

54. The cell of claim 53, wherein the cell is selected from the group consisting of bacteria, yeast, mammalian cells, plant cells, and insect cells.

55. An antibody, and fragments, derivatives, homologs and analogs thereof, which immunospecifically binds to the peptide of any one of claims 43-49.

56. An antibody of claim 55 labeled with a detectable label.

57. An antibody of claim 55, wherein said antibody is generated using any one of the peptides of SEQ ID NOS:10 and 11, and fragments, derivatives, homologs, and analogs of said peptide.

58. An antibody or fragment of claim 55, wherein the antibody is a polyclonal antibody.

59. An antibody or fragment of claim 55, wherein the antibody is a monoclonal antibody.

60. A kit comprising in one or more containers a Swirl peptide according to any one of claims 43-49, a portion of the nucleic acid sequence of SEQ ID NO:1, or an antibody that recognizes a Swirl protein according to any one of claims 55-59.

61. A recombinant non-human animal containing a nucleic acid, wherein the nucleic acid is an isolated nucleic acid comprising a nucleotide sequence encoding any one of the Swirl related peptides of SEQ ID NOS:10 and 11, and fragments, derivatives, homologs, and analogs thereof of those peptides.

62. A non-human transgenic animal having cells that carry a exogenous promoter and a cDNA corresponding to at least the open reading frame of SEQ ID NO:1 wherein said cells constituitively over express a Swirl peptide with a sequence as given in SEQ ID NOS:10 and 11, and fragments, derivatives, homologs, and analogs thereof of those peptides.

63. The transgenic animal of claim 62, wherein said exogenous promoter is an actin promoter.

64. The transgenic animal of claim 62, wherein said non-human animal is a mouse.