

sites of LIF can hold mannose-6 phosphate residues, creating a ligand site for the mannose-6 phosphate receptor (CIMPR, calcium-independent mannose-6 phosphate receptor), which participates in the cellular recycling of the LIF ligand [33, 34].

LIF exists in at least three isoforms, *i.e.* a soluble form called LIF-D, an intracellular form found in the nucleus, called LIF-i or LIF-T, and a third form localized in the extracellular matrix, termed LIF-M [35-37]. LIF-M and LIF-D are translated from alternative transcripts differing in the first exon, which encodes partially for different signal peptides, which target the mature protein to different locations. The LIF-T isoform is a truncated protein because of the absence of the ATG codon in the first

exon, leading to the initiation of translation at the first ATG codon of exon 2. This isoform has pro-apoptotic activity in the COS and 293T cell lines [37], but the function of this internal form of LIF has not been investigated in other cell systems or tissues. Expression of these three isoforms is regulated in an independent way during embryogenesis and adult life, whereas other isoforms have also been identified in liver [38, 39], but their functions await further clarification.

LIF is secreted by many cell types such as fibroblasts, activated T-cells, spleen or macrophage cells, chondrocytes, bone marrow stromal cells, mesenchymal stem cells, endothelial cells, astrocytes and also tumor cells [17, 40, 41]. *In vivo*, LIF production is associated with inflammation and autoimmune diseases [42-44]. It also promotes N-cadherin-mediated cell adhesion *via* the STAT3/ Wnt5 pathway in cardiomyocytes [45]. LIF is also naturally produced by the uterine decidua under the control of the estradiol peak, before implantation [14, 46-48] and thereafter is sustained by progesterone, presumably to induce a tolerant environment for the foetus during gestation [49]. Indeed, in endometrium, LIF directly induces the production of the class I non-classical HLA-G protein, whose function is essential for immune tolerance at the maternal-foetal interface during the establishment of gestation [50]. A high level of active LIF is also associated with transplantation tolerance, with direct regulation of Treg cell function in which the expression of the *Foxp3* gene seems to be controlled, at least in part, by LIF [11, 51]. Recent studies, conducted with KO model mice, have also revealed that LIF is a direct transcriptional target of the Fos-related protein Fra2, involved in the regulation of osteoclast functions [52]. A deleterious immunosuppressive function of LIF, which allows tumor cells to escape the immune system, has also been described in a model of ovarian cancer. Indeed, it was shown that LIF was a tumor-secreted factor that induces differentiation of monocytes to highly immunosuppressive TAM cells (tumor associated macrophages), [9].

Excess of LIF

The effect of an excess of LIF has been investigated in mice injected with the FDCP1 hematopoietic stem cells engineered to constitutively produce biologically active, murine LIF. These cells were engrafted normally into bone marrow, spleen and lymph nodes. After two to three months, engrafted animals lost weight, became hyperactive, developed osteopetrosis of long bones, calcifications in liver, heart, pancreas and skeletal muscles as well as abnormalities in the adrenal cortex and ovarian corpora lutea [53]. Studies of excess of LIF in the thymus of transgenic mice have led to the conclusion that LIF is important for maintaining a functional thymic epithelium that will support proper T cell maturation, a property also shared by oncostatin M [54, 55]. In embryos, excess of LIF-M blocks gastrulation by inhibiting the inner-cell mass differentiation into primitive ectoderm, a result also observed *in vitro* with embryoid bodies whose differentiation was blocked in the presence of an excess of LIF [56, 57]. These pioneering experiments, along with those showing that LIF maintains the pluripotency of

Abbreviations

AP1	activator-protein 1
BMP	bone morphogenetic protein
CD	cluster of differentiation
c-fos	FBJ murine osteosarcoma viral oncogene homolog
CIMPR	calcium-independent mannose-6 phosphate receptor
c-jun	avian sarcoma virus 17 oncogene homolog
CLC/CLF	cardiotrophin-like cytokine/cardiotrophin-like factor
c-myc	avian myelocytomatosis viral oncogene homolog
CNTF	ciliary neurotrophic factor
CNTFR	CNTF receptor
CREB	cAMP response element-binding
CT1	cardiotrophin-1
Dapp	dual adaptator of phosphotyrosine and PI3K
D-factor	differentiation factor
Eed	embryonic ectoderm development
EGF	epidermal growth factor
Egr	early growth response
ERK	extracellular signal-regulated kinase
ES cells	embryonic stem cells
FGF	fibroblast growth factor
Foxp3	forkhead box protein3
Fra	Fos-related antigen
HDAC	histone deacetylase
Hgf	hepatocyte growth factor
HLA	human leukocyte antigen
Ier	immediate-early response
Igfbp3	insulin growth factor binding protein-3
IL	interleukin
IL-6R	IL-6 receptor
IL-11 R	IL-11 receptor
iPS cells	induced pluripotent stem cells
Irg1	immune response gene-1
JAK	Janus kinase
junB	oncogene JUN-B
KLF	Kruppel-like factor
KO	knock-out
LIF	leukaemia inhibitory factor
Lifnd	LIF-induced genes
LIFR	LIF receptor
MW	molecular weight
NANOG	from Tir Na Nog
OCT	octamer-binding transcription factor
OSM	oncostatin M
OSMR	OSM receptor
p53	Tp53, tumor protein 53
PI3 kinase	phosphatidylinositol 3-kinase
RSK	ribosomal S6 kinase
RT-PCR	reverse transcriptase polymerase chain reaction
SHP2	Src homology region 2, phosphatase 2
SOCS	suppressor of cytokine signaling
SOX	SRY-related-HMB-box
STAT	signal transducer and activator of transcription
SWS	Stuve-Wiedemann syndrome
TAM cells	tumor associated macrophages cells
Treg	T regulatory cells
VEGF	vascular endothelial growth factor
Wnt	wingless-type mmtv integration site family
Zfp	zinc finger protein

mouse embryonic stem (ES) cells *in vitro* [23, 58-61], have led to numerous studies aimed at elucidating the mechanisms of action of LIF in stemness.

LIF and pluripotency

Knowledge of LIF signaling in the mouse ES cell system, along with years of expertise in manipulating mouse embryos, have led to the understanding of the species-dependent requirement of LIF for the maintenance of ES cell pluripotency. At first glance, it was puzzling to find that while mouse ES cells (mES) required LIF for maintenance of pluripotency, human ES cells (hES) did not need LIF, but rather have to be grown under the influence of activin and FGF factors in order to maintain their undifferentiated state [62-65]. A pioneering study, conducted using the mouse ES cell system, has already depicted a LIF-independent paracrine activity (named ESRF), secreted by differentiated cells, which allows the maintenance of mES cells pluripotency [66]. However, this activity has not been characterized further and its potential activity on human ES cells has not been evaluated. Since these first observations, transcriptome studies have led to the characterization of similarities and differences in expression profiles of genes in mES and hES cells, suggesting that these cells are probably not derived from equivalent parts of the early embryo [67, 68]. More recently, key results from two independent laboratories have been obtained which demonstrated that hES cells were probably not LIF-dependent because of their derivation from late rather than early epiblast [69-71]. These studies point to the fact that there is a short time frame for LIF dependency, and for maintenance of pluripotency in early embryos, which can be different between species and which deserves careful exploration (see also paragraph "LIF signaling: oldies and novelties"). However, the potential requirement of LIF for hES cell derivation and maintenance, which could depend on the maturity states of the embryos used to derive hES, might explain why some laboratories have used LIF in their culture medium, for growing hES cells [72].

LIF knock-out models

If homozygous LIF^{-/-} mice are viable, they nevertheless present many defects, including a decrease in the survival of hematopoietic stem cells and of their primordial germ cell pools [73], a profound loss of motor neurons [74] and of glial cells, along with an alteration in oligodendrocyte function [75]. In addition, maturation of olfactory neurons is impaired [76]. Recent studies have also shown that LIF represses hypoxia-induced VEGF expression, resulting in regulated capillary network formation [77]. Of major importance, LIF^{-/-} females are fertile, but their blastocysts cannot implant, leading to the definition of LIF as being the "nidation hormone" [73]. This implantation defect is due to the absence of LIF production by the uterus. LIF production is normally induced by estradiol *via* the TP53 loop. Indeed, there are functional TP53 binding sites in the LIF promoter [13, 78-80]. Of note, p53^{-/-} mice display the same implantation defect phenotype as LIF^{-/-} mice [13]. Interestingly, LIF^{-/-} or

p53^{-/-} blastocysts develop normally if implanted in a wild-type female or upon direct injection of LIF into the vagina of TP53^{-/-} or LIF^{-/-} mutated mice. None of the other IL6-related ligands has this specific effect on implantation, as deduced from the knock-out phenotypes reported for these ligands (table 1).

THE LIF RECEPTOR

Members of the IL-6 subfamily activate preformed, heteromeric receptors, which do not have any intrinsic catalytic activity and which all share the gp130 subunit [27, 28, 81-83]. The association of the ubiquitous gp130 (also called "subunit α ") with subunits specific for one or a few sub-family members (the so-called " β subunit" (*e.g.* gp190/ LIFR β ; CNTFR β ; gp80/IL-6R β ; OSMR β ; IL-11R β), and whose expression is more or less restrained, is responsible for both the diversity and the redundancy of the cell responses in this sub-family [84]. The functional LIF receptor is an heteromer comprising LIF low affinity binder gp190 together with the high affinity-converter gp130, both being transmembrane subunits with signalling ability. Preformed, inactive receptors are most probably present at the cell surface in the absence of ligand, as shown by co-precipitation of the heterodimeric complex without ligand, with anti-gp130 or anti-gp190 antibodies. However LIF binding increases interaction between subunits, and is essential for cellular responses [85-87]. The stoichiometry of the functional ligand/receptor complex is not known, but recently crystallographic analysis has demonstrated that this complex is a tetramer consisting of two LIF/gp190 molecules, [88, 89]. The intracellular part of both gp130 and gp190 associates with kinases of the JAK family, recruiting transcription factors of the STAT family, especially STAT3, as well as attenuators of LIF signaling such as the SHP2 tyrosine phosphatase and SOCS3 [90-92].

Mice knocked-out for the gp190 subunit, which also has low affinity binding for CT-1, display reduction of bone volume, severe osteopenia, metabolic liver disorder and reduction in astrocyte and motor neuron numbers in cerebral trunk and spinal chord [93-95]. They die perinatally, in part due to feeding difficulties because of their lack of development of sucking muscles. The placenta is also profoundly affected.

Gp130^{-/-} mice have also been generated in several laboratories, but the phenotypes reported are discrepant. Mutant mice produced by Yoshida *et al.* die between days 12 to 16 of embryogenesis with cardiac, hematopoietic and neuronal disorders [96], whereas those generated by Nichols *et al.* showed a critical function of gp130 in the completion of embryogenesis, only after diapause induction. This phenotype suggests a specialized function of gp130 as a response to environmental stress [97]. The reasons for these discrepancies have not been further investigated. Conditional gp130 deficient mouse mutants have also been derived in which gp130 was deleted in specific tissues or organs such as liver, lung or heart. These studies revealed a key role for gp130 signals in counterbalancing stress-dependent apoptotic signals [98].

HUMAN PATHOLOGY ASSOCIATED WITH LIF DEFICIENCY

LIF and fertility

In humans, as demonstrated in mice, LIF is expressed by the decidua following the estradiol peak and seems to be involved in blastocyst implantation. Gp190 is expressed in the luminal epithelium during the proliferative and secretory phases of the uterine cycle [99]. In addition, significant differences in the level of the soluble form of the gp190 protein (sgp190) have been founded in the serum of pregnant *versus* non-pregnant women, suggesting a role for this cytokine system throughout pregnancy, and more specifically in the functioning of the placenta [100]. LIF deficiency may be associated with a subset of female infertility due to an implantation defect. However, the direct effect of LIF is still a matter of debate since sterility has been associated with a decrease in LIF expression [101, 102] or to mutations in the *LIF* gene [103, 104], while other studies have shown that a low LIF level was a good implantation predictor [105]. However, in sterile women with endometriosis, LIF is not detected in the endometrium at the implantation stage [106].

The Stüve-Wiedemann syndrome

The Stüve-Wiedemann syndrome (SWS) or type 2 Schwartz-Jampel syndrome is a severe, autosomal recessive condition characterized by bowing of the long bones, respiratory distress, feeding difficulties, and hyperthermic episodes responsible for early lethality [107]. The molecular defect has been identified as null mutations in the gene encoding for the gp190 subunit of the LIF receptor. Functional studies have indicated that these mutations alter the stability of gp190 transcripts, resulting in the absence of this LIF receptor protein subunit and in the impairment of the JAK/STAT3 signaling pathway in patient cells. Of note, the phenotype of the gp190^{-/-} mice mimicked the complex phenotype of SWS patients, especially regarding the bone and nerve defects and early death [94].

REDUNDANCY AND PLEIOTROPY

LIF induces differentiation of the M1 cell line and apoptosis of normal mammary gland cells, after the lactating period. LIF is a pro-differentiative cytokine for adipocytes, [108], for cardiac muscle cells in a dose-dependent way and in synergy with BMP2 [109], and it induces differentiation of cardiac stem cells into endothelial cells [110]. Conversely, LIF maintains self-renewal of murine ES cells in synergy with serum or BMP4 or Wnt family members (Wnt3A and Wnt5) [111-113]. In addition, LIF regulates the differentiation process of stromal cells from bone marrow. Indeed, LIF secretion by human mesenchymal cells decreases when cells differentiate towards the adipogenic or osteoblast lineages. The LIF level, which is controlled by specific miRNA, is an essential, regulated parameter for proper differentiation of these cells [114]. LIF also favors the proliferation and survival of germ cells, hematopoietic progenitors, megakaryocytes, myoblasts and neural cells [1-3]. Some of these effects have been reported with other IL-6 family members [84]. Indeed, OSM, CNTF, CT1 and IL6 (in the presence of its α receptor subunit soluble gp80, which is not expressed by ES cells) are all endowed with the ability to maintain murine ES cell pluripotency [115, 116]. Additionally, OSM, CT1 and IL-6 induce macrophage differentiation of the M1 cell line [117, 118]. Gene ablation of LIF, CT-1 or CNTF or of their receptors (*tables 1, 2*), demonstrate their involvement in motor neuron survival [93, 119-121]. Double *Lif*^{-/-}/*Cntf*^{-/-} and triple *Lif*^{-/-}/*Cntf*^{-/-}/*Ct-I*^{-/-} knock-outs prove that these three cytokines have distinct functions for motor neuron survival and that LIF has an important role in post-natal maintenance of distal axons and motor neuron junctions [74].

LIF signaling: oldies and novelties

First identified as an EGF, IL-6 and LIF-dependent phosphorylated protein, STAT3 is present and active in all cells where LIF has an effect, whatever it may be [122-128]. Other factors that are always involved in LIF sig-

Table 1
Physiological effects of IL-6 cytokine family members revealed by KO mice models

Cytokines	Physiological effects	References
LIF	Survival of <i>lif</i> ^{-/-} adult mouse, but decreased numbers of stem cells in spleen and bone marrow	[73]
	No implantation of blastocysts in mouse lacking LIF gene. Implantation and development to term of the blastocysts when transferred to wild-type pseudopregnant recipients or by injection of LIF	[46, 78]
	Role in survival and differentiation of glial cells and oligodendrocytes of the hippocampus. Alteration of olfactory receptor neuron maturation	[75, 190]
IL-6	Normal development of IL-6-deficient mice. Impairment of the T-cell-dependent antibody response against vesicular stomatitis virus and the inflammatory acute-phase response after tissue damage or infection	[191, 192]
	Hematopoietic stem cell regulation	
OSM	Role in survival of neurons in the adult trigeminal and dorsal root ganglia and in the development of a subtype of nociceptive neurons	[193]
CNTF	Implicated in survival of motor neurons in adult mice	[120, 194]
CT-1	Implicated in survival of motor neurons in spinal cord and brainstem nuclei of mice during a period between embryonic day 14 and the first postnatal week	[121]
LIF/CNTF	Important implication of LIF and CNTF in survival, and in the function of motor neurons in the postnatal period. Co-operation of the two cytokines in the maintenance of motor neurons after lesion in deficient mice of four weeks	[120]
LIF/CNTF/CT-1	Different functions of CNTF, LIF and CT-1 for the survival and the function of motor neurons. A more important role of LIF for postnatal maintenance of distal axons and motor endplates	[74]

Table 2
Physiological effects of IL-6 subunit receptor members revealed by KO mice models

Cytokines	Physiological effects	References
Gp130	Death of embryos homozygous for the gp130 mutation between 12.5 days <i>postcoitum</i> and term. Crucial role in myocardial development and hematopoiesis during embryogenesis	[96]
	Importance of gp130 signalling for the prolonged maintenance of epiblast <i>in vivo</i> during diapause period induced by ovariectomy	[97]
LIFR β /gp190	Disruption of normal placental development in mutant mice leading to poor intrauterine nutrition, but foetuses reach term. Alterations in fetal liver metabolism and formation of bone. Role in the survival of astrocytes and motor neurons in the spinal cord and brain stem	[93, 94]
IL-11R β	Infertility in female mice due to a defective decidualization	[195, 196]
OSMR β	Role in regulation of hematopoiesis. Key role in liver regeneration	[197, 198]
CNTFR β	Mutant death perinatally. Role of CNTFR in motor neuron survival. Critical effects of CNTFR on the developing nervous system	[119]

naling are the activated JAK tyrosine kinases [129, 130]. JAK1 is essential for LIF signaling in mES cells [131, 132] and in trophoblast differentiation [133], and JAK2 seems to play a critical role in LIF-dependent muscle satellite cell proliferation [134]. The third obligatory component of LIF signaling is the feedback control regulator, which includes members of the *Socs* gene family [135-141]. SOCS3, a STAT3-dependent repressor that attenuates LIF signaling, is critical in many cell types and tissues in which LIF has an effect. Indeed, SOCS3 is essential for maintenance of murine ES cell pluripotency [142-144], for trophoblast differentiation [133, 145, 146] and for the involution of the mammary gland at the end of the lactation period [147, 148]. SOCS3 is also essential for regulation of the immuno-tolerant function of LIF recently described in Treg cells [149].

Other genes are induced by cytokine response, in general. This is the case for the primary response genes *junB*, *c-jun* and *egr1* that are all induced upon LIF treatment in M1 or ES cells, see *tables 3* and *4* [142, 150, 151].

However, so far, the mechanism of LIF pleiotropy has not been elucidated and both transcriptomic and proteomic/phosphoproteomic approaches should help to resolve this complex issue. Several cell-type specific targets of LIF such as hepatocyte growth factor (*Hgf*) induced in SEK1 cells or the insulin growth factor binding protein 3 (*Igfbp3*), amphiregulin and the immune response gene

1 (*Irg1*), identified in endometrium cells, also indicate that different end point transcriptional targets might explain pleiotropy [152, 153].

In mouse ES cells, LIF also induces the PI3Kinase pathway, which maintains cell pluripotency [154-156] while activating the ERK/RSK/CREB pathways which, along with the FGF pathway induce pro-differentiative programs [157-159]. Thus, several LIF induced pathways are concomitantly required to maintain ES cell plasticity, a peculiar property of stem cells.

Recent transcriptomic analyses performed in mouse ES cells and early derivatives, treated for short period (30 min) with LIF, have allowed identification of common and cell-specific LIF-regulated genes (summary in *table 3*). Primary response genes (*c-fos*, *JunB*, *Egr1* and *2*, *Ier2*), the *Socs3* inhibitor and regulators of mRNA stability (such as *Zfp36* and its direct target *Ier3*, [160]), are among the common LIF-induced (*Lifind*) genes found in ES cells and early derivatives [161]. Indeed, these genes are induced by LIF after a 24 or a 48 h period of LIF withdrawal, which respectively correspond to a LIF-dependent reversible (24 h) or irreversible (48 h) state of committed cells [158, 162-164]. These genes are also expressed in differentiated cells which re-express LIF and its receptor, after 10 days of LIF withdrawal [161]. This study has led to the characterization of different time-frames of LIF activity in the ES cell model. It will be a

Table 3
LIF transcriptional targets in different cell contexts

Cell types	Transcriptional targets	References
ES cells	Pluripotent cells (+LIF)	<i>JunB</i> ; <i>c-fos</i> ; <i>Socs3</i> ; <i>Zfp36</i> ; <i>Stat3Loc</i> ; <i>c-Myc</i> ; <i>Cd9</i> ; <i>Ypel2</i> ; <i>Plscr1</i> ; <i>Dapp1</i>
	ES-derived, reversible committed state (-LIF 24h, induced 30 min. with LIF)	<i>JunB</i> ; <i>c-fos</i> ; <i>Socs3</i> ; <i>Zfp36</i> ; <i>stat3Loc</i> ; <i>Egr1</i> ; <i>Egr2</i> ; <i>Ier2</i> ; <i>Ier3</i> ; <i>Klf4</i> ; <i>Klf5</i> ; <i>Rasd1</i> ; <i>Nfkbiz</i> ; <i>Dapp1</i> ; <i>Ypel2</i> ; <i>Dystonin</i> ; <i>Pabpc1</i> ; <i>Etv6</i> ; <i>Sbno2</i> ; <i>Plscr1</i>
	ES-derived, irreversible committed state (-LIF 48 h, induced 30 min. with LIF)	<i>JunB</i> ; <i>c-fos</i> ; <i>Socs3</i> ; <i>Zfp36</i> ; <i>stat3Loc</i> ; <i>Egr1</i> ; <i>Egr2</i> ; <i>Ier2</i> ; <i>Ier3</i> ; <i>Klf4</i>
	ES-derived, differentiated cells (10 days without LIF)	<i>JunB</i> ; <i>c-fos</i> ; <i>Socs3</i> ; <i>Zfp36</i> ; <i>Egr1</i> ; <i>Egr2</i> ; <i>Ier3</i> ; <i>Nfkbiz</i> ; Expression of endogenous LIF and of LIFR subunits
Tumor cells	M1 myeloid cell line	<i>JunB</i> ; <i>c-jun</i> ; <i>JunD</i> ; <i>Cis</i> ; <i>Gp49B1</i> ; <i>Socs1</i> ; <i>Egr1</i>
	SEK1 (human melanoma)	<i>Hgf</i>
Normal tissues	Endometrium	<i>Igfbp-3</i> ; <i>Amphiregulin</i> ; <i>Irg-1</i>
	Cardiomyocytes	<i>Zfp36</i> ; <i>Socs1</i> ; <i>Socs2</i> ; <i>Socs3</i>
	Fibroblasts	<i>Egr-1</i> ; <i>c-fos</i> ; <i>Socs3</i>
	Neural progenitors	<i>Socs2</i> ; <i>Socs3</i>

Table 4
Potential actors of the pleiotropic effects of LIF

	ES $\xrightarrow{\text{LIF}}$ Proliferation Pluripotency		M1 $\xrightarrow{\text{LIF}}$ Differentiation in macrophages		
	-LIF	+LIF	-LIF	+LIF	
c-jun	-	++	-	++	T.
JunB	-	++	-	++	
JunD	++	++	-	++	
Socs1	+	+	-	++	
Socs2	+	+	-	-	
Socs3	-	++	-	-	
Egr1	-	++	-	+	Post-T.
Egr2	-	++	N.D.	N.D.	
STAT3	+	+	+	+	
P-STAT3	-	++	-	++	

The expression profiles of Jun, Socs and Egr family members (detected by northern blots or RT-PCR) and of STAT3 and Phospho-STAT3 (detected by western blots) in mouse ES and M1 cell lines, in which LIF has opposite effects. While STAT3 activation is transient in ES cells, it is sustained in M1 cells.

T: Transcriptional regulation; Post-T: post-translational regulation. - : not expressed or not phosphorylated; + : expressed; ++ : highly expressed or highly phosphorylated.

Compilation of results are from these references: 135, 136, 137, 138, 142, 143, 158, 170, 171, 172, 200.

future goal to unravel the functions of these LIF targets in pluripotent ES cells and at various stages of ES-derived cell maturation. STAT3 was also re-expressed in differentiated cells, and characterization of its interaction networks in stem cells *versus* differentiated cells remains a challenging issue for the further understanding of LIF pleiotropy. Novel *Lifind* genes, whose induction is restricted to ES-derived committed cells (24h of LIF withdrawal), have also been identified. This is the case of *Yippee-like2*, *Strawberry Notch2* (Drosophila orthologs), *Dystonin*, *Phospholipid scramblase1* and *Dapp1* (a regulator of PI3K), whose functions in mouse are still poorly understood and which deserve further attention.

Mechanisms underlying LIF pleiotropy

STAT3/SOCS3 are the common, obligatory, LIF-dependent effectors found in almost all LIF-sensitive cell lines. Surprisingly, it has been shown, in at least two mouse cell systems (ES cells and pituitary tumor cells), that cell type-specific effectors of LIF and STAT3 only partly overlap [161, 163, 165, 166]. Also, depending upon the cell context, STAT3 could be associated with various partners such as NANOG, as recently shown in certain cancer cells [167]. In addition, the proteins encoded by the primary response genes, which are activated in many LIF-sensitive cell types, are themselves part of various transcriptional complexes (*e.g.* AP1 complexes), whose associations with different partners could lead to pleiotropic effects. Interestingly, different members of the Socs and Jun families are induced by LIF in M1 or ES cells (table 4). *Egr1* is induced in both cell systems and is critical for the macrophage differentiation of M1 cells, but its effect in ES cells has not yet been investigated [168, 169].

Another parameter, potentially involved in the pleiotropic effects of LIF, is the duration of the LIF signal. Indeed, while STAT3 activation is transient in ES cells (it starts decreasing after 1h of LIF stimulation), it is sustained in M1 cells where it lasts up to 36h [170-172].

Also and not yet tested in various LIF-sensitive cell types, epigenetic regulations could account for pleiotropic LIF effects. For example, in the ES cell system, a high level of phosphoacetylation of histone H3 has been reported as being a feature of ES-derived differentiated cells [173, 174]. In addition, repression of HDAC (histone deacetylase) activities by chemicals such as TSA (trichostatin A), in mouse ES cells grown with LIF, induces the expression of differentiation markers along with morphological changes similar to those observed upon LIF withdrawal [175, 176]. Furthermore, a specific epigenetic hallmark has been characterized, that is absent in differentiated cells: by mapping the histone methylation pattern in 2.5 % of mouse genome, it has been shown that a bivalent, tri-methylation mark at the histone H3 (H3K4 triMe / H3K27 triMe) was enriched in pluripotent cells only at differentiation gene loci, leading to silencing of these genes in undifferentiated cells. Upon cell differentiation, these bivalent modifications disappear and differentiation genes are expressed according to the remaining level of single H3K4 triMe (correlated with gene activation) or H3K27 triMe (correlated with gene repression). These crucial data led to the hypothesis that bivalent domains silence developmental genes in ES cells while keeping them poised for activation [177, 178]. It has also been demonstrated that Eed, the core component of the repressive polycomb complex, is a LIF-dependent STAT3 target in ES cells that is associated with high levels of H3K27 triMe. Eed could be the critical effector in silencing differentiation genes in pluripotent ES cells [179]. We would therefore propose the hypothesis that the absence of Eed or of a related repressive protein in M1 cells leads to a pro-differentiative effect of LIF, despite the presence of activated STAT3. It will be of great interest to determine the status of phosphorylation, acetylation and methylation at the histone H3 protein in ES and M1 cell lines treated with LIF for various periods of time and to determine whether pleiotropy could also rely on differential epigenetic regulation [176, 180, 181]. We propose a model in which LIF signalling would lead to opposing effects depending on whether it occurs in a context of opened or closed chromatin. Accordingly, some genes would always be activated in the presence of LIF (such as *Stat3*, *JunB* or *Socs3*), because of an unregulated chromatin status at these gene loci, an assumption that remains to be demonstrated. In this regard, the fact that LIF is a direct transcriptional target of the p53 protein, a known chromatin regulator [182, 183], opens also new avenues for understanding the mechanisms underlying LIF pleiotropy.

CONCLUSION

LIF orthologs have been characterized in many species, even in kangaroo in which gestation does not proceed through classical internal implantation [184]. Also intrigu-

ing, LIF ortholog has been cloned in chicken [185], but the function of LIF in these species remains to be studied. The evolution of this particular cytokine to become the “nidation hormone” in eutherian mammals is a challenging research area, which deserves particular attention as regards EVO-DEVO concerns, as well as for its potential relevance in the treatment of human infertility.

Let us hope that with accumulating understanding of LIF, and with technical advances in protein function analyses, it will not take another 40 years to unveil LIF's secrets and to understand how some LIF targets (such as c-MYC [186, 187] and KLF4 [143], both shown to be essential for self-renewal of mouse ES cells) can reprogram mouse and human somatic cells to become iPS cells (induced pluripotent stem cells), along with pluripotent factor companions such as OCT4 and SOX2 [61, 188, 189].

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