THE EXPRESSION OF INSULIN-LIKE GROWTH FACTORS AND THEIR RECEPTORS AT PREIMPLANTATION STAGE IN REPRODUCTIVE TISSUE OF DIABETIC MOUSE

by

RAHIMAH BINTI ZAKARIA

Thesis submitted in fulfilment of the
requirements for the degree of
Doctor of Philosophy

NOVEMBER 2006

ACKNOWLEDGEMENTS

In the name of Allah, the Most Merciful and the Most Compassionate

I would like to express my deepest gratitude and indebtedness thanks to my supervisors, Associate Professor (Dr) Nik Soriani Yaacob and Professor (Dr) Norazmi Mohd Nor for their fine and dedicated supervision throughout my studies and their thorough criticisms during my thesis writing. I am also thankful to my field supervisor, Professor Mohd Hamim Rajikin for his encouragement and criticisms throughout my study until I completed my thesis writing. I would like to thank Professor (Dr) Harbindar Jeet Professor, Head of Department of Physiology, for his support during my study.

My thanks to our Dean of School of Medical Sciences, Professor (Dr) Abdul Aziz Baba, and Deputy Deans of School of Medical Sciences for their encouragement throughout my studies.

I would like to thank Professor (Dr) Asma Ismail, Director of INFORMM and Professor (Dr) Zainul Fadziruddin Zainuddin, Dean of School of Health Sciences for giving me the opportunity to work in their laboratories. My thanks to staff of Department of Physiology (USM and UKM, Kuala Lumpur), Animal

House, Department of Pathology, INFORMM and School of Health Sciences for their kind assistance.

My special thanks to my dearest friend, Dr Asma Hayati Ahmad, for her encouragement during my study and her criticisms during my thesis writing. To all my friends in the department, Dr Mahaneem, Dr Che Badariah, Dr Wan Malihah, Dr Liza and Dr Adibah, and also my research group members, Mar, Ima, Teo, Asma, Rafezul, Dr Zul, Syam and Ayu, thank you to all of them for their assistance and support.

Finally to both my parents, my husband, my sons, Haikal, Haziq and Hadif, my sisters and brother, a very special thanks to all of them for their love, understanding and encouragement which allow me to complete my studies and thesis writing.

I would like to acknowledge Ministry of Science and Technology for financially support this research work via Fundamental Research Grant Scheme (FRGS).

TABLE OF CONTENTS

CHAPTER ONE : GENERAL INTRODUCTION

CHAPTER TWO : MATERIALS AND METHODS

CHAPTER THREE: THE EFFECT OF DIABETES MELLITUS ON *IN VITRO* DEVELOPMENT OF MOUSE PREIMPLANTATION EMBRYO

CHAPTER FOUR : QUANTIFICATION OF mRNA EXPRESSION OF INSULIN-LIKE GROWTH FACTORS AND THEIR RECEPTORS IN THE FALLOPIAN TUBES AND UTERI OF DIABETIC MICE DURING PREIMPLANTATION EMBRYO DEVELOPMENT

CHAPTER FIVE : IMMUNOHISTOCHEMICAL DETECTION AND LOCALIZATION OF INSULIN-LIKE GROWTH FACTORS AND THEIR RECEPTORS IN THE FALLOPIAN TUBES AND UTERI OF DIABETIC MICE DURING PREIMPLANTATION EMBRYO DEVELOPMENT

CHAPTER SIX : GENERAL DISCUSSION

APPENDICES

LIST OF PUBLICATIONS

LIST OF TABLES

LIST OF FIGURES

LIST OF PLATES

LIST OF ABBREVIATIONS

AA	arachidonic acid
ACTH	adrenocorticotropic hormone
AGE	advanced glycation end products
Akt	protein kinase B
ALS	acid-labile subunit
ATP	adenosine triphosphate
BAD	Bcl-xL/Bcl-2-associated death protein
BSA	Bovine Serum Albumin
$CaCl_2$	calcium chloride
cDNA	complementary DNA
cds	coding region
COX-2	cyclooxygenase-2
C-peptide	connecting peptide
$cPLA_2$	cytosolic phospholipase A_2
CRK	CT10 regulator of kinase
C_T	threshold cycle
Da	Dalton
DAB	3, 3'-diaminobenzidine tetrahydrochloride
DEPC	diethylpyrocarbonate

DHA	dehydroascorbate
DNA	deoxyribonucleic acid
DPX	distyrene plasticiser xylene
ECM	extracellular matrix
EDTA	ethylenediamine-tetra acetic acid
ERα	oestrogen receptor-α
ERK	extracellular signal-related kinase
EtBr	ethidium bromide
FBP	fructose 1,6-biphosphate
FGF	fibroblast growth factor
FSH	follicle stimulating hormone
GAPDH	glyceraldehyde-3-phosphate dehydrogenase
GDP	guanine diphosphate
GH	growth hormone
GLUT	glucose transporters
Grb	growth factor receptor-bound protein
GTP	guanine triphosphate
H & E	hematoxylin and eosin
H_2O_2	hydrogen peroxide
hCG	Human Chorionic Gonadotropin
HCl	hydrochloric acid
HIF-1α	hypoxia-inducible factor 1α
HPRT	hypoxanthine phosphoribosyltransferase
ICM	inner cell mass
ICR	Institute of Cancer Research

IGF-1	insulin-like growth factor-1
IGF-1R	IGF-1 receptor
IGF-2	insulin-like growth factor-2
IGF-2R	IGF-2 receptor
IGFBP	IGFs binding proteins
IGFBP-rPs	IGFBP-related proteins
IGFs	insulin-like growth factors
IgG	Immunoglobulin G
IHC	immunohistochemistry
IL-1β	interleukin-1ß
IP3	inositol triphosphate
IR	insulin receptor
IRS	insulin-receptor substrate
JNK	c-Jun N-terminal kinase
kb	kilobase
kDa	kiloDalton
LB	Luria-Bertani
LH	luteinizing hormone
M6P	mannose-6-phosphate
MAPK	mitogen-activated protein kinase
MEK	MAP/ERK kinases
MEKK	MEK kinase
$MgCl_2$	magnesium chloride
mRNA	messenger ribonucleic acid
MSA	multiplication-stimulating activity

mSOS	Son of sevenless
NaOH	sodium hydroxide
NCBI	National Center For Biotechnology Information
NIH	National Institute of Health
NOD	non-obese diabetic
NSILA	non-suppressible insulin-like activity in serum
NTC	no template control
PBS	phosphate-buffered saline
PCR	Polymerase Chain Reaction
PDFG	platelet-derived growth factor
PDK	3-phosphoinositide dependent kinases
PGE_2	prostaglandin E_2
PGF_2	prostaglandin F_2
PH	plekstrin homology
PI	phosphoinositides
PI-3K	phosphatidylinositol-3 kinase
PIP	phosphatidylinositol phosphate
PIP_2	phosphatidylinositol bisphosphate
PKB	protein kinase B
PKC	protein kinase C
PMSG	Pregnant Mare Serum Gonadotropin
PTB	phosphotyrosine binding
R^2	square regression coefficient value
RNA	ribonucleic acid
ROS	reactive oxygen species

SAPK	stress-activated protein kinase
SDS	sodium-dodecyl sulphate
SFA	sulfation factor activity
SH	Src-homology
SHC	Src homology-containing protein
SOC	sodium citrate medium
SOD	superoxide dismutase
STZ	streptozotocin
TBE	Tris-Borate-EDTA
TCA	tricarboxylic acid
TE	trophectoderm
TGF-β	transforming growth factor-β
Tm	melting temperature
TNF-α	tumour necrosis factor- α
TSH	thyrotropin
UNG	uracyl-N-glycosylase
X-gal	5-bromo-4-chloro-3-indolyl-beta-D-galactopyranoside

EKSPRESI "INSULIN-LIKE GROWTH FACTORS" DAN RESEPTORNYA PADA PERINGKAT PRAIMPLANTASI DALAM TISU REPRODUKTIF MENCIT DIABETES

ABSTRAK

Kami menghipotesis bahawa embrio praimplantasi yang berkembang dalam persekitaran diabetes mengalami kekurangan faktor pertumbuhan tertentu. Tujuan utama kajian ini adalah untuk menentukan kesan diabetes ke atas perkembangan embrio praimplantasi mencit secara *in vitro* dan menganalisis ekspresi mRNA dan protein IGF-1, IGF-2, IGF-1R dan IGF-2R dalam tisu fallopio dan uterus mencit kontrol dan diabetes. Mencit ICR betina yang matang secara seksual berusia 6 hingga 8 minggu dijadikan diabetes dengan suntikan streptozotosin (200 mg/kg, intra peritoneum). Embrio normal dalam peringkat 2-sel diperolehi daripada mencit kontrol dan diabetes yang diseperovulasi pada 48 jam pasca rawatan korionik gonadotropin manusia (hCG). Embrio dikultur secara berasingan dan diperiksa di bawah mikroskop songsang selama 3 hari berturut-turut. Tisu fallopio dan uterus diperolehi daripada mencit kontrol dan diabetes yang disuperovulasi pada 48, 72 dan 96 jam pasca rawatan hCG. Kuantifikasi ekspresi mRNA menggunakan tindak balas polimerase masa nyata menggunakan piawai internal homologus yang dibangunkan secara spesifik untuk setiap gen. Ekspresi protein menggunakan pewarnaan imunohistokimia dijalankan ke atas tisu dan skor semikuantitatif dibuat berdasarkan sistem 5-skala piawai. Bilangan embrio 2-sel yang diperolehi daripada mencit diabetes adalah sangat berkurangan apabila dibanding dengan mencit kontrol. Walau bagaimanapun, tiada perbezaan yang signifikan dalam peratus perkembangan embrio 2-sel mencit kontrol dan diabetes. Ekspresi mRNA IGF-1 tisu fallopio dan uterus mencit diabetes rendah secara signifikan masing-masing pada 72 dan 96 jam pasca rawatan hCG. Ekspresi mRNA IGF-1R kekal tinggi dalam tisu fallopio tetapi rendah secara signifikan dalam tisu uterus mencit diabetes pada 96 jam pasca rawatan hCG. Ekspresi mRNA IGF-2 tisu fallopio mencit diabetes tinggi secara signifikan pada 48 dan 96 jam pasca rawatan hCG tetapi rendah secara signifikan dalam tisu uterus mencit diabetes pada 96 jam pasca rawatan hCG. Ekspresi mRNA IGF-2R tisu fallopio dan uterus mencit diabetes tinggi secara signifikan masing-masing pada 48 dan 96 jam, dan 48 jam pasca rawatan hCG. Untuk ekspresi protein, skor imunohistokimia IGF-1 dan IGF-1R berkurang secara signifikan dalam tisu fallopio pada 96 jam pasca rawatan hCG. Skor IGF-2 dan IGF-2R sebaliknya bertambah secara signifikan dalam tisu fallopio mencit diabetes masing-masing pada 48 dan 72 jam, dan pada 72 jam pasca rawatan hCG. Walau bagaimanpun, tiada perbezaan skor yang signifikan bagi IGFs dan reseptornya dalam tisu uterus mencit kontrol dan diabetes. Sebagai kesimpulan, peratus perkembangan embrio 2-sel kepada blastosista adalah serupa di dalam mencit kontrol dan diabetes tetapi tidak dapat disahkan sama ada kualiti embrio tersebut sama atau tidak. Ekspresi mRNA dan protein IGFs dan reseptor masing-masing mengalami perubahan yang signifikan akibat kesan diabetes ibu, mencadangkan wujudnya peranan mereka dalam patogenesis embriopati diabetes.

THE EXPRESSION OF INSULIN-LIKE GROWTH FACTORS AND THEIR RECEPTORS AT PREIMPLANTATION STAGE IN REPRODUCTIVE TISSUES OF DIABETIC MOUSE

ABSTRACT

We hypothesized that the alteration in the expression of IGFs and their receptors may create an abnormal intrauterine environment thus affect embryos development. Therefore, the aims of the present study were to determine the effects of diabetes on *in vitro* development of mouse preimplantation embryos and to determine the mRNA and protein expression of IGF-1, IGF-2, IGF-1R and IGF-2R in the fallopian tube and uterine tissue of control and diabetic mice. Sexually mature female ICR mice of 6-8 weeks old were made diabetic by streptozotocin (200 mg/kg, intraperitoneal). The normal two-cell embryos were obtained from superovulated control and diabetic mice at 48 post-hCG treatment. Embryos were separately cultured and examined under an inverted microscope for 3 consecutive days. Fallopian tubes and uterine tissues were obtained from the superovulated control and diabetic mice at 48, 72 and 96 hours post-hCG treatment. The mRNA expression was measured using Real-time PCR using specifically developed homologous internal standards for each gene. Protein expression was measured by immunohistochemical staining and a semiquantitative scoring was performed using a standardized 5-scale system. The number of normal two-cell embryos obtained from diabetic mice was much reduced when compared to control mice. However, there was no significant difference in the percentage of two-cell embryo development in control and diabetic mice. The mRNA expression of IGF-1 in the fallopian tube and uterus of diabetic mice was significantly low at 72 hours and 96 hours post-hCG treatment, respectively. The mRNA expression of IGF-1R remained high in the fallopian tube but was significantly low in the uterus of diabetic mice at 96 hours post-hCG treatment. The mRNA expression IGF-2 in the fallopian tube was significantly high at 48 and 96 hours post-hCG treatment but was significantly low in the uterus of diabetic mice at 96 hours post-hCG treatment. The mRNA expression of IGF-2R in the fallopian tube and uterus of diabetic mice was significantly high at 48 and 96 hours, and at 48 hours post-hCG treatments, respectively. For protein expression, the immunohistochemical scoring for both IGF-1 and IGF-1R was significantly decreased in the fallopian tube of diabetic mice at 96 hours post-hCG treatment. In contrast, the score for IGF-2 and IGF-2R was significantly increased in the fallopian tube of diabetic mice at 48 and 72 hours; and at 72 hours post-hCG treatment, respectively. However, there was no significant difference in the score of IGFs and their receptors in the uterus of control and diabetic mice. In conclusion, the percentage of the two-cell stage embryos which developed to blastocysts was similar in control and diabetic groups but whether the quality of these embryos were the same could not be confirmed. Both the mRNA and protein expression of IGFs and their receptors were significantly altered by maternal diabetes, which suggest their role in the pathogenesis of diabetic embryopathy.

CHAPTER ONE

GENERAL INTRODUCTION

1.1 PHYSIOLOGY OF PREIMPLANTATION EMBRYO DEVELOPMENT

1.1.1 Proliferation and differentiation of preimplantation embryo

Fertilization of the mouse ovum by sperm occurs in the ampullary region of the fallopian tube. Subsequent development occurs as the embryo moves down the fallopian tube and into the uterus over a period of about four days in mice, as compared to five and seven days in rats and humans, respectively (Figure 1.1). Approximately 24 hours after fertilization, the embryo undergoes relatively synchronous cell division resulting in the formation of two cells or blastomers. There are no junctions established between the individual cells, which are held together by ionic attractions on the opposing plasma membranes (Chavez, 1984). The cells are constrained within a physical shell, the zona pellucida, which is a matrix of four glycoproteins (Wassarman and Mortillo, 1991). During this period, each blastomere is totipotent, retaining the capacity to form a complete fetus. Further mitotic divisions occur asynchronously at progressively shorter intervals so that from the eight-cell stage onwards, one cell cycle is approximately six hours. At the eight-cell stage, generation of two distinct lineages commences with the process of compaction when individual blastomers polarize, become epithelial-like and flatten on each other,

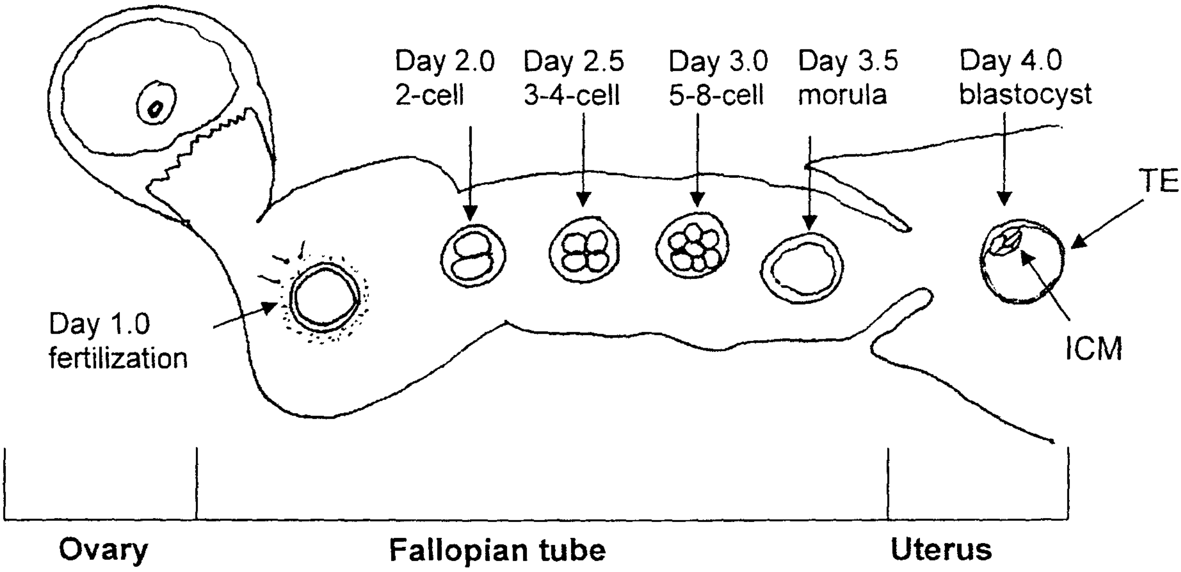

Figure 1.1 Development of the preimplantation embryo in mice from embryonic Day 1 through Day 4
(Adapted from Hogan *et al.*, 1986)

The fertilization takes place in the ampullary region of the fallopian tube and the developing embryo traverse down to the site of implantation in the uterine cavity.

maximising cell contact and forming tight and gap junctions (Ducibella *et al.*, 1977; Magnuson and Epstein, 1981; Chavez, 1984; Fleming *et al.*, 1992). This compacted morula stage coincides with the arrival of the embryo at the utero-tubal junction. In the compacted morula, fluid is transported across the newly formed epithelium to form a blastocoel and at this point the embryo is referred to as a blastocyst. At this stage, two distinct cell populations can be recognized (Johnson, 1981). The eccentrically placed inner cell mass (ICM) eventually forms the embryo proper and some extraembryonic tissues. The trophectoderm (TE), which is a single epithelial layer of flattened cells surrounding the blastocoel and ICM, establishes the foci of adhesion with the uterine epithelium and gives rise to the fetal component of the placenta (Hogan *et al.*, 1986).

1.1.2 Metabolic activity of preimplantation embryo

Mouse oocyte and zygote have an absolute requirement for pyruvate (Biggers *et al.*, 1967); i.e. glucose cannot support early embryo development until the eight-cell stage (Biggers, 1971). From the two-cell to the blastocyst stage, the embryos experience an increase in the tricarboxylic acid (TCA) cycle metabolites and a dramatic increase in fructose 1, 6-biphosphate (FBP). The dramatic switch from a dependence on the TCA to a metabolism based on glycolysis occurs at the time of compaction. The only source of adenosine triphosphate (ATP) for the preimplantation embryo would be conversion of glucose to pyruvate and lactate via glycolysis.

The blastocyst stage marks a new peak in cellular proliferation and growth. These changes create new biosynthetic demands on the embryos.

Maintenance of a high rate of glycolysis is important for providing a "dynamic buffer" of metabolic intermediates for the biosynthesis of macromolecules (Newsholme and Newsholme, 1989) and increasing amount of glucose are converted to lactate at this stage in humans and rodents (Leese and Barton, 1984). Interspecies variations in the rate of glycolysis have been reported, higher in human blastocysts (Leese *et al.*, 1993) and lower in mouse blastocysts (Leese, 1991) compared to rat embryos.

Blastocysts are actively engaged in the uptake and metabolism of maternally derived nutrients such as glucose (Leese, 1991). The major site of uptake regulation is likely to be the system of facilitative glucose transporters (GLUT) situated at the basolateral surface of the TE in mouse blastocysts (Aghayan *et al.*, 1992).

1.1.3 Influence of maternal factors on preimplantation embryo development

Although the activation of the embryonic genome provides the conceptus with a number of vital developmental signals (Kidder, 1992; Schultz and Heyner, 1992), its progression through the preimplantation period is also influenced by maternal factors present in the oviductal and uterine environment.

Biggers (1981) proposed a theoretical model summarizing the physiological processes that influence the microenvironment of the preimplantation embryo. The composition of the microenvironment is determined by several transport mechanisms: between the embryo and the secretions in which it is bathed, between the fallopian tube and uterus and the bathing secretions and further mixing is produced as the secretions flow up and down the reproductive tract as shown in Figure 1.2.

Maternally-derived nutrients/factors can either be transudates from the maternal circulation such as glucose (Leese *et al.*, 1979, Wales and Edirisinghe, 1989; Gonzalez *et al.*, 1994) and insulin (Heyner *et al.*, 1989; Smith *et al.*, 1993), or secretions by various uterine cells into the lumen such as growth factors (Pollard, 1990; Song *et al.*, 2000) and cytokines (Pampfer *et al.*, 1991; Robertson *et al.*, 2001) during the preimplantation period.

1.2 DIABETIC PREGNANCY

The association between maternal diabetes and the increased risk of congenital malformations has a long history and was first reported by LeCorche (1885). It is generally accepted that congenital malformations are the leading cause of death in the offspring of diabetic women (Kitzmiller *et al.*, 1978). The incidence of congenital malformations is approximately 6 to 9% in diabetic pregnancies, which is three- to four-fold higher than in the general population, and accounts for 33 to 66% of perinatal deaths (Reece and Hobbins, 1986). The congenital malformations most commonly associated with maternal diabetes are listed in Table 1.1 (Reece and Hobbins, 1986). However, none of the reported congenital malformations is pathognomonic for the diagnosis of diabetic embryopathy.

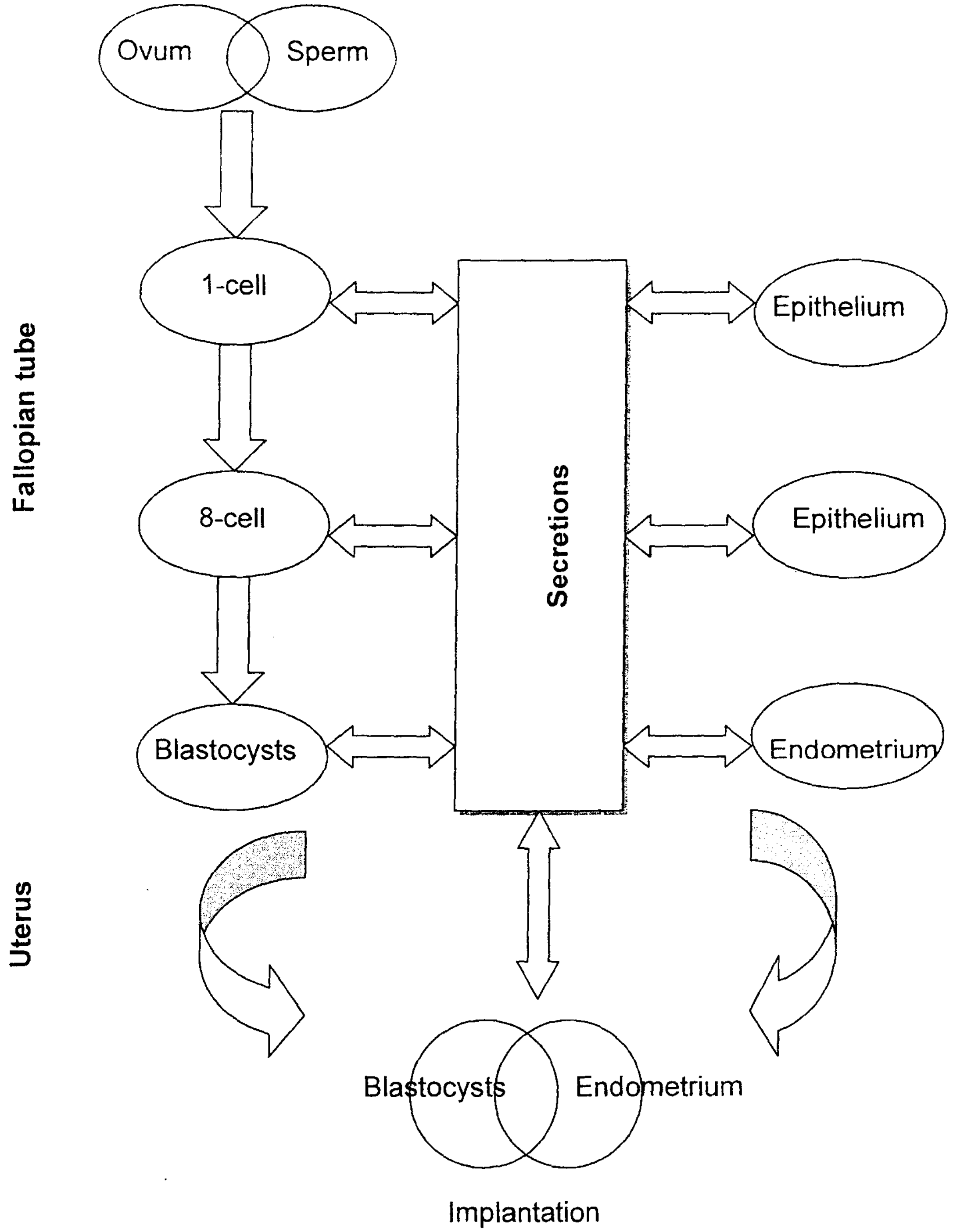

Figure 1.2 A theoretical model summarising the physiological processes that influence the microenvironment of the preimplantation embryo (Adapted from Biggers, 1981).

Table 1.1 Congenital malformations in infants of diabetic mothers

(Adapted from Reece and Hobbins, 1986)

Structure	**Anomaly**
Skeletal and Central Nervous System	Caudal regression syndrome
	Neural tube defects excluding anencephaly
	Anencephaly with or without herniation of neural elements
	Microcephaly
Cardiac	Transposition of the great vessels with or without ventricular septal defects
	Ventricular septal defects
	Coarctation of the aorta with or without ventricular septal defects or patent ductus arteriosus
	Atrial septal defects
	Cardiomegaly
Renal Anomalies	Hydronepherosis
	Renal agenesis
	Ureteral duplication
Gastrointestinal	Duodenal atresia
	Anorectal atresia
	Small left colon syndrome
Others	Single umbilical artery

1.3 DEFINITION OF "DIABETIC EMBRYOPATHY"

The term "embryopathia diabetica" was coined by Mayer (1952) and was later replaced by the term "diabetic embryopathy" (Passarge and Lenz, 1966). The concept of diabetic embryopathy initially encompassed the long-recognized newborn features such as macrosomia and organomegaly but was later broadened to include congenital malformations (Mayer and Camara, 1964). Presently, the same concept was separated into two different entities, diabetic embryopathy and diabetic fetopathy. Diabetic embryopathy occurs during embryogenesis, mainly from the end of blastogenesis until the period of organogenesis (between the 3rd and 7th week of gestation) and is associated with congenital malformations (Kousseff, 1999). In contrast, diabetic fetopathy occurs during fetal development, after the 10th week of gestation, and is not associated with malformations (Kousseff, 1999). Occasionally, diabetic embryopathy is associated with diabetic fetopathy. However, these two entities, both induced by maternal diabetes mellitus, have different windows of vulnerability and perhaps, different pathogenesis.

1.4 AETIOLOGICAL FACTORS ASSOCIATED WITH DIABETIC EMBRYOPATHY

It has been suggested that the absence of a specific malformation pattern for diabetic embryopathy signals the presence of several aetiological factors and mechanisms in diabetic pregnancy (Khoury *et al.*, 1989). Likewise, the number of different teratogenic agents identified indicates that diabetic embryopathy is of complex aetiology (Sadler *et al.*, 1989; Zusman *et al.*, 1989; Buchanan *et al.*, 1994).

1.4.1 Maternal Hyperglycemia

Hyperglycemia-induced teratogenic effects have been demonstrated in animal studies both *in vivo* and *in vitro* (Cockroft and Coppola, 1977; Baker *et al.*, 1981; Horton and Sadler, 1983; Kalter and Warkany, 1983a & 1983b; Freinkel *et al.*, 1986; Reece and Hobbins, 1986). The percentage of congenital malformations correlated with blood glucose levels (Reece *et al.*, 1985) and glycosylated hemoglobin levels (Rose *et al.*, 1988).

The period and time of exposure to hyperglycemia as well as the level of hyperglycemia are all important for dysmorphogenesis to occur. The critical period of exposure to hyperglycemia is during organogenesis, which is considered to be between days 9.5 to 11.5 in rats and 8.0 to 9.6 in mice (Freinkel, 1988), corresponding to the first 5 or 6 weeks of human pregnancy. A minimum exposure time of two or more hours is needed to induce these malformations. A 20% malformation rate was induced at glucose levels that were approximately two-fold above normal concentrations; an almost 50% malformation rate was seen at glucose levels three-fold above normal concentrations; and approximately 100% rate at six times above normal concentrations (Reece *et al.*, 1985).

Maternal hyperglycemia adversely affects not only the postimplantation embryos but also preimplantation progression from one-cell to the blastocyst stage in a streptozotocin (STZ)-induced or a non-obese diabetic (NOD) mouse model (Diamond *et al.*, 1989; Moley *et al.*, 1991 & 1994). In the NOD model at 96 hours after superovulation and mating, only 20% of the recovered embryos reached blastocyst stage in the diabetic compared to 90% among the non-diabetic. This developmental delay is reversible by treating the mothers with insulin before superovulation and mating and during the first 96 hours of gestation. This early preimplantation delay may be manifested later in gestation as fetal loss, early growth delay or congenital malformation. There is now convincing evidence that severe developmental anomalies leading to fetal resorption or malformation can occur as a consequence of subtle damage inflicted to the embryos before or at the time of implantation (Rutledge, 1997).

The mechanism of hyperglycemia-induced congenital anomalies remains unclear. Hyperglycemia-induced reduction in GLUT has been proposed to be one of the possible mechanisms. A paradoxical reaction to hyperglycemia has been demonstrated in preimplantation embryos (Moley, 1999). In embryos of diabetic mice, a pronounced intracellular hypoglycemia was found despite maternal hyperglycemia (Moley *et al.*, 1998b). The decreased intracellular glucose concentration was associated with decreased GLUT namely, GLUT-1, GLUT-2 and GLUT-3 isoforms; both at the protein and mRNA levels (Moley *et al.*, 1998b).

Reduced availability of glucose associated with decreased GLUT in diabetic embryos, results in significantly lower FBP and higher pyruvate, indicating decreased glycolysis and increased pyruvate uptake by the embryos, respectively. The glycolytic changes lead to dysfunction of the outer mitochondrial membrane and subsequently trigger the apoptotic cascade (Chi *et al.*, 2002).

The decrease in GLUT especially GLUT-1 and -3 isoforms also explains the elevated extracellular dehydroascorbate (DHA) and reduced intracellular ascorbic acid (Rumsey *et al.*, 1997) related to hyperglycemia as described previously (Ely, 1981). Ely (1981) proposed that reduced intracellular ascorbic acid resulted in decreased hexose monophosphate shunt activity (DeChatelet *et al.*, 1972), which might suppress deoxyribonucleic acid (DNA) synthesis as shown in Figure 1.3. Reduced DNA synthesis may slow cell division, leading to impaired cell proliferation or anomalies. It has also been suggested that elevated extracellular DHA may inhibit mitosis or cell proliferation (Edgar, 1970).

This decrease in intracellular glucose concentration leads to a lower cell number in the ICM, either by increased apoptotic rate (Pampfer *et al.*, 1997b; Moley *et al.*, 1998a), or by diminished proliferation of these cells (Pampfer *et al.*, 1990). Decrease in glucose transport and metabolism is not only related to progressive decrease in embryo viability but served as important regulatory points in the early apoptotic cascade (Johnson *et al.*, 1996; Li *et al.*, 1998; Shim *et al.*, 1998; Bialik *et al.*, 1999, Lin *et al.*, 2000). Maternal hyperglycemia, moreover, can cause direct disruption of the highly regulated gene program that controls the expression pattern of crucial developmental determinants during early embryogenesis, including apoptosis (Phelan *et al.*, 1997; Cai *et al.*, 1998; Moley *et al.*, 1998a; Pampfer *et al.,* 2001).

Three cell death paradigms that are linked to decreased GLUT include, (i) induction of ATP depletion and stimulation of the mitochondrial death cascade or (ii) induction of oxidative stress and triggering of Bax-associated

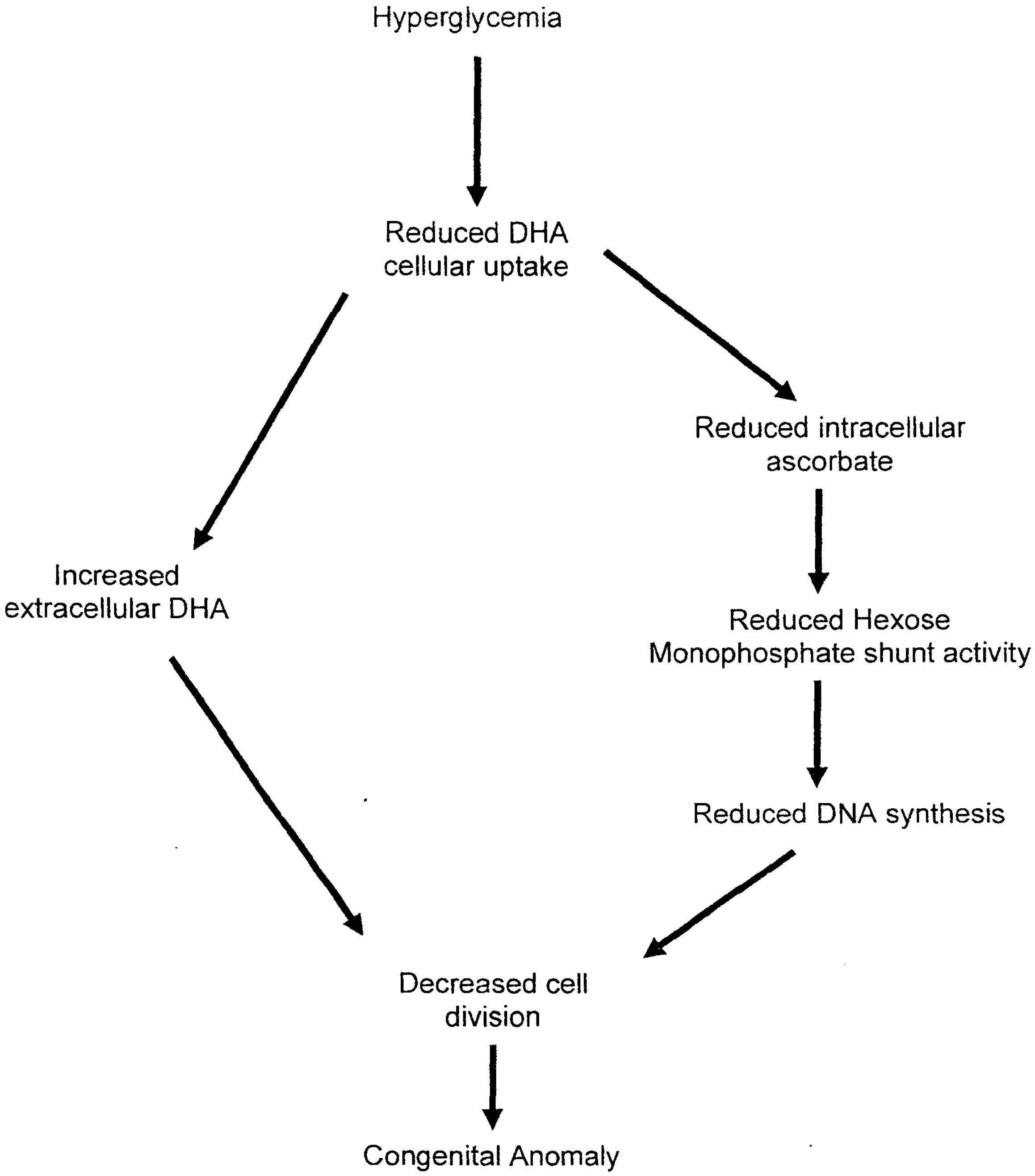

Figure 1.3 Mechanism of hyperglycemia-induced alterations in cell division and congenital anomalies

(Adapted from Ely, 1981)

events including the c-Jun N-terminal kinase (JNK) and mitogen-activated protein kinase (MAPK) signalling pathways or (iii) regulation of expression of the gene encoding hypoxia-inducible factor 1α (HIF-1α) and the stabilization of p53 by HIF-1α binding, leading to an increase in p53-associated apoptosis and, in turn, increased expression of Bax, and thus exaggerated apoptosis within blastocysts during glucose deprivation (Chi *et al.*, 2000; Moley and Mueckler, 2000; Keim *et al.*, 2001).

The outcome of apoptosis during preimplantation stage will depend on the percentage of cell death, if more than 60% of ICM undergo cell death, the pregnancy may result in fetal loss and resorption. However, the death of fewer cells (e.g. 40-45%) can result in either fetal resorption or malformation if this cell death involves key progenitor cells in development (Tam, 1988; Moley, 2001).

Another possible mechanism of hyperglycemia-induced congenital anomalies that has been put forward is related to dysregulation in the uterine cytokine secretion (Pampfer, 2001). Diabetes-induced modifications in the oviductal and uterine concentrations of nutrients (such as increased glucose levels), hormones (such as decreased insulin levels), growth factors, and cytokines (increased local synthesis of inhibitory factors or decreased local synthesis of stimulatory factors) are likely to elicit alterations in embryo development before implantation and organogenesis.

Studies in STZ- and alloxan-treated diabetic mice exhibit an increased amount of tumour necrosis factor-α (TNF-α) messenger ribonucleic acid (mRNA) and protein in the uterus and placenta of diabetic mice (Pampfer *et al.*, 1995; Flein *et al.*, 2001) as well as a marked reduction in pregnancy rate and a high incidence of litters with severely malformed fetuses (Torchinsky *et al.*, 1997, Machado *et al.*, 2001). In addition, overexpression and excessive secretion of TNF-α by uterine cells in diabetic pregnancy may induce a decrease in cell number of the ICM as reported in an earlier study (Pampfer *et al.*, 1997b; Wuu *et al.*, 1999).

TNF-α acts in a cell type- and stimulus-dependent manner, to generate apoptotic-signalling pathways (Baud and Karin, 2001; Gupta, 2001). The apoptotic action of TNF-α could occur mainly through its binding to the type 1 receptor TNF-α, followed by the activation of caspase 8 (Slee *et al.*, 1999; Mohr *et al.*, 2002; Torchinsky *et al.*, 2003), which is considered to be among the main mediators of apoptosis (Baud and Karin, 2001; Gupta, 2001). The apoptotic action of TNF-α could be mediated through interleukin-1ß (IL-1ß) secreted by macrophages (Pampfer *et al.*, 1999) localized at the subepithelial region of the uterine stroma (Takacs *et al.*, 1988).

The mechanism of hyperglycemia-induced IL-1ß secretion has been proposed to be via the formation and interaction of advanced glycation end products, AGE (Vlassara *et al.*, 1988). Macrophages have a receptor that recognizes the AGE moiety and mediates the uptake and degradation of AGE proteins. This removal process is associated with the production and secretion of TNF-α and IL-1. The localized release and action of these cytokines may play a role in the coordinated removal and replacement of senescent extracellular matrix (ECM) components in normal tissue homeostasis (Vlassara *et al.*, 1988).

1.4.2 Maternal Hyperketonemia

The elevated glucagon-insulin ratio in diabetes mellitus enhances triglyceride hydrolysis by hormone-sensitive lipase and thereby increases plasma free fatty acid levels and also increases the uptake of these fatty acids by the liver. Acetyl-CoA carboxylase activity and malonyl-CoA concentrations are decreased in diabetes mellitus. Increased fatty acids and decreased malonyl-CoA result in increased β-oxidation of fatty acids and the generation of acetyl-CoA. As a result, pyruvate carboxylase for gluconeogenesis is stimulated and ketone bodies production is increased. The ketone bodies are potential teratogens as they freely cross the placenta (Herrera, 2002) and may serve as a fuel source to the fetus under conditions of maternal fasting (Ruwe *et al.*, 1991). A high concentration of ketone bodies (β-hydroxybutyrate and acetoacetate) leads to a decreased production of purines and pyrimidines by fetal rat brain tissue (Shambaugh *et al.*, 1984).

Frienkel and colleagues (Freinkel *et al.*, 1986; Freinkel, 1988) have also shown that β-hydroxybutyrate induced malformations in cultured rat embryos in a dose-related fashion. Combination of minimally teratogenic amounts of both glucose and β-hydroxybutyrate during culture of rat embryos resulted in significantly greater reductions of somite number, crown-rump length, and mean embryo protein content than by either of these metabolites alone (Freinkel *et al.*, 1986). Clinical studies, however, showed inconclusive correlation between maternal ketonuria and an increased risk of psychomotor impairment in children but not malformation rates (Rizzo *et al.*, 1991).

1.4.3 Maternal Hypoglycemia

The effect of hypoglycemia in the genesis of birth defects remains unclear. Discrepancies exist between human and animal data regarding the teratogenic effect of hypoglycemia. In animal models, Buchanan and colleagues (1986) demonstrated that mild hypoglycemia caused a significant reduction in somite number, protein and DNA content of the embryos, which are suggestive of growth retardation. In contrast to the animal models, there is little evidence in humans that hypoglycemia is teratogenic (Kitzmiller *et al.*, 1991).

1.4.4 Free Oxygen Radicals

Hyperglycemia-induced oxidative stress or generation of reactive oxygen species (ROS) by the embryos is implicated by indirect evidence, such as phospholipid peroxidation, reduction in the intracellular levels of antioxidant enzymes (superoxide dismutase (SOD), catalase and glutathione peroxidase) and depletion of antioxidant (glutathione) buffer capacity (Eriksson and Borg, 1993; Cederberg *et al.*, 2000). .

Hyperglycemia impairs inositol uptake by the embryos (Weigensberg *et al.*, 1990). The immediate effect of lowered inositol concentration would be decreased levels of the phosphoinositides (phosphoinositides, PI; phosphatidylinositol phosphate, PIP; and phosphatidylinositol bisphosphate, PIP_2) and their products in the embryonic tissue (Strieleman *et al.*, 1992). A lack of PIP_2 would subsequently yield less inositol triphosphate (IP3) and diacylglycerol, both of which are stimulators of protein kinase C (PKC) activity. A lowered PKC activity would then exert a number of effects, including lowered activity of cytosolic phospholipase A_2 ($cPLA_2$), the key enzyme in the metabolism of triglycerides and phospholipids.

Two major pathways of phospholipid peroxidation have been suggested in embryos under hyperglycemic conditions. One of them involves arachidonic acid (AA), which is released from the membrane by $cPLA_2$ and converted into prostaglandin E_2 (PGE_2) by cyclooxygenase-2 (COX-2). A decrease of $cPLA_2$ activity would subsequently diminish the availability of free AA, and thus diminish the production and metabolism of PGE_2 during critical period in organogenesis (Goldman *et al.*, 1985). In another pathway, AA is converted into PGE_2-like isoprostanes, such as 8-iso-PGF_2 and 8-iso-$PGF_{2\alpha}$. These PGE-like isoprostanes have been shown to have damaging effects in animal models and embryos. Studies have suggested a relationship between deficiency of AA with hyperglycemia and embryopathy, and conversely, the protective effect of supplementation with AA and decrease incidence of diabetic embryopathy (Goldman *et al.*, 1985, Pinter *et al.*, 1988, Reece *et al.*, 1996).

There is evidence that hyperglycemia can degrade antioxidant enzyme defenses i.e. lower glutathione reductase and SOD activity (Li *et al.*, 1999), thereby allowing ROS to damage other enzymes and also structural proteins. Moreover, both glucose and its glycation products will generate radicals if free iron (or copper) is present. In addition, ketone bodies are also reported to be able to generate ROS via cytochrome P450 (Christopher *et al.*, 1995).

Hyperglycemia-induced increase in ROS either from increased of its production (Liu and Gutterman, 2002) or from diminished antioxidant defense capacity (Li *et al.*, 1999) in the tissue results in mitochondrial swelling (Yang *et al.*, 1995b), DNA mutations (Lee *et al.*, 1999) and apoptosis (Phelan *et al.*, 1997).

Chronic and excessive oxidative stress disturbs a variety of stress-sensitive signalling pathways that are associated with apoptosis, including the MAPK signalling pathway (Torres and Forman, 2003; Kyosseva, 2004). It has been demonstrated that the activity of extracellular signal-related kinase (ERK) 1 and ERK 2 were decreased and the activity of JNK 1 and JNK 2 were increased in oxidative stress. ERKs are involved in cell survival, whereas JNKs play a role in promoting apoptosis through regulation of transcription factors (Lin, 2003; Wada and Penninger, 2004). Similarly, maternal diabetes impairs ERK and activates JNK signalling pathways, resulting in excessive apoptosis and embryonic malformations (Reece *et al.,* 2006) as illustrated in Figure 1.4.

1.4.5 Genetic Susceptibility

Women with similar metabolic control have different outcomes with regard to fetal malformations, suggesting the existence of genetic differences among women with diabetes. A genetic predisposition towards an increased

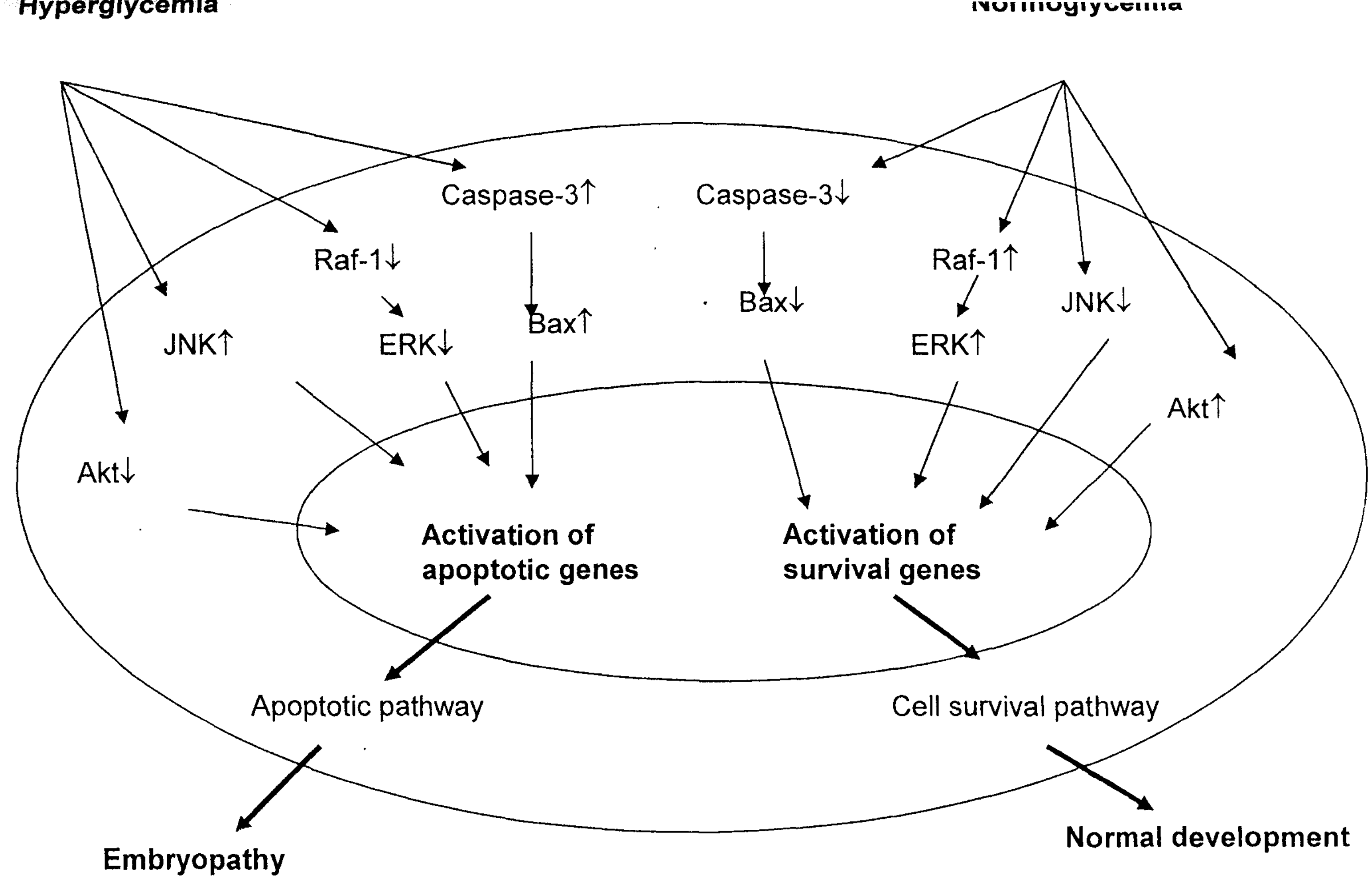

Figure 1.4 Potential molecular pathways involved in diabetice embryopathy

(Adapted from Reece *et al.*, 2006)

rate of embryonic dysmorphogenesis (Eriksson, 1988) may result from a diminished capacity to scavenge endogenously formed ROS. This is a capacity that can vary between strains (Salganik *et al.*, 1994; Hagay *et al.*, 1995) and tentatively, among pregnant diabetic women and their offsprings.

One study reported that the frequency of congenital malformations in the offspring of STZ-induced diabetic rats differed among Sprague-Dawley substrains (Eriksson *et al.*, 1986) despite similar levels of carbohydrate and lipid metabolism. In the rat model, diabetic teratogenesis in the susceptible mothers appears to be potentiated in the presence of genetically predisposed embryos. However, Eriksson's data in rats are inconsistent with human studies. In human studies, no significant differences were found in the incidence of congenital malformation in the offspring of diabetic and non-diabetic fathers (Comess *et al.*, 1969; Chung and Myrianthopoulos, 1975). The anomaly rates, however, were found to be significantly higher among infants whose mothers were diabetic compared with offspring of normal parents. These human data do not support, although do not entirely exclude, a genetic factor as a major determinant of diabetes-associated congenital malformations (Eriksson *et al.*, 1986).

1.4.6 Other Maternal Factors

A variety of additional factors shown to be associated with diabetic malformation have also been investigated. Zinc deficiency has been reported in a few clinical studies as a cause of fetal malformation (Eriksson, 1984). A decrease in zinc content has been demonstrated in the rat offspring of diabetic mother, however, the exact role of zinc deficiency in diabetes-related embryopathy remains to be elucidated (Eriksson, 1984).

Insulin, which is teratogenic in chickens (Julian and Abbott, 1998), produces no abnormalities when added in very high concentrations (250 times physiologic) to mouse embryos (Sadler and Horton, 1983). Moreover, serum collected from diabetic rats receiving insulin therapy is less teratogenic than that collected from diabetic animals receiving no insulin supplements (Wentzel and Eriksson, 1996).

1.5 FUEL-MEDIATED TERATOGENESIS

Earlier concept in developmental biology implies that the damaged preimplantation embryos would either abort at the time of implantation or survive free of anomalies (Russell and Russell, 1950). This concept has been challenged by observations that alterations in the embryonic milieu or exposure to certain agents before implantation can contribute to the occurrence of fetal abnormalities long after the time of the primary insult (Freinkel and Metzger, 1978, Iannaccone *et al.*, 1987, Kimmel *et al.*, 1993).

The concept of "pregnancy as a tissue culture experience" is still accepted until today. It was first introduced by Freinkel and Metzger (1978). This concept proposed that the placenta and the fetus develop in an incubating medium that is totally derived from maternal metabolites. The latter cross the placenta in a concentration-dependent fashion, and this limits the incubation medium in the fetal circulation. Since all these constituents are mainly regulated by maternal insulin, disturbances in its supply and action will influence the whole nutrient composition to which the fetus is exposed and may lead to fetal hyperinsulinemia.

Based on this concept, the abnormal maternal mixture of metabolites gains access to the developing fetus *in utero*, modifying the phenotypic gene expression in newly formed cells, which in turn may lead to short- and long-term effects in the offspring. The fetal tissues most likely to be affected are neural cells, adipocytes, muscle cells and pancreatic β-cells. Exposure during the early first trimester can lead to early intrauterine growth retardation and organ malformations, described by Freinkel as 'fuel-mediated teratogenesis'. During the second trimester, when the formation and development of the brain cells take place, altered behavioral, intellectual or psychological patterns may occur. During the third trimester, proliferation of fetal adipocytes, muscle cells, pancreatic β-cells and neuroendocrine systems is the basis for development later in life of obesity or type 2 diabetes mellitus.

1.6 INSULIN-LIKE GROWTH FACTORS (IGFs)

The present understanding of IGFs results from a union of knowledge from three different areas of research (i) the mediators of the growth promoting actions of growth hormone (GH), namely sulfation factor activity, SFA (Salmon and Daughaday, 1957), (ii) the nature of the non-suppressible insulin-like activity in serum, NSILA (Froesch *et al.*, 1963), and (iii) the identity of serum factors that stimulate cellular multiplication *in vitro*, namely multiplication-stimulating activity, MSA (Dulak and Temin 1973).

The term "somatomedin" was introduced to replace the terms SFA, NSILA and MSA (Daughaday *et al.*, 1972). This term was later replaced by IGFs (Daughaday and Rotwein 1989).

The components of the IGFs system include (i) IGF-1, IGF-2 and insulin; (ii) their corresponding receptors, IGF-1R, IGF-2R and insulin receptors (IR); (iii) six IGFs binding proteins (IGFBP 1-6); (iv) nine additional IGFBP-related proteins (IGFBP-rPs 1-9); (v) IGFBP cleaving proteases; (vi) and a glycoprotein known as acid-labile subunit (ALS) (Clemmons, 1993; Cohick and Clemmons, 1993; LeRoith *et al.*, 1995; Collett-Solberg and Cohen, 2000).

1.7 INSULIN-LIKE GROWTH FACTOR-1 (IGF-1)

IGF-1 is a 7649 Dalton (Da) single-chain polypeptide with three intrachain disulphide bridges consisting of 70 amino acids (Rinderknecht and Humbel, 1978a). Structurally IGF-1 is divided into domains A and B (similar to insulin), domain C (analogous to the connecting peptide (C-peptide) of proinsulin but no sequence homology to C-peptide of insulin) and domain D (not present in insulin). IGF-1 displays approximately 62 percent sequence homology with IGF-2 and 47 percent with insulin.

The primary structure of IGF-1 has been characterized in five mammalian species. Bovine, porcine and human IGF-1 are identical, whereas rat and mouse IGF-1 differ from human by three and four amino acid residues, respectively. Only one amino acid residue difference is observed between rat and mouse IGF-1 (Rinderknecht and Humbel, 1978a; Bell *et al.*, 1986;

Honegger and Humbel, 1986; Murphy *et al.*, 1987a; Shimatsu and Rotwein, 1987a & 1987b; Tavakkol *et al.*, 1988).

In addition to the classical IGF-1 molecules, a truncated form of IGF-1 known as DES (1-3) IGF-1 has been isolated from human fetal tissue (Sara *et al.*, 1986) and adult brain (Carlsson-Skwirut *et al.*, 1986) as well as from bovine colostrum (Francis *et al.*, 1986). DES (1-3) IGF-1 is the product of posttranslational modification of proIGF-1 lacking the first three residues at the amino terminus: Gly-Pro-Glu. The biologic potency of this truncated form is 10 times higher than that of the full length form and is explained by reduced binding to IGFBP (Francis *et al.*, 1988; Carlsson-Skwirut *et al.*, 1989; Simes *et al.*, 1991; Beck *et al.*, 1993; Ballard *et al.*, 1996).

17.1 IGF-1 gene

The IGF-1 gene consists of six exons, five introns and is transcribed from two promoters as shown in Figure 1.5 (Rotwein, 1991, Zarrilli *et al.*, 1994). It spans a large region of chromosomal DNA, ranging in size from 50 kilobase (kb) in the chicken to 80 kb in the rat; the human gene is localized on chromosome region 12q22-q24.1 (Brissenden *et al.*, 1984; Zarrilli *et al.*, 1994).

Exons 1 and 2 are leader exons, and encode 5' untranslated regions and signal peptide sequences. From the two leader exons, two types of IGF-1 transcripts are encoded (Hall *et al.*, 1992; Shemer *et al.*, 1992; Pell *et al.*, 1993; Yang *et al.*, 1995a). Exon 1 transcripts are found in all tissues and regulated by factors other than GH. It represents the "autocrine and/or paracrine