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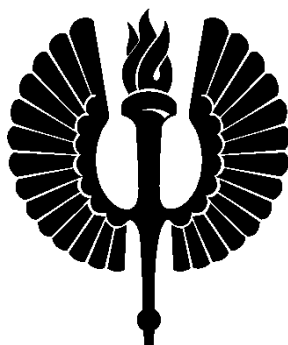
SARJA – SER. D OSA– TOM. 908

MEDICA - ODONTOLOGICA

**THE ROLE OF INTEGRINS IN ENTEROVIRUS  
INFECTIONS AND IN METASTASIS OF CANCER**

by

**Åse Karttunen**



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UNIVERSITY OF TURKU  
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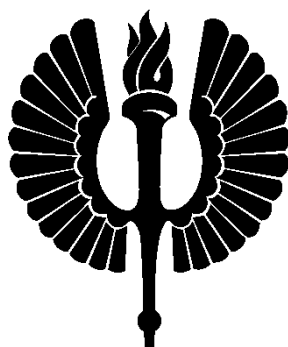
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*To my Family*

# ABSTRACT

Åse Karttunen

## THE ROLE OF INTEGRINS IN ENTEROVIRUS INFECTIONS AND IN METASTASIS OF CANCER

The Department of Virology, University of Turku, Turku, the Department of Virology, Haartman Institute, and the Helsinki Biomedical Graduate School, University of Helsinki, Helsinki, and the Department of Biochemistry and Pharmacy, Åbo Akademi University, Turku, Finland. *Annales Universitatis Turkuensis, Medica-Odontologica, Yliopistopaino, Helsinki, 2010.*

Integrins are a family of transmembrane glycoproteins, composed of two different subunits ( $\alpha$  and  $\beta$ ). Altered expression of integrins in tumor cells contributes to metastasis tendency by influencing on the cells' attachment to adjacent cells and their migration. Viral pathogens, including certain enteroviruses, use integrins as receptors. Enteroviruses have also been suggested to be involved in the etiopathogenesis of type 1 diabetes.

The study focuses on the role of integrins in the pathogenesis of metastasis to cortical bone and on type 1 diabetes (T1D) and echovirus 1 infection. In **the first part** of the thesis, the role of different integrins in the initial attachment of MDA-MD-231 breast cancer cells to bovine cortical bone disks was studied. A close correlation between  $\alpha 2\beta 1$  and  $\alpha 3\beta 1$  integrin receptor expression and the capability of the tumor to attach to bone were observed. In **the second part**, a possible correlation between susceptibility to enterovirus infections in diabetic children and differences in enterovirus receptor genes, including certain integrins, was investigated. In parallel, virus-specific neutralizing antibodies and diabetic risk alleles were studied. In the diabetic group, an amino acid change was detected in the polio virus receptor and the neutralizing antibody titers against echovirus 30 were lower. However, to obtain statistically sustainable results, a larger number of individuals should be analyzed. Echovirus 1 (EV1) enters cells by attaching to the  $\alpha 2I$  domain of the  $\alpha 2\beta 1$  integrin. In **the third part** EV1 was shown to attach to a chimeric receptor construct of the transferrin receptor and the  $\alpha 2I$  domain and to enter cells through clathrin-mediated endocytosis that is normally not used by the virus. The chimeric receptor was recycled to the plasma membrane, whereas the virus remained in intracellular vesicles. The virus replication cycle was initiated in these cells, suggesting that evolution pressure could possibly cause the virus to evolve to use a different entry mechanism. Moreover, a cDNA microarray analysis of host gene expression during EV1 replication showed that 0.53% of the total genes, including several immediate early genes, were differently expressed.

**Keywords:** Integrin, breast cancer, metastasis, human enterovirus, echovirus 1, type 1 diabetes, clathrin mediated endocytosis

# TIIVISTELMÄ

Åse Karttunen

## INTEGRIINIEN MERKITYS ENTEROVIRUSINFEKTIOSSA JA SYÖVÄN ETÄPESÄKKEIDEN MUODOSTUMISESSA

Virusoppi, Turun Yliopisto, Haartman-instituutti, Virologian osasto ja Biolääketieteellinen tutkijakoulu, Helsingin Yliopisto, Helsinki, ja Biokemian ja farmasian laitos, Åbo Akademi, Turku. Annales Universitatis Turkuensis, Yliopistopaino, Helsinki, 2010.

Integriinit ovat solukalvon läpäiseviä glykoproteiineja, jotka koostuvat kahdesta alayksiköstä (alfa ja beta). Ne ovat vuorovaikutuksessa solukalvon kanssa soluadheesiossa ja migraatiossa. Muuttunut integriinien ilmentyminen syöpäsoluissa vaikuttaa soluadheesioon ja soluliikkuvuuteen ja voi täten vaikuttaa solun taipumukseen muodostaa etäpesäkkeitä. Tiettyjen integriinien tuotto rintasyövässä korreloituu sairauden ennusteeseen ja metastasointiherkkyyteen. Eräät enterovirukset hyödyntävät solun integriinejä päästääkseen solun sisälle. Enterovirusten aiheuttamat taudinkuvat ihmisissä vaihtelevat nuhakuumeista sydänlihastulehduksiin ja keskushermostoinfektioihin. Enterovirusinfektioilla voi olla merkitystä myös tyypin I diabeteksen puhkeamisessa.

Tässä väitöskirjatyössä on tutkittu integriinien osuutta syövän etäpesäkkeiden leviämisessä luukudokseen sekä niiden toimintaa enterovirusten, kuten echovirus 1:n reseptoreina ja reseptorien ilmentymistä suhteessa tyypin I diabetekseen. Väitöskirjan **ensimmäisessä osatyössä** tutkittiin integriinien merkitystä rintasyöpäsolujen varhaisessa kiinnittymisessä kortikaalisille luukiekkoille. Vahva yhteys nähtiin  $\alpha 2\beta 1$  ja  $\alpha 3\beta 1$  integriinien ilmentymisessä ja kyvyssä sitoutua kortikaaliseen luukudokseen. **Toisessa osatyössä** tutkittiin, voisivatko muutokset enterovirusten reseptorimolekyyleissä korreloida tyypin I diabeteksen puhkeamiseen. Sekvenssianalyysi tehtiin kuuden tunnetuimman enterovirusreseptorin (PVR, ICAM-1, DAF, CAR,  $\alpha v\beta 3$  ja  $\alpha 2\beta 1$  integriini) geenialueilta, ja virusspesifiset vasta-aineet määritettiin seerumista. Diabetesryhmästä geenivaihtelua löytyi PVR:sta ja vasta-aineet echovirus 30:tä vastaan olivat matalammat kuin kontrolliryhmässä. Tulokset pitää kuitenkin vielä varmistaa suuremmassa ryhmässä tilastollisen luotettavuuden selvittämiseksi. Echovirus I (EV1) sitoutuu  $\alpha 2\beta 1$  integriinin  $\alpha 2$  alayksikön I-domeeniin ( $\alpha 2I$ ), ja **kolmannessa osatyössä** osoitettiin että virus pystyi infektoimaan solut, jotka ilmensivät pinnallaan reseptorikimeeraa, missä  $\alpha 2I$ -jakso oli liitetty transferriinireseptoriin. Virus kuljetettiin soluun klatrinivälitteisesti, mikä eroaa EV1:n normaalisti käyttämistä soluuntukeutumisreiteistä. Lisäksi cDNA-mikrosiruanalyysi isäntäsolun geeniekspressiosta EV1-replikaation aikana osoitti, että 0.53% geeniekspressiosta oli muuttunut, sisältäen monia solun toiminnalle keskeisiä geenejä.

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## ABBREVIATIONS

<b>Ad</b>	Adenovirus
<b><math>\alpha</math>2I</b>	I domain of the integrin $\alpha$ 2 subunit
<b>ALS</b>	amyotrophic lateral sclerosis
<b>Arf</b>	ADP-ribosylation factor
<b>ATF</b>	activating transcription factor
<b><math>\beta</math>2-m</b>	$\beta$ 2 microglobulin
<b>BSA</b>	bovine serum albumin
<b>CAMs</b>	cell adhesion molecules
<b>CAR</b>	coxsackievirus-adenovirus receptor
<b>CAV</b>	coxsackievirus A
<b>CBV</b>	coxsackievirus B
<b>CD155</b>	poliovirus and vitronectin receptor
<b>Cdk</b>	cyclin-dependent kinase
<b>cDNA</b>	complementary DNA
<b>CLIC</b>	clathrin-independent carrier
<b>CPE</b>	cytopathic effect
<b>CI-MPR</b>	mannose 6-phosphate receptor
<b>CPV</b>	canine parvovirus
<b>CTGF</b>	connective tissue growth factor
<b>CXCL10</b>	CXC chemokine ligand 10
<b>DAF</b>	decay-accelerating factor
<b>ECM</b>	extracellular matrix
<b>ECV</b>	endosomal carrier vesicle
<b>EE</b>	early endosome
<b>EEA1</b>	early endosome antigen 1
<b>eIF4F</b>	eucaryotic initiation factor 4F
<b>EGF</b>	epidermal growth factor
<b>EGR1</b>	early growth response 1
<b>ER</b>	endoplasmic reticulum
<b>ERC</b>	endocytic recycling compartment
<b>EV</b>	echovirus
<b>FACS</b>	flow cytometry (fluorescence activated cell sorting)
<b>FAK</b>	focal adhesion kinase
<b>FasL</b>	fas ligand
<b>FPV</b>	feline panleukopenia virus
<b>Fra-1</b>	fos related antigen-1
<b>GAD65</b>	glutamic acid decarboxylase 65
<b>GAP</b>	GTPase activating protein
<b>GDI</b>	rho dissociate inhibitor
<b>GEEC</b>	GPI-anchored, protein-enriched early endosomal compartment
<b>GEFs</b>	guanine nucleotide exchange factors

<b>GPI</b>	glycosylphosphatidylinositol
<b>GRP78</b>	glucose-regulated protein 78
<b>HAVcr-1</b>	HAV cellular receptor 1
<b>HBV</b>	hepatitis B virus
<b>FMDV</b>	foot-and-mouth-disease
<b>HEV</b>	human enteroviruses
<b>HIV-1</b>	human immunodeficiency virus type I
<b>HPEV</b>	human parechovirus
<b>HRV</b>	human rhinovirus
<b>HS</b>	heparan sulphate
<b>HSV</b>	herpes simplex virus
<b>ICAM-1</b>	intercellular adhesion molecule 1
<b>IEG</b>	immediate early gene
<b>IF</b>	immunofluorescence
<b>IFN</b>	interferon
<b>IgSF</b>	immunoglobulin superfamily
<b>IRES</b>	internal ribosome entry site
<b>JNK</b>	c-Jun NH2-terminal kinase
<b>LDLR</b>	low density lipoprotein receptor
<b>LE</b>	late endosome
<b>LFA-1</b>	lymphocyte function associated antigen-1
<b>VLDLR</b>	very low density lipoprotein receptor
<b>LRP1</b>	LDLR related protein 1
<b>MAb</b>	monoclonal antibody
<b>MAPK</b>	p38 mitogen-activated protein kinase
<b>MIDAS</b>	metal-ion-dependent adhesion site
<b>MMP</b>	matrix metalloproteinase
<b>MOI</b>	multiplicity of infection
<b>OPN</b>	osteopontin
<b>OPV</b>	oral polio vaccine
<b>PABP</b>	poly(A)-binding protein
<b>PARP</b>	poly(ADP-ribose) polymerase
<b>Pak</b>	p21-activated kinase
<b>PBS</b>	phosphate-buffered saline
<b>PCR</b>	polymerase chain reaction
<b>PI3K</b>	phosphoinositide 3-kinase
<b>PI(3)P</b>	phosphatidylinositol 3-kinase
<b>PLC</b>	phospholipase C
<b>PBMC</b>	peripheral blood mononuclear cell
<b>pol II</b>	RNA polymerase II
<b>PSI</b>	plexin-semaphorin-integrin
<b>PV</b>	poliovirus
<b>PVR</b>	poliovirus and vironectin receptor
<b>RabGDI</b>	Rab GDP dissociation inhibitor

<b>REP</b>	Rab escort protein
<b>RGD</b>	arginine-glycine-aspartic acid
<b>SDS</b>	sodium dodecyl sulfate
<b>SFV</b>	Semliki forest virus
<b>SNP</b>	single nucleotide polymorphism
<b>SRC</b>	short consensus repeats
<b>SV40</b>	simian virus 40
<b>T1D</b>	type 1 diabetes
<b>Tf</b>	transferrin
<b>TF</b>	transcription factor
<b>TfR</b>	transferrin receptor
<b>TJ</b>	tight junction
<b>TM</b>	transmembrane
<b>TNF</b>	tumor necrosis factor
<b>u-PAR</b>	urokinase-plasminogen activator receptor
<b>UTR</b>	untranslated region
<b>VCAM-1</b>	vascular cell adhesion molecule-1
<b>VLDL-R</b>	very-low-density lipoprotein receptor
<b>vp1</b>	enteroviral capsid protein vp1
<b>VWA</b>	von Willebrand A domains
<b>vRNA</b>	viral RNA

## LIST OF ORIGINAL PUBLICATIONS

This thesis is based on the following original publications, which are referred to in the text by Roman numerals (I-III). In addition, results about cellular gene expression during echovirus 1 infection are reported.

**I Lundström, Å., Holmbom, J., Lindqvist, C. & Nordström, T.** 1998. The role of  $\alpha 2\beta 1$  and  $\alpha 3\beta 1$  integrin receptors in initial anchoring of MDA-MB-231 human breast cancer cells to cortical bone matrix. *Biochemical and Biophysical Research Communications* 250:735-40.

**II Karttunen, Å., Pöyry, T., Vaarala, O., Ilonen, J., Hovi, T., Roivainen, M. & Hyypiä, T.** 2003. Variation in enterovirus receptor genes. *Journal of Medical Virology* 70:99-108.

**III Karttunen, Å., Pietiäinen, V., Pukkila, V., Heino, J., Waris, M., Marjomäki, V., & Hyypiä, T.** Targeting of echovirus 1 to the clathrin pathway. Submitted

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# 1 INTRODUCTION

Integrins are a family of transmembrane glycoproteins that interact with the extracellular matrices in cell adhesion and migration. Altered expression of integrins in tumor cells contribute to metastasis tendency by affecting attachment to adjacent cells and migration tendency. Breast cancer is characterized by frequent skeletal metastasis. One possibility that might explain the bone selectivity is that the breast cancer cells express surface adhesion molecules that facilitate their adherence to proteins present in the bone microvasculature matrix. In addition to natural ligands (such as vitronectin and collagen), viral pathogens, including certain enteroviruses, utilize the cellular integrin receptors to enter the host cells. Enteroviruses belonging to the picornavirus group are among the most common viruses infecting humans globally. Several studies have suggested that enteroviruses could also be involved in the etiopathogenesis of type 1 diabetes.

This thesis aims to elucidate the role of enterovirus receptors including the integrins in the pathogenesis of metastasis to cortical bone and type 1 diabetes and echovirus 1 infection in four different subprojects. In the first subproject, the most important integrins in initial anchorage of human breast cancer to cortical bone matrix were investigated. In the second subproject, a possible correlation between the susceptibility to enterovirus infections and/or frequent occurrence of enterovirus antibodies in prediabetic and diabetic children with differences in integrin and other enterovirus receptor genes were studied. In parallel, virus-specific neutralizing antibodies and diabetic risk alleles were investigated. The third and fourth subproject concentrated on echovirus 1 (EV1) which uses  $\alpha 2\beta 1$  integrin as a cellular receptor. In the third subproject, the EV1 entry via a chimeric receptor construct of transferrin receptor and  $\alpha 2$  I domain was studied. The aim was to analyze if EV1 is able enter cells by clathrin directed entry which is normally not used by the virus, and establish productive infection. In the fourth subproject the host gene expression was investigated during EV1 endocytosis and replication.

## 2 REVIEW OF THE LITERATURE

### 2.1 INTEGRINS

Integrins are a family of cell surface glycoproteins composed of at least 18 different  $\alpha$  subunits and eight  $\beta$  subunits that attach noncovalently forming 24 different heterodimers (Hynes, 2002) (Fig 1., Table 1). The extracellular N-domain of the  $\alpha$ - and  $\beta$ -subunits have up to 1104 residues and 778 residues respectively, a single transmembrane (TM) domain and a C-terminal, cytoplasmic tail. Integrins function as receptors for extracellular matrix (ECM) proteins and are important in cell-cell interactions during differentiation, malignant transformation, immune recognition and blood coagulation. Integrins bind to diverse ligands, including many ECM proteins such as collagen, fibronectin, laminin, vitronectin, von Willebrand factor and thrombospondin, ICAMs, members of the immunoglobulin superfamily, (IgSF) and plasma proteins, like fibrinogen (Hynes & Lander, 1992). In addition, a restricted number of proteins interact with integrins within the plasma membrane bilayer. These include caveolins, leukocyte surface antigen CD47, urokinase-plasminogen activator receptor (u-PAR) and certain tetraspanins (Barberis *et al.*, 2000, Chapman *et al.*, 1999, Giancotti, 2000, Hemler *et al.*, 1985).

Nine of the vertebrate  $\alpha$ -subunits contain an approximately 190 amino acids long I ("inserted") domain (Whittaker & Hynes, 2002). In those I domain integrins, the domain is the major ligand binding site. The I domain is a member of a family of von Willebrand A domains (VWA). The globular domain is composed of a GTPase-like domain, with a metal-ion-binding site (MIDAS). Dependent of the conformation of MIDAS, I domains can exist in both high affinity and low affinity ligand-binding conformation (Emsley *et al.*, 2000, Lee *et al.*, 1995a, Lee *et al.*, 1995b) that is essential for binding of some ligands, e.g. collagen (Emsley *et al.*, 2000). The I domain interacts with a  $\beta$ -propeller, which is a G-protein-like domain formed from seven similar structural units (Springer, 1997). In integrins lacking a  $\alpha$ I domain, the main ligand-binding sites are in the  $\beta$ I domain, the  $\beta$ -propeller and the upper surface of the  $\alpha$  subunit (Xiong *et al.*, 2001).

The leg of the  $\alpha$ -subunit is composed of a thigh domain and two calf domains. All  $\beta$ -subunits contain a head with an I-like domain, which shares common structures with the  $\alpha$ I domains (Lee *et al.*, 1995a) including MIDAS. The leg of the  $\beta$ -subunit consists of a plexin-semaphorin-integrin (PSI) domain, hybrid domain, four cystein-rich repeats (I-EGF; epidermal growth factor domains) and a novel cystatin-like fold (Hynes, 2002). The cytoplasmic tail is crucial for modulating ligand-integrin interactions into dynamic cellular responses, such as cell spreading or migration and endocytosis. The intracellular

**Table 1.** Human Integrins (Modified from Johnson et al., 2009)

<b>Integrin Ligands</b>	
<b>Integrins recognize the RGD peptide</b>	
$\alpha 5\beta 1$	Fibronectin
$\alpha 8\beta 1$	Fibronectin, vitronectin, tenascin C, osteopontin, nefronectin
$\alpha V\beta 4$	Fibronectin, vitronectin
$\alpha V\beta 3$	Fibrinogen, fibronectin, vitronectin, tenascin C, osteopontin, bone sialoprotein, MMP-2, CYR61
$\alpha V\beta 5$	Vitronectin
$\alpha V\beta 6$	Fibronectin, TGF- $\beta$ -LAP
$\alpha V\beta 8$	Vitronectin
$\alpha IIb\beta 3$	Fibrinogen, fibronectin, vitronectin
<b>The Integrin Collagen receptor subfamily</b>	
$\alpha 1\beta 1$	Collagens, semaphorin 7A (laminins)
$\alpha 2\beta 1$	Collagens, tenascin C, (laminins)
$\alpha 10\beta 1$	Collagens
$\alpha 11\beta 1$	Collagens
<b>Leucocyte integrin subfamily</b>	
$\alpha D\beta 2$	ICAM, VCAM
$\alpha M\beta 2$	ICAM, VCAM, iC3b, factor X, fibrinogen
$\alpha L\beta 2$	ICAM,
$\alpha X\beta 2$	Fibrinogen, plasminogen, heparin, iC3b
$\alpha 4\beta 7$	Fibronectin, VCAM
$\alpha E\beta 7$	E-cadherin
<b>Integrins containing an <math>\alpha 3</math>, <math>\alpha 4</math>, <math>\alpha 6</math>, <math>\alpha 7</math> or <math>\alpha 9</math> <math>\alpha</math> subunit</b>	
$\alpha 3\beta 1$	Laminins (collagens)
$\alpha 4\beta 1$	Fibronectin, VCAM
$\alpha 6\beta 1$	Laminins
$\alpha 6\beta 4$	Laminins
$\alpha 7\beta 1$	Laminins
$\alpha 9\beta 1$	Tenascin C, osteopontin, ADAMs, factor XIII, VCAM, VEGF-C, VEGF-D

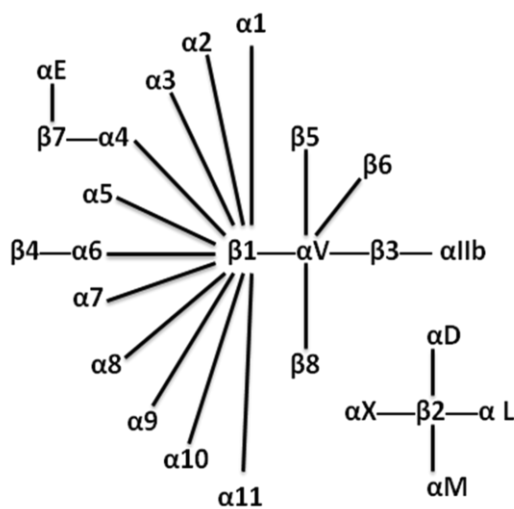
domains are linked to the actin cytoskeleton and several adapter molecules including vinculin, talin or  $\alpha$ -actin (Zamir & Geiger, 2001). All integrins, except  $\alpha 6\beta 4$ , are coupled to the actin cytoskeleton. The  $\beta 4$  integrin subunit differs from the others by having a long cytoplasmic tail of about 1000 amino acids instead of around 50 amino acids that interact with the intermediate filaments. Conserved regions of TM and cytoplasmic tail of both  $\alpha$  and  $\beta$  integrin subunits have been reported to be essential in the regulation of integrin activation. The integrin can be locked in an inactive state by disulfide-bonds in the TM domain. Constitutive activation of integrin can be maintained by mutation in TM region or truncation of tail sequence (Banno & Ginsberg, 2008). Binding of talin to the cytoplasmic part of the  $\beta$  subunit induces a series of conformational changes that

induce formation of an active extracellular domain with high affinity for ligands (Ulmer *et al.*, 2003, Vinogradova *et al.*, 2002).

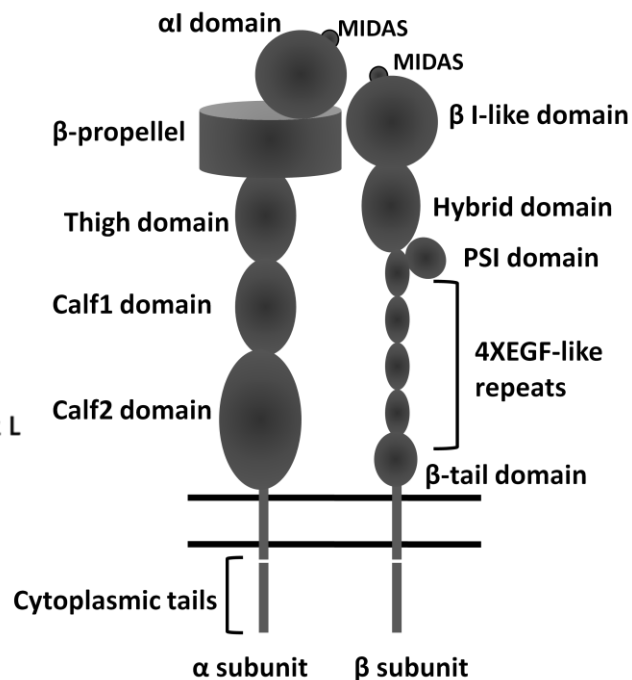
Collagens are the most abundant proteins in the mammalian body. The collagen family contains at least 13 different proteins. Collagen fibers and fibrils give the structural support that is needed in the skeletal tissue, blood vessel and in the extracellular matrix in different tissues in the body. Type I collagen is the most abundant of the collagens and is expressed predominantly in tissues like skin, tendons and in the ECM of the skeleton where it is the major protein of the bone matrix. Amino acid residues of the I domain of an integrin determine its ligand-binding specificity to different collagens (Dickeson *et al.*, 1998, Nykvist *et al.*, 2000). The  $\alpha 2I$  domain D219 has been suggested to be important for collagen I binding (Smith *et al.*, 2000), while in the  $\alpha 1$  I domain that has higher affinity for collagen IV the corresponding amino acid is R218. In  $\alpha 10$  and  $\alpha 11$  this position has

R241 and T238 respectively. In addition,  $\alpha 1\beta 1$  and  $\alpha 2\beta 1$  attach to some non-collagen ligands involved in cell adhesion, such as laminin 1 and 2. Furthermore,  $\alpha 1\beta 1$  can bind to the cartilage protein matrilin-1 (Makihira *et al.*, 1999) and  $\alpha 2\beta 1$  to the cartilage protein chondroadherin (Camper *et al.*, 1997). All ligands for  $\alpha 1\beta 1$  and  $\alpha 2\beta 1$ , except chondroadherin, support cell spreading.  $\alpha 10\beta 1$  attaches to type II collagen (Camper *et al.*, 1998), while  $\alpha 11\beta 1$  is known to attach to fibrillar collagen I-III (Popova *et al.*, 2007).

The other five integrins with I domain ( $\alpha D$ ,  $\alpha E$ ,  $\alpha M$ ,  $\alpha L$  and  $\alpha X$ ) (Rose *et al.*, 2007) are leukocyte integrins. The leukocyte integrins bind to counter receptors, including E-cadherin and intercellular and vascular adhesion molecules (ICAMs or VCAM correspondingly). Some of them also attach to plasma proteins such as plasminogen and fibrinogen or iC3b in the complement system (Table 1).



**Figure 1.** 18  $\alpha$  integrin subunits and eight  $\beta$  integrin subunits are able to form 24 heterodimeric integrins.



**Figure 2.** Schematic structure of collagen binding integrin. (Modified from Humphries, 2002; Hynes, 2002; White *et al.*, 2004).

Several members of the integrin family, including  $\alpha 5\beta 1$ ,  $\alpha 8\beta 1$ ,  $\alpha I\text{Ib}\beta 3$ ,  $\alpha V\beta 3$ ,  $\alpha V\beta 5$ ,  $\alpha V\beta 6$  and  $\alpha V\beta 8$ , (Table 1), recognize an arginine-glycine-aspartic acid (RGD) tripeptide sequence in molecules such as fibrinogen, fibronectin, vitronectin, von Willebrand factor and laminins. Peptides containing the RGD motif, can efficiently block these integrin-ligand interactions (Hynes, 1992, Ruoslahti & Pierschbacher, 1987).

Other integrins containing neither the I domain nor the RGD sequence include the subunits  $\alpha 3$ ,  $\alpha 4$ ,  $\alpha 6$ ,  $\alpha 7$  and  $\alpha 9$ . The integrin subunits  $\alpha 3$ ,  $\alpha 6$  and  $\alpha 7$  are all part of laminin-



binding integrins and are needed for the integrity of tissues such as kidney, skin and muscle (Table 1).  $\alpha 4$  and  $\alpha 9$  integrin subunits recognize ECM proteins, some plasma proteins, counter receptors belonging to the immunoglobulin superfamily and vascular endothelial cell growth factors (Vlahakis *et al.*, 2007) (Table 1).

Outside-in signaling may be propagated by ligand binding to the extracellular domain, which initiates conformational changes that are mediated to the TM and cytoplasmic domains, and causes integrin clustering into discrete domains, such as focal adhesion domains (Arnaout *et al.*, 2005). Integrin ECM site focal adhesion is formed by aggregation of several signalling and structural molecules, including focal adhesion kinase (FAK), Src, PI-3-Kinase, RhoGAP, paxillin, talin, p130CAS, integrin linked kinase (ILK) and Caveolin-1 in ECM (Gahmberg *et al.*, 2009). The downstream signals following integrin ligation can modify cell function by altered cell morphology, cell migration or stability, regulation of cell differentiation and apoptosis. Inside-out signalling occurs by action of non-integrin cellular receptors or cytoplasmic molecules causing activation of signalling pathways inside the cell leading to either activation/deactivation of integrins.

Integrins have been implicated in various diseases and disease processes from inflammation, atherosclerosis to cancer. Altered expression of integrins in cancer cells contributes to metastasis tendency by influencing the cells' attachment to adjacent cells and their migration. Moreover, several viral pathogenes, including adenoviruses (Wickham *et al.*, 1993), cytomegaloviruses (Feire *et al.*, 2004), flaviviruses (La Linn *et al.*, 2005), picornaviruses (Bergelson *et al.*, 1992, Berinstein *et al.*, 1995, Roivainen *et al.*, 1994), rotaviruses (Ciarlet *et al.*, 2002, Guerrero *et al.*, 2000) and togaviruses (La Linn *et al.*, 2005) use integrins as receptors to enter the host cell.

## **2.2 THE ROLE OF INTEGRINS IN BREAST CANCER METASTASIS TO THE SKELETON**

Breast cancer is characterized by frequent skeletal metastasis. One possibility that might explain the common bone metastases is that the breast cancer cells express adhesion molecules that facilitate their adherence to the cell surface molecules present in the bone microvasculature matrix. Integrins mediate cellular adhesion and are crucial for the regulation of tissue integrity and several other functions in mammalian tissues. Integrins are involved in all steps of the metastasis process, including migration, invasion and colonization of target tissues (White & Muller, 2007), as well as in forming the vasculature crucial for tumor growth (Akalu *et al.*, 2005, Goel & Languino, 2004).

The first stage of metastasis in a primary breast tumor is weakened adhesion to adjacent cells and migration from the primary tumor. This involves two properties that include forward movement of the cells and crossing the dense collagenous tissue

surrounding the tumor by degrading the extracellular matrix or, alternatively, squeezing through interstitial spaces (Wolf *et al.*, 2003).

Integrins control the motility of cells. Migration movements include such as, synchronized processes of integrin engagement and actin cytoskeleton rearrangements (Giannone *et al.*, 2004, Ridley, 2001). Integrin clustering at focal contact sites activates actin polymerization, mediated by members of the Rho family of small GTPases, including Rho, Rac and cdc42, providing the physical force for forward migration (Ridley *et al.*, 2003). Furthermore, integrins are also implicated in the directionality of cell movement and breakdown of restrictive cell-cell adhesive structures. These properties are mediated through amplification of growth factor-derived signals (White & Muller, 2007).

Spreading of cells from the primary tumor requires simultaneous ability to degrade surrounding ECM barrier and to pass through the endothelial cell layer surrounding blood vessels. Degradation needs activation of membrane-bound or secreted proteases, generated by both tumor cells and inflammatory stromal cells. Matrix degradation includes membrane-bound or secreted proteases, such as members of the matrix metalloproteinase (MMP) family, which in invasive breast cancer cells are dependent on integrin expression (Baum *et al.*, 2007, Brooks *et al.*, 1996). Integrins have been shown to both promote MMP-mediated proteolysis and increase their expression (White & Muller, 2007). Inhibition of integrin expression in invasive breast tumor cells decreases MMP activity leading to reduction in invasive activity (Morini *et al.*, 2000). Metastatic cancer cells have been reported to utilize integrins for attachment to the basement membrane in a distant environment (Van der Velde-Zimmermann *et al.*, 1997, van der Pluijm *et al.*, 1997). Basement membrane is composed of thin sheets of dense ECM enveloping all epithelial organs and functions as a barrier to macromolecules and cells (Albini *et al.*, 2004).

Normal human breast epithelial cells express  $\alpha 1\beta 1$ ,  $\alpha 2\beta 1$ ,  $\alpha 3\beta 1$ ,  $\alpha 6\beta 4$  and  $\alpha v\beta 3$  integrins (Alford & Taylor-Papadimitriou, 1996, Damjanovich *et al.*, 1997, Glukhova *et al.*, 1995), whereas a common feature of breast tumors is altered expression of  $\alpha 1\beta 1$ ,  $\alpha 2\beta 1$ ,  $\alpha 3\beta 1$ ,  $\alpha 6\beta 1$  and  $\alpha 6\beta 4$  integrins (Alford & Taylor-Papadimitriou, 1996, Koukoulis *et al.*, 1991).

$\alpha v\beta 3$  integrin mediates adhesion of cancer cells and osteoclasts to the bone matrix (Harms *et al.*, 2004). It can bind to an RGD peptide sequence present in many bone matrix proteins including vitronectin, osteopontin (OPN) and bone sialoprotein (Cacciari & Spalluto, 2005, Harms *et al.*, 2004). Adhesive proteins, such as  $\alpha v\beta 3$ , may mediate malignant cell adhesion to platelets (Nash *et al.*, 2002), an association that could protect tumor cells from clearance by the immune system (Nieswandt *et al.*, 1999). The  $\alpha v\beta 3$  integrin may also favour tumor cell adhesion to the vessel endothelium and their subsequent extravasation into distant tissues (Pontier & Muller, 2008).

The  $\alpha v\beta 3$  integrin has been shown to mediate certain cellular responses to OPN, a bone-derived phosphoglycoprotein related to aggressive disease progression and skeletal

metastasis (Furger *et al.*, 2003). This can lead to upregulation of metastasis-promoting factors, such as MMPs and the Met/HGF receptor (Tuck *et al.*, 2000). Induced expression of the  $\alpha\beta3$  integrin in malignant breast cancer has been shown to improve the survival of tumor cells after intravasation (Pontier & Muller, 2008). The  $\alpha\beta3$  integrin has also been implicated to be important in the metastasing process of breast cancer cells to bone. Breast metastatic cells and breast cancer-derived bone metastasis expressed high levels of the integrin (Liapis *et al.*, 1996). In vivo -selected MDA-MB-231 cells that metastase only to bone show increased expression of the  $\alpha\beta3$  integrin (Hall *et al.*, 2006). Inhibitors of the  $\alpha\beta3$  were shown to reduce bone metastasis in breast cancer patients and in an animal model after intracardiac injection of MDA-MB-435 cells (Harms *et al.*, 2004). In a study with prostate cancer cells, blocking antibodies against the  $\alpha\beta3$  integrin inhibited attachment to crude bone protein extract by over 90% (Hullinger *et al.*, 1998).

Furthermore, the  $\alpha\beta3$ , together with the  $\alpha5\beta1$  integrin, has been implicated in breast cancer to promote proliferation signaling by interacting with growth receptor partners (Pontier & Muller, 2008). These events have been reported to regulate migration of malignant cells by coupling, for instance, to MMP9 metalloprotease (Felding-Habermann *et al.*, 2001, Rolli *et al.*, 2003). In animal models, administration of peptides designed to block the integrins  $\alpha5\beta1$  and  $\alpha\beta3$  impaired growth and metastasis of invasive breast cancer (Khalili *et al.*, 2006, White & Muller, 2007).

Increase in the expression of the collagen/laminin receptor  $\alpha2\beta1$  has been reported in many-human malignancies (Jones *et al.*, 1992, Pignatelli *et al.*, 1990, Suzuki *et al.*, 1993). In animal models, the  $\alpha2\beta1$  and the fibronectin receptor  $\alpha4\beta1$  have been shown to be responsible for selective metastasis of cancer cells to the skeleton (Chan *et al.*, 1991, Matsuura *et al.*, 1996). Controversially, reduction or loss of the  $\alpha2\beta1$  integrin has been observed in several breast cancers (Alford *et al.*, 1998, Lanzafame *et al.*, 1996) and it has associated with increased metastatic potential (Arihiro *et al.*, 1993).

$\beta1$  integrin subunit expression is abnormal in approximately 30-50% of breast cancers and correlates with poor differentiation of the tumor (Cordes & Park, 2007).  $\beta1$  integrin signaling has been observed to be involved in various stages of cancer progression, including invasion, migration and metastasis (Elliott *et al.*, 1994, Fujita *et al.*, 1995). The signaling depends on binding to extracellular ligands, including fibronectin and laminin-1. Decreased  $\beta1$  integrin expression in breast tumors has been reported to correlate with more aggressive disease (Gonzalez *et al.*, 1999, Lanzafame *et al.*, 1996, Pignatelli *et al.*, 1992). Conversely, increased  $\beta1$  integrin signaling has also been reported to promote tumorigenesis by facilitating the activity of growth factor receptors (Wang *et al.*, 1998, Wang *et al.*, 2002). Inhibitory antibody against the  $\beta1$  integrin induced apoptosis and decreased proliferation in three-dimensional cell cultures and in animal models of breast cancer (Yao *et al.*, 2007). Overexpression of the  $\beta1$  integrin was further reported to be associated with decreased survival in invasive cancer of breast (Yao *et al.*, 2007) and

pancreas (Bottger *et al.*, 1999), and cutaneous melanoma (Nikkola *et al.*, 2004). The controversial tumor-promoting effect of both reduced and induced  $\beta 1$  integrin gene expression could be explained by different cellular regulation mechanisms (Yao *et al.*, 2007).

Some other integrins have also been associated in the biology of breast cancer.  $\beta 4$  integrin-coupled signaling has been reported to be involved in breast cancer progression.  $\alpha 3\beta 1$  was suggested to be critical for migration, invasion and metastasis of a breast cancer cell line MDA-MB-231 to the skeleton (Morini *et al.*, 2000) and the expression levels of the  $\alpha 3\beta 1$  integrin were higher in breast cancer metastases than in primary tumors. Furthermore, invasion was suggested to be dependent on the activity of MMP-9 (Morini *et al.*, 2000). In an *in vivo* study, expression of signaling-defective  $\beta 4$  integrin in mammary epithelium delayed breast tumor progression in mice (Guo *et al.*, 2006). The  $\alpha 6\beta 1$  and  $\alpha 6\beta 4$  integrins have been shown to contribute to breast cancer cell survival during cellular stress (Chung & Mercurio, 2004).

Some of the published results concerning the role of integrins in the breast cancer skeletal metastasis process are controversial, which could partly be explained by different surface expression of integrins on tumor cells. The  $\alpha v\beta 3$  integrin has been shown in numerous studies to be crucial for breast cancer cell attachment to bone surface. However, in the MDA-MB-231 cells that express low levels of the  $\alpha v\beta 3$  integrin, other integrins were suggested to be important in the metastasis to bone (Morini *et al.*, 2000, Wong *et al.*, 1998). Differences in experimental procedures may also affect the experimental results, for instance in studies by Morini *et al.* and Wong *et al.* showing the  $\alpha v\beta 3$  integrin not to be important in the initial attachment of MDA-MB-231 cells to bone (Morini *et al.*, 2000, Wong *et al.*, 1998). Pluijm *et al.* suggested the opposite in a study where cells were permitted to attach and spread on bone matrix over a long time span, possibly causing upregulation of additional surface integrins at the plasma membrane (van der Pluijm *et al.*, 1997). In addition, factors other than the integrin expression profile could also affect the cell metastatic potential.

## 2.3 PICORNAVIRUSES

Picornaviruses are small (30 nm) nonenveloped animal viruses with a single-stranded infectious RNA genome. The family *Picornaviridae* is divided into twelve genera (aphto-, avihepato-, cardio-, entero-, erbo-, hepato-, kobu-, parecho-, seneca-, sapelo-, tescho- and tremoviruses) (<http://www.picornaviridae.com>) (Table 2). Every genus is further divided into species consisting of virus serotypes. Previously, picornavirus classification was based mainly on their pathogenesis in laboratory animals and antigenic properties (Hyypiä *et al.*, 1997), but the current classification utilizes the genomic sequences of the

viruses. Picornaviruses are responsible for a diversity of diseases, such as poliomyelitis (polioviruses, PVs), common cold (human rhinoviruses; HRVs), hepatitis (hepatitis A virus), and foot-and-mouth-disease in cattle (foot-and-mouth-disease viruses; FMDVs) (Table 2).

Enteroviruses are among the most common viruses infecting humans globally. Human enteroviruses (HEVs) have former been classified into echoviruses (EVs), coxsackie A viruses (CAVs), coxsackie B viruses (CBVs) and polioviruses (PVs). In the current classification, HEVs are grouped into seven species: enterovirus A, B, C, and D, and rhinovirus A, B and C (Table 1). Enteroviruses are associated with a wide variety of illnesses, in all age groups, ranging from minor febrile disease to more severe conditions, including poliomyelitis, meningitis, encephalitis, myocarditis and neonatal generalized infection (Li *et al.*, 2007). Most infections are, however, mild or asymptomatic (Grist *et al.*, 1978). The principal site of infection is the epithelium of the respiratory or the gastrointestinal tracts. This can be followed by viremia (occurrence of viruses in the blood) that may cause transfer of the infection to secondary target organs. Enteroviruses have also been suggested to be involved in the development of some chronic diseases, such as type 1 diabetes (T1D) (Hyöty & Taylor, 2002) and dilated cardiomyopathy (Knowlton, 2008).

PVs were discovered as early as in 1908 and are the best-known enteroviruses (Landsteiner & Popper, 1909). PV infection can cause poliomyelitis which can lead to permanent paralysis. The virus has infected human populations for thousands of years. Although the poliovirus vaccination campaign has almost eradicated the disease, it is still a problem in some parts of the world. On the basis of coxsackievirus pathogenicity in laboratory animals, they have originally been divided into subgroups A and B (Dalldorf & Sickles, 1948). All CBVs can be propagated in cell culture, while some CAVs can only replicate in newborn mice. Echoviruses (enteric, cytopathogenic, orphan viruses) were originally recognized due to their ability to replicate exclusively in cell culture, in contrast to other enteroviruses which infected laboratory animals (Anonymous, 1955).

Oncolytic enteroviruses are potential agents for future cancer therapy. In 2004 Shafren *et al.* reported that CAV21 induced rapid oncolysis of human melanoma cells, overexpressing the virus receptors DAF and ICAM-1 in vitro and in vivo in mice bearing multiple melanoma xenografts (Shafren *et al.*, 2004). This study was followed by additional reports implicating CAV21 to possess oncolytic potential in multiple melanoma (Au *et al.*, 2007), breast tumors (Skelding *et al.*, 2009) and prostate tumors (Berry *et al.*, 2008) both in vitro and in vivo. CAV21 administered to end-stage melanoma patients showed no adverse effect (Parato *et al.*, 2005). In 2005 Shafren *et al.* showed EV1 to be oncolytic for cultured malignant ovarian cells expressing high levels of  $\alpha 2\beta 1$  integrin, but not for nonmalignant control cells (Shafren *et al.*, 2005). The oncolytic effect was further determined by using human ovarian cancer xenografts in mice in which the tumor burden

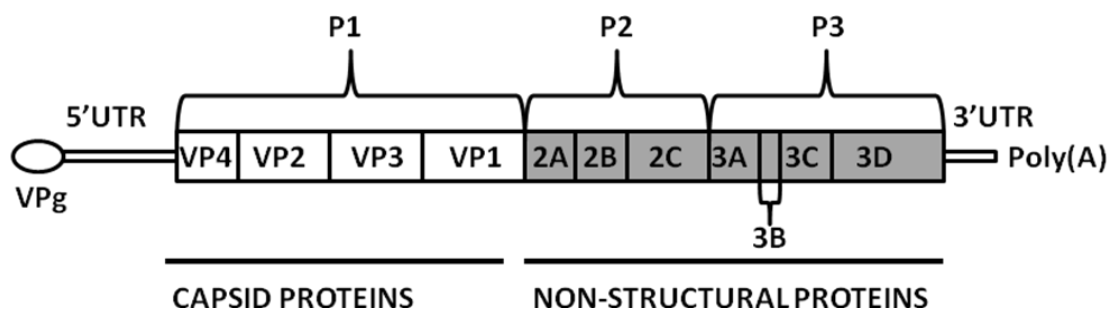
was rapidly reduced, and in prostate and gastric cancer models (Berry *et al.*, 2008, Haley *et al.*, 2009, Shafren *et al.*, 2005).

**Table 2.** Contemporary classification of picornaviruses (<http://www.picornaviridae.com>)

<b>Genus</b>	<b>Species (No. of serotypes)</b>
<b>Enteroviruses</b>	<b>Human enterovirus A (21 types) (HEV-A)</b>
	-Human coxsackieviruses A2-A8, A10, A12, A14, A16
	-Human enterovirus 71
	-Human echoviruses 76, 89, 90, 91
	-Simian enteroviruses enterovirus 92, SV19, SV43, SV46, A13
	<b>Human enterovirus B (59 types) (HEV-B)</b>
	-Human coxsackieviruses B1-B6
	-Human coxsackieviruses A9
	-Human echoviruses 1-7, 9, 11-21, 24-27, 29-33
	-Human enteroviruses 69, 73-75, 77-88, 93, 97-98, 100-101, 106-107
	-Simian enterovirus SA5
	<b>Human enterovirus C (19 types) (HEV-C)</b>
	-Human coxsackieviruses A1, A11, A13, A17, A19, A20-A22, A24
	-Human poliovirus 1-3
	- Human enteroviruses 95-96, 99, 102, 104-105, 109
	<b>Human enterovirus D (3 types) (HEV-D)</b>
	-Human enteroviruses 68, 70, 94
	<b>Simian enterovirus A (3 types)</b>
	<b>Bovine enterovirus (2 types)</b>
<b>Porcine enterovirus B (2 types) (PEV-B)</b>	
<b>Human rhinovirus A (74 types)</b>	
-Human Rhinovirus 1-2, 7-13, 15-16, 18-25, 28-34, 36, 38-41, 43-47, 49-51, 53-68, 71, 73-78, 80-82, 85, 90, 94-96, 98, 100	
<b>Human rhinovirus B (25 types)</b>	
-Human Rhinovirus 3-6, 14, 17, 26-27, 35, 37, 42, 48, 52, 69, 70, 72, 79, 83, 84, 72, 79, 83-84, 86, 91-93, 97, 99	
<b>Human rhinovirus C</b>	
<b>Cardiovirus</b>	<b>Encephalomyocarditis virus (1 type)</b>
	<b>Theilovirus (12 types)</b>
<b>Aphthovirus</b>	<b>Foot-and-mouth disease virus (7 types)</b>
	<b>Equine rhinitis virus (1 type)</b>
	<b>Bovine rhinitis B virus</b>
<b>Hepatovirus</b>	<b>Hepatitis A virus</b>
<b>Parechovirus</b>	<b>Human parechovirus (14 types)</b>
	<b>Ljungan virus</b>
<b>Erbovirus</b>	<b>Equine rhinitis B virus (3 types)</b>
<b>Kobuvirus</b>	<b>Aichi virus (1 type)</b>
	<b>Bovine kobuvirus (1 type)</b>
<b>Teschovirus</b>	<b>Porcine teschovirus (11 types)</b>
<b>Sapelovirus</b>	<b>Porcine sapelovirus</b>
	<b>Simian sapelovirus</b>
	<b>Avian sapelovirus</b>
<b>Senecavirus</b>	<b>Seneca Valley virus</b>
<b>Tremovirus</b>	<b>Avian encephalomyelitis virus</b>
<b>Avihepatovirus</b>	<b>Duck hepatitis A virus</b>

### 2.3.1 Structure of picornaviruses

The picornavirus genome is enclosed in an icosahedral capsid containing 60 copies of each of the four structural proteins VP1 to VP4. The capsid proteins bound together form the structural unit of the capsid, the protomer. Five protomers are arranged into a pentamer and 12 pentamers form the capsid. VP1, VP2 and VP3 remain external, while VP4 is buried within the capsid. The picornavirus genome is a positive-strand RNA molecule of 7.2 to 8.5 kilobases (kb) (Figure 3). It has a small virus-encoded protein (VPg) covalently linked to its 5' terminus, while the 3' end is polyadenylated. The 3' and 5' ends contain untranslated regions (5'UTR and 3'UTR, respectively). 5'UTR includes an internal ribosome entry site (IRES) and a cloverleaf secondary structure. IRES directs the initiation of translation in a cap-independent manner (Pelletier & Sonenberg, 1988), whereas the cloverleaf structure is a multifunctional replication element which interacts with viral and cellular proteins to form a ribonucleoprotein complex (Li *et al.*, 2007). The 3'UTR contains a secondary structure, a pseudoknot, that has an important role in the regulation of viral RNA synthesis (Jacobson *et al.*, 1993). The open reading frame (ORF) is translated into one single large polyprotein (between 2100-2400 amino acids, aa), which is further proteolytically cleaved into three precursor proteins P1, P2 and P3 and finally into four structural proteins (VP1-4) and seven nonstructural proteins (2A-C, 3A-D). 2A functions as a protease only in enteroviruses and rhinoviruses, and 3C in all picornaviruses (Hanecak *et al.*, 1982, Toyoda *et al.*, 1986). 3D is an RNA-dependent RNA polymerase.



**Figure 3.** The enterovirus genome. The polyprotein is initially proteolytically cleaved into P1, P2 and P3 regions. The P1 region is processed into the structural proteins VP1-VP4, while P2 and P3 are processed into non-structural proteins.

### 2.3.2 Picornavirus infection cycle

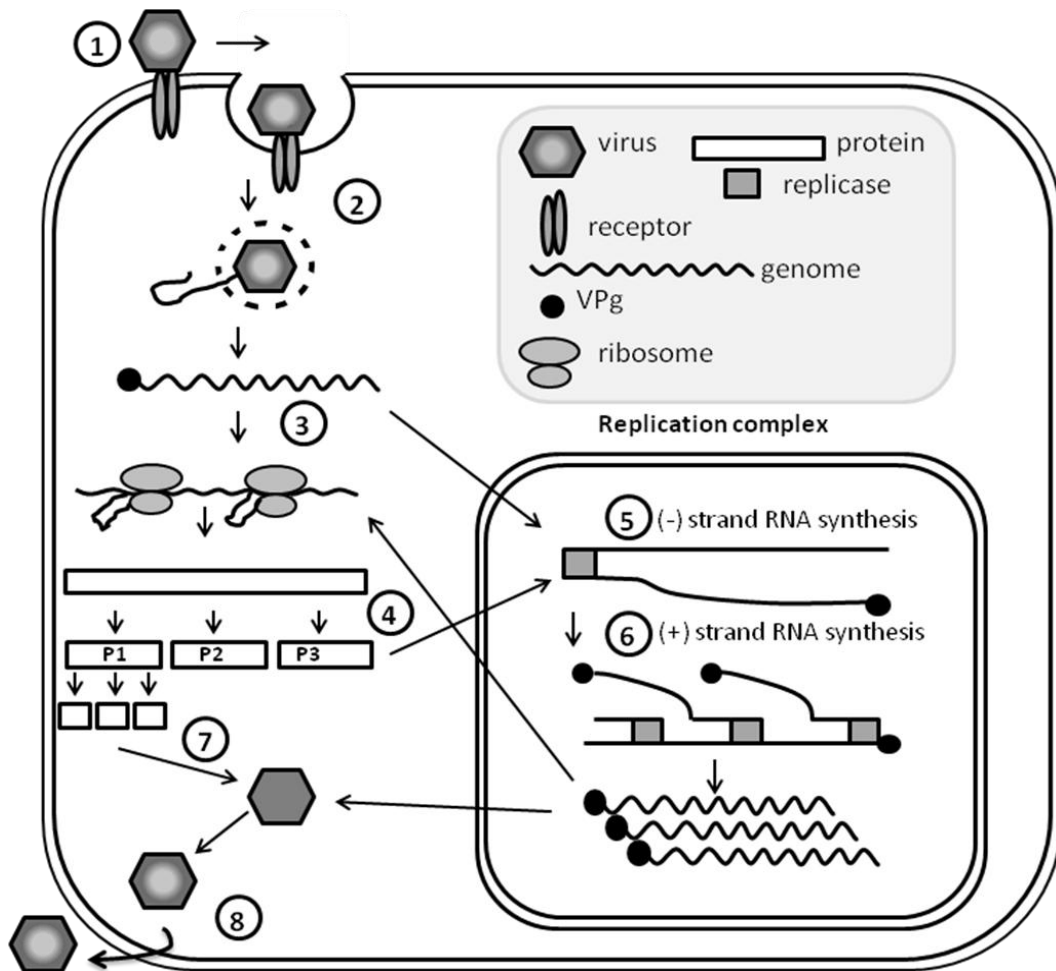
To initiate infection, the virus needs to attach to a receptor on the cell surface (see step 1 in Fig. 4). The infection of most picornavirus infections is associated with major structural

modifications of the virion to the altered ('A') particle in order to release the viral RNA (vRNA). VP4 is absent in A particles, and the amino terminus of VP1 is externalized. For many enteroviruses, this structural change is known to be triggered by receptor binding (Rossmann *et al.*, 2002). For other picornaviruses, such as the minor receptor group of HRVs, it is driven by the acidic pH within the endosomes (Dreschers *et al.*, 2007). Enteroviruses are subsequently endocytosed and the viral genome is released into the cell cytosol (Pietiäinen *et al.*, 2005) (see step 2 in Fig. 4). The VPg protein is removed from the 5'UTR in the cytoplasm and the genome is translated (see step 3 in Fig. 4) to a polyprotein precursor, which is then cleaved to provide the viral proteins crucial for genome replication and particle assembly particles (see step 4 in Fig. 4).

In picornaviruses, like in other RNA viruses, the virus genome synthesis occurs in replication complexes on membraneous vesicles that are induced by virus proteins (Egger *et al.*, 2002). All the nonstructural proteins are involved in the viral RNA replication. In the initial step in replication, the positive strand viral RNA is copied to minus strand RNA (see step 5 in Fig. 4). This is followed by the production of new positive strand RNA molecules (see step 6 in Fig. 4). Enteroviruses inhibit cellular protein synthesis by cleaving the cellular initiation factor eIF4G, thus preventing the binding of the 5' cap-binding initiator factor eIF4E to cellular mRNAs with specific activity of the 2A protein (Etchison *et al.*, 1982, Gradi *et al.*, 1998). Already 2 h after the initiation of the PV infection translation of nearly all cellular genes is replaced by viral mRNA translation (Etchison *et al.*, 1982). However, the translation of the picorna viral genome is not affected because of the IRES that allows cap-independent translation of RNA (Dorner *et al.*, 1984, Pelletier & Sonenberg, 1989). Alternatively, picornaviruses can dephosphorylate two low-molecular-weight cellular proteins 4E-BP1 and 4E-BP2, which are then able to bind to EIF4E and block its binding to EIF4G (Gingras *et al.*, 1998). Furthermore, a picornavirus infection can inhibit cellular RNA synthesis by inhibiting the DNA-dependent RNA polymerases I, II and III (Clark & Dasgupta, 1990, Falk *et al.*, 1990, Yalamanchili *et al.*, 1996).

After sufficient synthesis of picornavirus capsid proteins and genomic RNA, the encapsidation of viral particles is initiated (see step 7 in Fig. 4). The viral particles are released by cell lysis (see step 8 in Fig. 4). The replication cycle of enteroviruses ranges from 5 to 10 h in cell culture. Approximately 50 000 new virus particles are produced in one cell but only 0.1-2% of them are infectious (Racaniello, 2001).

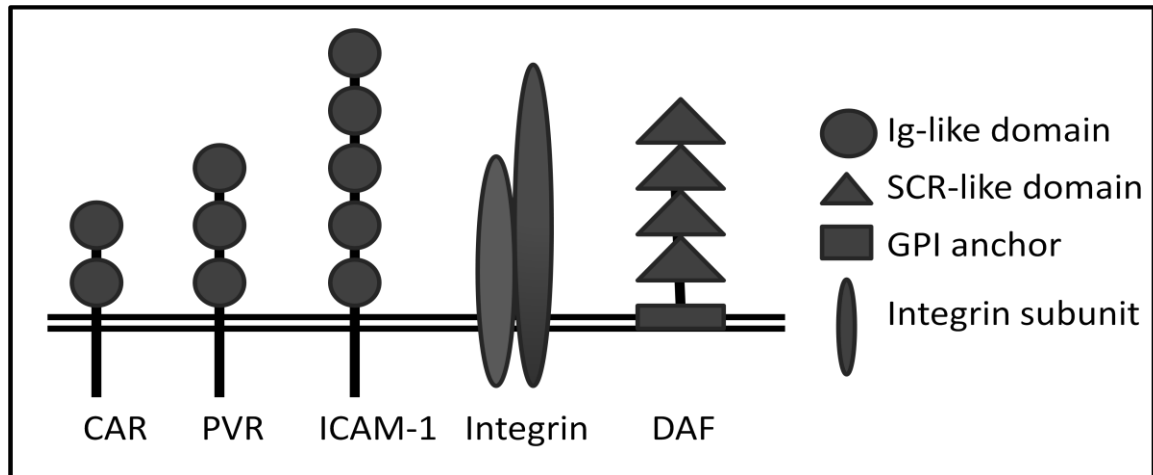




**Figure 4.** Schematic overview of the picornavirus replication cycle: 1) Attachment, 2) Entry and uncoating, 3) Translation, 4) Protein processing, 5-6) RNA replication, 5) (-) strand RNA synthesis, 6) (+) strand RNA synthesis, 7) Assembly and 8) Release.

## 2.4 CELLULAR RECEPTORS FOR PICORNAVIRUSES

To infect cells, viruses need to attach to molecules on the cell surface. Viruses use as receptors a wide range of molecules including proteins, carbohydrates and glycolipids. Virus-induced change in the receptor structure may induce signaling that activates the host-cell and regulates the entry process. The receptor binding can alter the virus structure triggering uncoating. Furthermore, accessory molecules may be needed for successful cell entry and virus uncoating. Picornaviruses may attach to several different molecules, including members of the immunoglobulin superfamily (IgSF) and integrins (Table 3 and Fig. 5).



**Figure 5.** Schematic picture of proteins known to function as enterovirus receptors. (Modified from Evans and Almond, 1998).

**Integrins** are used as receptors by some picornaviruses.  $\alpha$ v-integrin-binding picornaviruses, such as human parechoviruses (HPV1) (Joki-Korpela *et al.*, 2001), CAV9 (Roivainen *et al.*, 1994, Williams *et al.*, 2004), some EV9 strains (Zimmermann *et al.*, 1995) and FMDVs (Fox *et al.*, 1989) possess an RGD motif in their VP1 capsid protein that functions as a binding site for  $\alpha$ v-integrins (Chang *et al.*, 1992, Fox *et al.*, 1989) (Table 3). However, RGD-independent infection of CAV9 (Hughes *et al.*, 1995, Roivainen *et al.*, 1991, Roivainen *et al.*, 1996) and FMDV (Jackson *et al.*, 1996, Sa-Carvalho *et al.*, 1997) has been reported, indicating that these viruses can use alternative receptors. Indeed, FMDV with mutated RGD sequence uses as receptor heparan sulphate (HS) (Baranowski *et al.*, 2000).

Glucose-regulated protein 78 (GRP78, a member of the heat shock protein-70 family), is a coreceptor for CAV9 (Triantafilou *et al.*, 2002) while MHC class I (Triantafilou *et al.*, 2002) and beta2 microglobulin (Triantafilou *et al.*, 1999, Heikkilä *et al.*, 2010) participates in the endocytotic process of the virus. In HPEV1 infection, the RGD motif has been shown to be critical for the infection initiation (Boonyakiat *et al.*, 2001), other molecules like MMP9 may participate in the entry process (Pulli *et al.*, 1997). In addition, several non-RGD EVs were recently shown to attach to  $\alpha$ v integrins (Ylipaasto *et al.*, 2010) (Table 3).

The  $\alpha$ 2 $\beta$ 1 integrin (collagen and laminin receptor) functions as a receptor for EV1 (Bergelson *et al.*, 1992, Bergelson *et al.*, 1993, Ohman *et al.*, 2001). The  $\alpha$ 2I domain can exist in either closed or open conformation (Emsley *et al.*, 2000). The open conformation occurs in activated integrins prior to ligand binding, suggesting that it represents a high avidity state of the  $\alpha$ 2I domain. EV1 and collagen interactions with the  $\alpha$ 2I domain differ considerably. The MIDAS amino acids and concomitant supporting by  $Mg^{2+}$  are crucial for collagen attachment to the  $\alpha$ 2I domain, while these factors are not necessary in EV1

attachment to the integrin (Bergelson *et al.*, 1993, King *et al.*, 1997). Collagen, like all natural ligands, favours binding to the open  $\alpha 2I$  domain (Aquilina *et al.*, 2002, Tulla *et al.*, 2001) and  $\alpha 2I$  domain binding triggers conformation change from closed to open conformation (Emsley *et al.*, 2000). Furthermore, clustering, either by collagen or antibody to the  $\alpha 2\beta 1$ , triggered rapid and transient activation of p38 MAPK (Jokinen *et*

**Table 3.** Examples of picornavirus host cell receptors (Joki-Korpela *et al.*, 2001, Racaniello, 2001, Williams *et al.*, 2004, Ruiz-Saenz *et al.*, 2009, Triantafilou *et al.*, 2002, Yamayoshi *et al.*, 2009, Yang *et al.*, 2009, Ylipaasto *et al.*, 2010).

RECEPTOR(S)	Virus
<b>Integrins</b>	
$\alpha 2\beta 1$ integrin	Echovirus 1
$\alpha \nu \beta 3$ integrin	Echovirus 25, 30, 32; Coxsackievirus A9
$\alpha \nu \beta 6$ integrin	Coxsackievirus A9
$\alpha \nu \beta 1$ and $\alpha \nu \beta 3$ integrin	Human parechovirus 1
$\alpha \nu \beta 1$ , $\alpha \nu \beta 3$ , $\alpha \nu \beta 6$ , $\alpha \nu \beta 8$ and $\alpha 5\beta 1$ integrin	Foot-and-mouth disease virus
<b>IgSF-like</b>	
Poliovirus receptor, PVR; CD155,	Polioviruses
Intercellular adhesion molecule 1, ICAM-1; CD54	Coxsackieviruses A13, A18, A21
	Major receptor group of rhinoviruses
Coxsackievirus-adenovirus receptor, CAR	Coxsackieviruses B1-B6
HAV cellular receptor 1, HAVcr-1	Hepatitis A virus
<b>SRC-like</b>	
Decay-accelerating factor, DAF; CD55	Coxsackieviruses A21; Echoviruses 3, 6, 7, 11-13, 20, 21, 24, 29, 30
	Enterovirus 70
	Coxsackieviruses B1, B3, B5
<b>Others</b>	
Sialic acid	Enterovirus 70, 71
	Rhinovirus 87
Heparan sulphate	Foot-and-mouth disease virus (culture adapted)
	Certain echovirus serotypes
Low-density lipoprotein receptor; LDL-R	Minor receptor group of rhinoviruses
$\beta 2$ microglobulin, $\beta 2m$	Certain echovirus serotypes
	Coxsackievirus A9
Glucose-regulated protein 78	Coxsackievirus A9
Scavenger receptor class B, memBer 2, SCARB2	Enterovirus 71
SA-linked glycans	Enterovirus 71

*al.*, 2010). EV1, unlike any other ligand known, preferred binding to the closed  $\alpha 2 I$  domain and inactive  $\alpha 2 \beta 1$  integrin (Jokinen *et al.*, 2010, Xing *et al.*, 2004). EV1-induced  $\alpha 2 \beta 1$  integrin clustering did not significantly activate the p38 MAPK signaling cascade (Jokinen *et al.*, 2010). Instead, EV1 clustering activated PKC $\alpha$ , which previously was shown to be needed for EV1 endocytosis (Upla *et al.*, 2004). This suggested that EV1 induced clustering does not trigger similar conformational change of  $\alpha 2 \beta 1$  integrin, caused by either collagen or antibodies (Jokinen *et al.*, 2010).

In Cryo-EM reconstruction of EV1 interactions with a  $\alpha 2 I$  domain-GST fusion protein, the  $\alpha 2 I$  domain was shown to attach to VP1, VP2 and VP3 in the canyon of the virus. The MIDAS motif faced the canyon floor, although not in close contact with the virus, making it impossible for the  $\alpha 2 I$  domain to bind collagen and virus simultaneously. Virus binding to  $\alpha 2 I$  domain did not, however, induce virus uncoating. EV1 was able to attach simultaneously to multiple GST- $\alpha 2 I$  fusion proteins supporting the observation that EV1 attachment induces  $\alpha 2 \beta 1$  clustering (Xing *et al.*, 2004).

**Immunoglobulin superfamily.** Poliovirus receptor (PVR; CD155), coxsackievirus-adenovirus receptor (CAR), ICAM-1 (CD54), and hepatitis A virus cellular receptor 1 (HAVcr-1) are members of the IgSF and function as receptors for many picornaviruses, including PVs, CBVs, major group HRVs, CAVs and hepatitis A virus (Table 3). These proteins have an extracellular part, consisting of a variable number of Ig-like domains with disulphide bonds, a transmembrane domain and a short cytoplasmic domain. The N-terminal part of these receptors binds to the canyon in the virus particle (Rossmann *et al.*, 2002).

All the three poliovirus serotypes utilize the PVR (Mendelsohn *et al.*, 1989). There are two different functional PVRs, produced by alternative splicing, that differ only in the cytoplasmic sequence. PVR contains three extracellular IgSF domains (D1, D2 and D3) (Chothia & Jones, 1997) (Fig. 5). In folding D1 exhibits similarities with Ig variable domain, whereas the two other domains resemble immunoglobulin constant domains. Residues in the domain D1 of PVR have been reported to be involved in PV binding (Rossmann *et al.*, 2002). The cytoplasmic domain of PVR attaches to the light chain of dynein motor complex and is suggested to transport vesicles containing intact PV in retrograde axonal transport to the neuronal-cell body (Mueller *et al.*, 2002, Ohka *et al.*, 2004).

ICAM-1 is recognized by members of the HRV major receptor group (Table 3), e.g. HRV14 and 16 (Greve *et al.*, 1989, Staunton *et al.*, 1989), and is also used by some CAVs, e.g. CAV 21 (Newcombe *et al.*, 2003, Shafren *et al.*, 1997a). ICAM-1 forms cell adhesions between leukocytes and endothelium by binding to lymphocyte function-associated antigen-1 (LFA-1; CD11a/CD18), a member of the integrin family, and the plasma protein fibrinogen, (Marlin & Springer, 1987). ICAM-1 contains five IgSF domains (Fig. 3). HRVs and CAV21 attach to the first aminoterminal IgSF of ICAM-1

(Kolatkar *et al.*, 1999, Olson *et al.*, 1993). Although the binding site of ICAM-1 to HRVs and CAV 21 canyons differs (Rossmann *et al.*, 2002, Xiao *et al.*, 2005), the interaction in both viruses induces conformational changes that destabilize the viruses and enhance the releases their genomes (Rossmann., 1994).

CAR functions as a cellular receptor for all CBVs (Bergelson *et al.*, 1997, Tomko *et al.*, 1997). It has two IgSF domains (Fig. 5) and is localized in intercellular contact sites in epithelial cell junctions, thus interacting in the regulation of the flow of ions and macromolecules, including viruses, across cell monolayers (Cohen *et al.*, 2001). These tight junctions contain integral membrane proteins, which adhere adjacent cell membranes in close contact with cytoplasmic scaffolding proteins that provide a contact to intracellular signaling molecules and cytoskeleton. An interesting aspect is that CAR is downregulated in some tumors (Fuxe *et al.*, 2003, Okegawa *et al.*, 2001, Sachs *et al.*, 2002) and expression of transfected CAR causes inhibition of cell proliferation, suggesting that it could operate as a tumor suppressor (Anders *et al.*, 2003). CBVs attach to several amino acids in the first domain of CAR (He *et al.*, 2001) and virus binding to receptor induces conformational changes in the capsid (Goodfellow *et al.*, 2005, Milstone *et al.*, 2005).

**Other picornavirus receptors.** In addition to integrins and IgSF receptors, picornaviruses can use some others receptors, such as decay-accelerating factor (DAF), very-low-density lipoprotein receptor (VLDL-R), heparan sulphate (HS), sialic acids and  $\beta$ 2 microglobulin ( $\beta$ 2-m). Decay-accelerating factor (DAF) is a glycoprotein that participates in the regulation of complement activity (Nicholson-Weller *et al.*, 1982) and can act as the cellular receptor for several echovirus serotypes (Bergelson *et al.*, 1994, Clarkson *et al.*, 1995, Powell *et al.*, 1998, Ward *et al.*, 1994), enterovirus 70 and as a secondary cellular receptor for CAV21 and CBV 1, 3 and 5 (Bergelson *et al.*, 1995, Shafren *et al.*, 1995) (Table 3). DAF is widely expressed in different mammalian cell types and contains four short consensus repeats (SRC) linked by a glycosylphosphatidylinositol (GPI) anchor (Medof *et al.*, 1987) (Fig. 5). EV7 (Clarkson *et al.*, 1995, He *et al.*, 2002), EV12 (Bhella *et al.*, 2004, Pettigrew *et al.*, 2006), EV11 (Lea *et al.*, 1998) and CBV3 (Bergelson *et al.*, 1995) bind to regions near and of the third SRC domain, while enterovirus 70 (Karnauchow *et al.*, 1996) and CAV21 (Shafren *et al.*, 1997b) interacts with the first SRC domain. Virus-DAF interaction appears not to be sufficient to induce virus uncoating and A particle formation (Milstone *et al.*, 2005).

The cellular receptors for the HRV minor receptor groups are members of the low density lipoprotein receptor (LDLR) family, including the low density lipoprotein receptor (LDLR), the very low density lipoprotein receptor (VLDLR) and LDLR related protein 1 (LRP1) (Nykjaer & Willnow, 2002, Vlasak *et al.*, 2005). HS is a glycosaminoglycan ubiquitously expressed in mammalian cells. HS is naturally involved in cell adhesion, migration, proliferation, and differentiation. In addition, it binds to several signaling

molecules and a number of other ligands (Tumova *et al.*, 2000). Some picornaviruses attach to HS, like FMDV (Jackson *et al.*, 1996), swine vesicular disease virus (Escribano-Romero *et al.*, 2004), CBV3 (Zautner *et al.*, 2003), Theiler's murine encephalomyelitis virus (Reddi & Lipton, 2002), some EVs (Goodfellow *et al.*, 2001) and HRV54 (Khan *et al.*, 2007) (Table 3).

Sialic acids are a family of negatively charged sugar molecules located at the cell surface, most often on glycans of glycoproteins, glycosphingolipids, and the proteoglycan keratan sulphate (Angata & Varki, 2002). A couple of enteroviruses, including enteroviruses 70 (Alexander & Dimock, 2002, Haddad *et al.*, 2004, Nokhbeh *et al.*, 2005) and 71 (Yang *et al.*, 2009) and RHV87 (Uncapher *et al.*, 1991), have been reported to use sialic acids.  $\beta$ 2-m associates with MHC class I molecules on the cell surface (Bjorkman *et al.*, 1987, Madden, 1995).

$\beta$ 2-m has been suggested in antibody inhibition studies to function as a receptor for CAV9 (Heikkilä *et al.*, 2010, Triantafilou *et al.*, 1999) and some EVs serotypes including EV1 (Ward *et al.*, 1998).

## 2.5 INTERNALIZATION OF PICORNAVIRUSES INTO HOST CELLS

**Table 4.** Internalization pathways of enteroviruses.

Endocytic pathway	Virus	Reference
<b>Chlathrin-dependent</b>	<b>CBV3</b>	(Chung <i>et al.</i> , 2005)
	<b>EV6</b>	(Leveque <i>et al.</i> , 2007)
	<b>PV</b>	(Kronenberger <i>et al.</i> , 1998, Willingmann <i>et al.</i> , 1989)
	<b>HRV2</b>	(Brabec <i>et al.</i> , 2003, Schober <i>et al.</i> , 1998)
	<b>HRV14</b>	(Grunert <i>et al.</i> , 1997, Schober <i>et al.</i> , 1998)
	<b>HRV16</b>	(Lau <i>et al.</i> , 2008)
	<b>HPEV1</b>	(Joki-Korpela <i>et al.</i> , 2001)
<b>Lipid raft /Caveolae-dependent</b>	<b>CAV9</b>	(Triantafilou & Triantafilou, 2003)
	<b>CBV4</b>	(Triantafilou & Triantafilou, 2004)
	<b>EV1</b>	(Karjalainen <i>et al.</i> , 2008, Marjomäki <i>et al.</i> , 2002, Pietiäinen <i>et al.</i> , 2004)
	<b>EV6</b>	(Leveque <i>et al.</i> , 2007)
	<b>PV</b>	(Coyne <i>et al.</i> , 2007a)
<b>Macropinocytosis</b>	<b>CAV9</b>	(Heikkilä <i>et al.</i> , 2010)
	<b>CBV3</b>	(Coyne <i>et al.</i> , 2007b)
	<b>EV1</b>	(Karjalainen <i>et al.</i> , 2008, Marjomäki <i>et al.</i> , 2002, Pietiäinen <i>et al.</i> , 2004)
<b>Other</b>	<b>PV</b>	(Brandenburg <i>et al.</i> , 2007)
	<b>HRV14</b>	(Khan <i>et al.</i> , 2010)

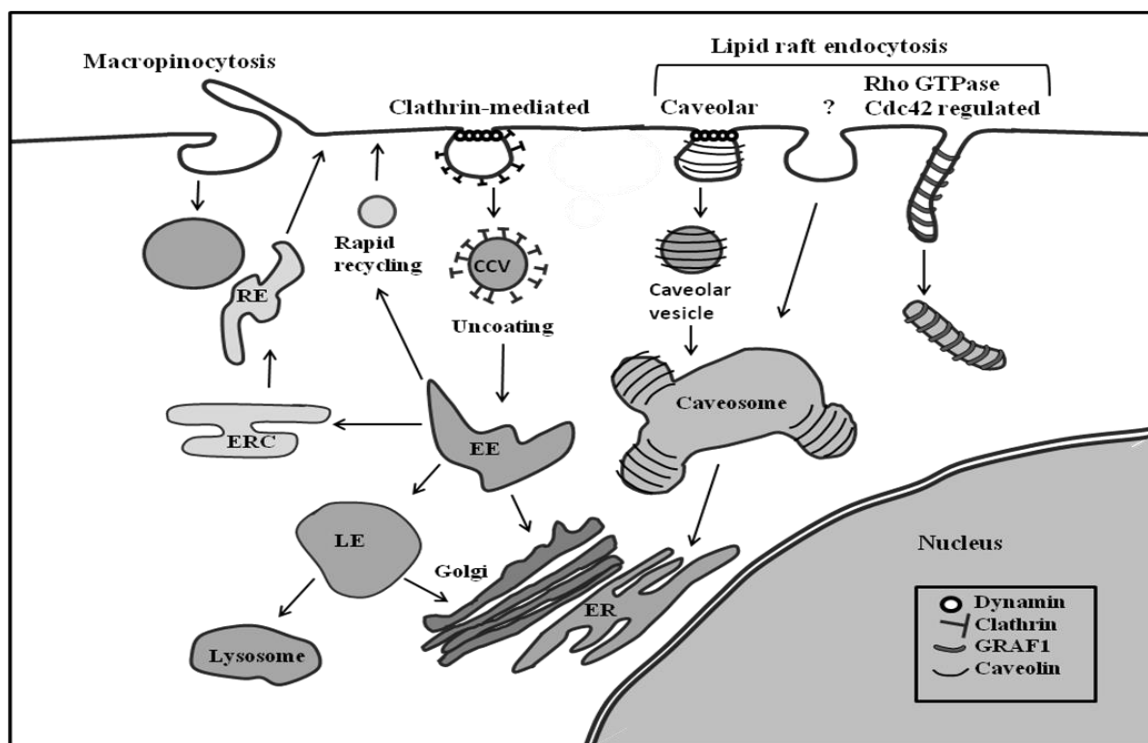
To infect the cell picornaviruses must penetrate the plasma membrane. Most nonenveloped viruses, like picornaviruses, use endocytosis for host cell entry. Picornaviruses enter the host cell by clathrin-dependent and lipid raft/caveolin-dependent pathways and by macropinocytosis (Table 4.). Many viruses are able to switch from one uptake mechanism to another or simultaneously utilize more than one endocytic route (Sieczkarski & Whittaker, 2005).

### 2.5.1 Clathrin-dependent endocytosis

Clathrin-mediated endocytosis is essential for several cellular mechanisms, including nutrient uptake, synaptic vesicle recycling, and transport of receptors and ion channels from the cell membrane (Brodsky *et al.*, 2001, Cremona & De Camilli, 1997, Hirst & Robinson, 1998, Marsh & McMahon., 1999). The clathrin molecule has a conformation of a triskelion with three kinked extensions that radiate from a central vertex (Kirchhausen, 2000). Clathrin-coated pits concentrate cargo proteins for internalization (Kirchhausen, 2000), and internalization can occur constitutively or in response to stimuli. Several proteins, including adaptor complex AP-2, dynamin GTPase, neuronal adaptor protein AP180, CALM (Nonet *et al.*, 1999, Zhang *et al.*, 1998) and Eps 15 regulate the assembly and fission of the pits (Benmerah *et al.*, 1999, Chen *et al.*, 1999). Dynamin GTPase catalyzes vesicle fission upon hydrolysis of GTP (Mettlen *et al.*, 2009). The internalized clathrin-coated vesicle is rapidly uncoated and fuses with early endosomes (EEs) (Chappell *et al.*, 1986). Some ligands detach from their receptors in the slightly acidic milieu of EEs. Endocytosed receptors can be recycled back to the plasma membrane from EEs in a fast (approximately 5 min) or a slow (approximately 15-30min) recycling pathway. In the latter the cargo is first shuttled to endocytic recycling compartment (ERC) before transport to recycling endosome (RE), while in fast recycling the cargo enters directly from EE in RE. Alternatively, the cargo can be transported from EEs to late endosome (LE), with a lower pH in 5 to 15 minutes. The transport from EE to LE has been suggested to be mediated by an endosomal carrier vesicle (ECV) (Clague *et al.*, 1994, Gu & Gruenberg, 1999, Gu & Gruenberg., 2000). Some cargoes are transported from LEs into lysosomes, which have an acidic pH and hydrolytic enzymes for degradation (Fig 6.).

Rab proteins belong to the Ras superfamily of GTPases, which includes four other families; Ras, Rho, Arf and Ran (Garcia-Ranea & Valencia, 1998, Takai *et al.*, 2001). Ras and Rho have a role in cell growth and motility, while Rab, together with the latter two, regulates intracellular trafficking. Several Rabs are involved in clathrin-dependent endocytosis in endosomal vesicles (Table 5). Examples of other important molecules in the clathrin-dependent entry route include the Rab5 effectors, EEA1 and PI(3)K, needed

in EE fusion. EEA1 functions as a tethering protein between two Rab5 positive membranes (Rothman & Warren, 1994).



**Figure 6.** Endocytic pathways. Internalization pathways for cargo include macropinocytosis, clathrin mediated endocytosis and lipid raft endocytosis mechanisms.

Transferrin (Tf) transport is a widely used marker for clathrin-mediated entry. Tf belongs to a family of iron-binding proteins. The iron-Tf complex binds to the transferrin receptor (TfR) and is rapidly endocytosed through clathrin-coated pits (Mellman, 1996). TfR is constitutively endocytosed, and the rate of recycling is further enhanced by Tf binding. From the clathrin-coated vesicle the Tf-TfR is transported to EEs. In the endosomal acidic environment of the EE, iron is released from Tf and the resultant apo-Tf-TfR is recycled to the plasma membrane (Hedman *et al.*, 1987, Morgan, 1996, Qian *et al.*, 1997) in either a rapid or slow recycling route (Grant & Donaldson, 2009).

Several viruses, including adenoviruses, alphaviruses, hantaviruses, orthomyxoviruses, parvoviruses and picornaviruses (DeTulleo & Kirchhausen, 1998, Evans & Almond, 1998, Marsh & Pelchen-Matthews, 2000), utilize clathrin-mediated endocytosis. The incoming viruses are most often exposed to the acidic milieu of endosomes. Many viruses respond to the pH decrease by undergoing changes that lead to endosomal membrane penetration and viral genome release. Some enteroviruses (Table 4), aphthovirus, FMDV and parechovirus HPEV1 are picornaviruses that have been shown to use clathrin-mediated entry.



**Table 5.** Rab proteins involved in clathrin-dependent endocytosis.

<b>Rab</b>	<b>Function</b>	<b>Reference</b>
<b>Rab 4</b>	Rapid recycling from EE to plasma membrane	(Deneka <i>et al.</i> , 2003, Yudowski <i>et al.</i> , 2009)
<b>Rab5</b>	Transport from EE to LE	(Bucci <i>et al.</i> , 1992, Gorvel <i>et al.</i> , 1991)
<b>Rab7</b>	Transport from EE to LE for certain molecules Transport from late LE to lysosome	(Fan <i>et al.</i> , 2003, Feng <i>et al.</i> , 1995, Press <i>et al.</i> , 1998) (Bottger <i>et al.</i> , 1996, Bucci <i>et al.</i> , 2000, Meresse <i>et al.</i> , 1995, Schimmoller & Riezman, 1993)
<b>Rab10</b>	Implicated to be involved in transport between EE and RE	(Babbey <i>et al.</i> , 2006, Chen <i>et al.</i> , 2006a)
<b>Rab11</b>	Transport from EE to ERC Recycling from EE to plasma membrane Transport from ERC to RE and recycling to the plasma membrane	(Naslavsky <i>et al.</i> , 2006) (Sheff <i>et al.</i> , 1999) (Weigert <i>et al.</i> , 2004)
<b>Rab22A</b>	Transport from EE to ERC	(Magadan <i>et al.</i> , 2006)
<b>Rab35</b>	Rapid recycling from EE to plasma membrane	(Kouranti <i>et al.</i> , 2006)

## 2.5.2 Lipid raft/caveolae-mediated endocytosis

Lipid rafts are small (10-200 nm), heterogeneous, highly dynamic, sterol and sphingolipid-enriched domains that compartmentalize cellular processes (Pike, 2006). The main components of lipid rafts are sphingolipids, (glycol-) phospholipids, and cholesterol. Cholesterol partition into sphingolipid bilayer makes it more flexible and enables substantial lateral movement of the lipid rafts in the membrane (Simons & Ikonen, 1997). Small lipid rafts can form larger platforms by protein-protein and protein-lipid interactions (Pike, 2006). Raft formation and/or stabilization is thought to be a highly regulated process that occurs only in response to activation by a stimulus, e.g. receptor clustering (Hammond *et al.*, 2005). Specific proteins, such as caveolins (Mukherjee *et al.*, 1999) and flotillins (Rajendran *et al.*, 2003) are thought to organize rafts into specialized membrane domains.

Lipid rafts have a role in the antigen presentation (Gombos *et al.*, 2004, Gombos *et al.*, 2006), signal transduction and act in sorting of trans-Golgi network (Keller & Simons, 1998, Simons & van Meer, 1988) and endosomes (Mukherjee *et al.*, 1999). Many pathogens, including bacteria (Lafont & van der Goot, 2005) and viruses (Chazal & Gerlier, 2003, Pelkmans, 2005), have evolved to use lipid rafts for their own internalization.

Several receptors and signaling proteins (e.g. Src, Lck, and CD4) are associated with lipid rafts, while others colocalize upon activation (Gupta & DeFranco, 2003, Kabouridis

*et al.*, 1997). Some proteins that lack transmembrane spans are targeted to lipid raft domains, particularly proteins with GPI-anchors (Brown & London, 1998, Gombos *et al.*, 2008). Transmembrane proteins are generally excluded from tightly packed lipid raft structures (Fastenberg *et al.*, 2003, van Duyl *et al.*, 2002). Nevertheless, transmembrane proteins can be directed to lipid rafts by addition of raft targeting signals. At least four different raft-dependent pathways are thought to exist in mammalian cells. These pathways differ in their requirements for dynamin and small GTPases organizing the endocytosis and cargo selection. Two of the pathways are dynamin-dependent, and of those two, one is regulated by caveolin and the other is dependent on RhoA. The two other dynamin-independent lipid rafts are controlled by Rho GTPases Cdc42 and GTPase Arf 6 respectively (Upla *et al.*, 2009).

Caveolae are flask-shaped invaginations in the plasma membrane that contain sphingolipids, cholesterol, polymerase I and transcript release factor (PTRF)-cavin and caveolin proteins (Anderson, 1998, Hill *et al.*, 2008, Simons & Ikonen, 1997). The caveolin proteins are thought to form a hairpin structure in the membrane. They have a central 33-amino acid long hydrophobic domain, with both the N-terminus and C-terminus facing the cytoplasm (Dietzen *et al.*, 1995, Dupree *et al.*, 1993, Monier *et al.*, 1995). Cholesterol binds tightly in a 1:1 ratio to caveolin, and it is crucial for stabilizing of the caveolin oligomers (Monier *et al.*, 1996) and involved in signaling and trafficking mechanisms of caveolae.

Caveolae have been implicated in several functions including cell signaling, vesicular transport and lipid regulation. Caveolar endocytosis is used by natural ligands (e.g. albumin, cholesterol) (Schnitzer *et al.*, 1994, Smart *et al.*, 1996), toxins (e.g. cholera toxin; CTx) (Montesano *et al.*, 1982, Nichols, 2002), bacteria (e.g. *E. coli*) (Shin *et al.*, 2000), viruses (Pelkmans & Helenius, 2002) and prions (Peters *et al.*, 2003). Due to the important regulatory role of caveolae in several signaling cascades, mutations or defects in caveolin proteins contribute to the pathogenesis of some diseases, including type 2 diabetes, cancer, cardiovascular diseases, atherosclerosis, pulmonary fibrosis and some types of degenerative muscular dystrophies (Schwencke *et al.*, 2006).

Caveolae have been suggested to be involved in the regulation of various pathways, including those regulated by integrins, by clearing proteins from the plasma membrane (Pelkmans *et al.*, 2005). Integrins regulate multiple pathways, some of which can be constitutively activated in cancer cells by the lack of cellular regulation by caveolin-1. Caveolin-1 expression is suppressed in some oncogenically transformed cells, leading to the absence of detectable caveolae (Koleske *et al.*, 1995). For instance, decreased caveolin-1 expression in breast cancer cells contributes to higher invasive potential (Sloan *et al.*, 2004). Reexpression of caveolin-1 in tumor cells restores anchorage-dependent growth (Engelman *et al.*, 1997).

Caveolae are partially immobile in the plasma membrane, and activation by ligand binding to receptor may trigger internalization. Tyrosin phosphorylation of caveolin-1 can activate caveolae endocytosis. Internalization activation temporarily recruits GTP-binding protein dynamin to caveolae, triggering fission of caveolae by subsequent hydrolysis of GTP and constriction of caveolae neck. Internalization of caveolae is further dependent on reorganization of the cytoskeleton by depolymerization of actin (Parton *et al.*, 1994). After pinching off from the plasma membrane, caveolae may connect to microtubule-associated proteins for transport (Schnitzer *et al.*, 1995). The cytoplasmic caveolae can fuse with caveosomes (Pelkmans *et al.*, 2001) or alternatively deliver their cargo to endosomal vesicles of the clathrin-mediated pathway (Pelkmans *et al.*, 2004). Caveosomes have a neutral pH, and they are caveolin-1 positive and rich in cholesterol and glycosphingolipids (Pelkmans *et al.*, 2001). The cargo can be delivered from caveolar vesicles and caveosomes further to the endosomes, Golgi, ER or lysosomes, a process that may involve microtubule-directed transport (Conrad *et al.*, 1995, Nichols, 2002).

**Virus entry by caveolar endocytosis.** Since SV40 was shown to enter the cell by caveolar endocytosis (Anderson *et al.*, 1996), a growing number of viruses, including the enteroviruses EV1 (Marjomäki *et al.*, 2002), PV (Coyne *et al.*, 2007a), respiratory syncytial virus (Brown *et al.*, 2002) and filoviruses (Empig & Goldsmith, 2002) were shown to utilize caveolin-mediated endocytosis. A benefit for viruses to use caveolae entry is that they avoid the acidic endosomes/lysosomes. The caveolae-dependent endocytosis transports the pathogens to a specific destination, e.g. SV40 to the endoplasmic reticulum (Pelkmans *et al.*, 2001), cholera toxin to the Golgi compartment (Nichols, 2002) and EV1 to the perinuclear space (Marjomäki *et al.*, 2002). EV1 attaches to the host cell by binding to the  $\alpha 2$  I domain ( $\alpha 2I$ ) of the  $\alpha 2\beta 1$  integrin on the cell surface (Bergelson *et al.*, 1992). In former studies, the virus has been shown to internalize together with the integrin receptor in either caveolin-1 positive or negative vesicles and is later transported to caveosomes (Marjomäki *et al.*, 2002, Pietiäinen *et al.*, 2004). The virus infection was shown to be dependent on dynamin-2 in some cell lines (Karjalainen *et al.*, 2008, Pietiäinen *et al.*, 2004) and partly on cholesterol (Marjomäki *et al.*, 2002, Pietiäinen *et al.*, 2004), and the need of an intact actin cortex was shown to vary according to cell type (Pietiäinen *et al.*, 2004). However, later studies indicate that the majority of the viruses use alternative entry process that is independent of both clathrin and caveolin.

**Picornaviruses utilizing both lipid raft/caveolae and clathrin entry routes.** A few picornavirus serotypes, including CBV3, FMDV and EV6, have been shown to use both lipid raft/caveolin and clathrin-dependent routes of endocytosis, depending on cell type or genetic variation in the virus genome (Chung *et al.*, 2005, Coyne *et al.*, 2007b, Leveque *et al.*, 2007, Wang *et al.*, 1993). CBV3 were found to use clathrin-dependent entry in Hela cells (Chung *et al.*, 2005), while another CBV3 strain infecting HeLa CCL-2 cells required dynamin and lipid rafts (Patel *et al.*, 2009). In polarized epithelial cells, virus

entry from tight junction (TJ) is dependent on caveolin, Ras, Rab5 and Rab34 GTPases involved in macropinocytoses and independent of dynamin (Coyne *et al.*, 2007b). FMDV that is virulent for susceptible animals has been shown to attach to five different integrins (table 3) (Ruiz-Saenz *et al.*, 2009). Tissue culture adaption of some FMDV serotypes causes loss of virulence in animals and integrins as cellular receptors. Instead, those serotypes utilize cell surface HS molecules as receptors. In two strains of genetically engineered FMDV, the first was able to bind to both HS and integrin and entered the cells by both clathrin and caveolin-mediated entry, while the second that only utilized HS as cellular receptor colocalized with caveolin (ODonnell *et al.*, 2008). The cell entry of two strains of EV6 was studied, where one had the ability to hemagglutinate human erythrocytes, a feature related to the virus attachment to DAF (Powell *et al.*, 1999), while the other virus strain had lost its hemagglutinating capacity due to inability to attach to DAF. DAF are concentrated in the plasma membrane within the lipid rafts domain. DAF-binding EV6 strain did enter through a lipid raft-dependent pathway, while the non-DAF-binding strain endocytosed through clathrin-directed pathway (Leveque *et al.*, 2007).

**Other endocytotic pathways through lipid rafts.** In addition to caveolae entry, at least three other lipid raft endocytotic pathways have been proposed to exist. These include a dynamin-dependent pathway regulated by RhoA. RhoA GTPases are important in the regulation of cytoskeletal dynamics and are connected to several cellular processes, including vesicular transport. The two other lipid rafts-mediated entry pathways are dynamin-independent. One of them is controlled by Rho GTPases Cdc42, while the other is regulated by GTPase Arf 6. Activity of Rac1, Cdc42, N-WASP and a GTPase regulator, connected with a focal adhesion kinase 1 upstream of Cdc42 (Lundmark *et al.*, 2008), triggers the forming of acidic endocytotic vesicles called clathrin-independent carriers (CLICs) (Chadda *et al.*, 2007, Kalia *et al.*, 2006, Kumari & Mayor, 2008, Sabharanjak *et al.*, 2002). The CLICs obtain Rab5 and EEA1 and fuse with other CLICs forming GPI-anchored, protein-enriched early endosomal compartments (GEECs). The GEECs subsequently fuse with the sorting endosomes of the clathrin pathway in a process that needs both PI3K and Rab5 (Kalia *et al.*, 2006).

Arf6-dependent lipid raft recycling internalization pathways have been reported to be utilized by GPI-anchors and some integral membrane proteins, such as  $\beta$ 1-integrins. The internalized molecules enter phosphatidylinositol-(4,5)-bisphosphate (PIP<sub>2</sub>)- and cholesterol-containing membranes before being transported to the sorting endosomes of the clathrin pathway. The cargo can be further transported to recycling endosomes by a Rab22-dependent process or alternatively shuttled to the lysosomal vesicles.

Flotilins are raft-associated proteins that are located in microdomains and able to form membrane curvature and endocytosis (Babuke & Tikkanen, 2007, Frick *et al.*, 2007, Glebov *et al.*, 2006). The regulation mechanism for this entry process is still unsolved. EV1 have been reported to use an alternative entry process that is independent of both

clathrin and caveolin and in some cell types of dynamin. The virus attached to a lipid raft is internalized in endosomes that mature further into multivesicular structures which recruit caveolin-1 by fusing with caveolae or caveosomal structures, thus forming structures that may be considered as late caveosomes (Karjalainen *et al.*, 2008).

### 2.5.3 Macropinocytosis

By macropinocytosis, cells are able to take up large quantities of extracellular fluids and macromolecules. Some microbial pathogens also utilize this pathway to enter the cells. Macropinocytosis is either a stimulated or constitutively active process depending on the cell type. Dendritic cells take up antigens and, after processing them into peptides, present them to T-cells. Macropinocytosis is driven by actin polymerization causing circular ruffles of the plasma membrane to form large endocytotic macropinosome vesicles. Mostly macropinocytosis is growth factor-induced, although various molecules can induce ruffling independent of growth factors (Mercer & Helenius, 2009). Macropinocytosis can be induced by external stimulation, e.g. by growth factors that trigger activation of receptor tyrosine kinase (RTKs), which leads to a signaling cascade that alters the dynamics of actin filaments and results in ruffling. Ras superfamily GTPases are important in this process, and RTK activation of Ras activates three parallel signaling pathways containing Rac1, Rab5, Arf6 and phosphatidylinositol-3-kinase (PI(3)K) (Bar-Sagi & Feramisco, 1986, Bar-Sagi *et al.*, 1987), which together cooperate to modulate ruffle formation, macropinosome closure and membrane transport (Lanzetti *et al.*, 2004).

Several kinases are crucial for macropinocytosis, and one of the most important is the p21-activated kinase 1 (Pak1), a serine/threonine kinase activated by Rac1 and Cdc42. Pak1 is needed during all stages of macropinocytosis. It regulates cytoskeleton dynamics and motility and activates numerous effectors needed for membrane ruffling and macropinosome closure (Dharmawardhane *et al.*, 2000, Liberali *et al.*, 2008, Parrini *et al.*, 2005). Other kinases, important for membrane ruffling and macropinosome formation are protein kinase C (PKC) (Amyere *et al.*, 2000, Miyata *et al.*, 1989) and c-Src. Na<sup>+</sup>/H<sup>+</sup> exchangers are also important markers for the macropinosome (West *et al.*, 1989).

Macropinocytosis has been reported in several studies to be used as an entry route by viruses, including vaccinia virus, rubella virus, human immunodeficiency virus type I (HIV-1), herpes simplex virus 1 (HSV1) and adenoviruses (Ad) (Mercer & Helenius, 2008). Some viruses are thought to use macropinocytosis as a direct endocytotic route, while others may use it indirectly to assist in viral infection and simultaneously use other endocytotic mechanisms (Mercer & Helenius, 2008). Two enteroviruses, EV1 and CBV3, have so far been suggested to use macropinocytosis in their entry. EV1 is attached to its receptor, the  $\alpha 2\beta 1$  integrin, and internalized into vacuolar structures. The infection was

shown to be dependent on several molecules known to be involved in macropinocytosis, such as Pak1, PI(3)K, PLC, Rac1 and Na<sup>+</sup>/H<sup>+</sup> exchangers. The infection required cholesterol and actin dynamics (Karjalainen *et al.*, 2008) and was further shown to be dependent on C-terminal-binding protein-1/brefeldinA-ADP ribosylated substrate (CtBP1/BARS) (Liberali *et al.*, 2008). In polarized epithelial cells, CBV3 enters cells from epithelial TJ within macropinosomes (Coyne *et al.*, 2007b). Virus entry was dependent on caveolin, Ras, Rab5 and Rab34 GTPases, Na<sup>+</sup>/H<sup>+</sup> exchangers and PKC, but independent of dynamin (Coyne & Bergelson, 2006).

## 2.6 HOST GENE EXPRESSION INDUCED BY ENTEROVIRUS INFECTION

Enterovirus infections are able to cause dramatic change in the host cell. Certain enteroviruses, such as PV1 (Johannes *et al.*, 1999), EV1 (Huttunen *et al.*, 1997, Huttunen *et al.*, 1998, Pietiäinen *et al.*, 2000) and EV7 (Huttunen *et al.*, 1997) have been shown to affect the expression of eukaryotic immediate early genes (IEGs). Many enteroviruses have been shown to control cell death by either activating or inhibiting apoptosis. In addition, in PV infected cells concomitant activation of both apoptotic and antiapoptotic pathways has been shown to occur (Autret *et al.*, 2008).

**Immediate early genes (IEGs)** are a class of genes that are rapidly and usually transiently activated in response to a wide variety of cellular stimuli (Soloaga *et al.*, 2003). The induction of IEGs occurs in the absence of de novo protein synthesis (Platenik *et al.*, 2000). IEGs function for instance as chemo-attractants, cytoplasmic enzymes, ligand-dependent transcription factors and inducible transcription factors (ITFs), including the Fos protein family (FOS, FOSB, Fra-1, Fra-2), Jun (JUN, JUNB, JUND) (Herdegen & Leah, 1998) and some members of activating transcription factors (ATF) (e.g ATFa, ATF-2 and ATF2, ATF3). These genes are components of the dimeric AP-1 transcription factor that regulates a wide range of cellular processes, such as cell proliferation, cell survival and differentiation (Shaulian & Karin, 2002).

Several IEGs have been determined to be increased during EV1 infection. The transcription of IEGs JUN, JUNB, and FOS has been shown to increase 5-10 h p.i. in EV1-infected cells in a Northern blot analysis (Huttunen *et al.*, 1997) and in studies measuring the transcriptional rate of the genes (Huttunen *et al.*, 1998). EV1 infection causes activation by phosphorylating both the stress-related p38 mitogen-activated protein kinase (MAPK) and the growth signal-related ERK1/2 MAPKs. The growth signal-related ERK1/2 MAPKs pathway leads to induction of FOS, whereas p38 MAPK were involved in the increased expression of JUNB (Huttunen *et al.*, 1998). Furthermore, in a microarray study, EV1 infection induced expression of two IEGs, Fos related antigen (Fra-1) and

early growth response 1 (EGR1) 6 h p.i. 10 h p.i induction of both of these IEGs was even more strongly induced and the expression of a few additional IEGs was increased, including JUN, Krueppel-like factor 10 (KLF10) and c-myc (Pietiäinen *et al.*, 2000).  $\alpha 2\beta 1$  integrin-mediated cell adhesion to type I collagen is known to induce certain IEGs. However, IEGs activation has not been observed during early time points of virus attachment and endocytosis, suggesting viral replication to be essential for the induction of these genes (Huttunen *et al.*, 1997, Pietiäinen *et al.*, 2000). This view was supported by the fact that transfection of cells with viral EV1 RNA induced the activation of JUNB and that the induction of FOS, JUN and JUNB were also observed in EV7 infected HOS  $\alpha 2\text{AW}$  cells (Huttunen *et al.*, 1997).

Similar pattern of induction of IEGS in host cells has been shown to occur during the infection of other enteroviruses. In PV-infected Hela cells, the expression of some IEGs was found to be increased upon the infection (Johannes *et al.*, 1999). These IEGs included ATF3, c-myc, cysteine-rich, angiogenic inducer, 61 (CYR61), Pim-1 and KLF10. In another study, PV-infection also induced increased expression of Pim-1, c-myc and JUN (Pietiäinen *et al.*, 2000). In line with these studies, CBV3 infection was found to transiently upregulate ATF3, JUN, FOS (McManus *et al.*, 2002), CYR61 and KLF10 (Kim *et al.*, 2004). Furthermore, the gene expression profile of CBV3-infected mouse hearts showed upregulation of the expression of ATF4, ATF3 and ATF4 (Shaulian & Karin, 2002). They can act as transcriptional repressors or attach to JUN in order to induce cellular transcription. In a murine model of chronic CBV3 myocarditis, the expression of connective tissue growth factor (CTGF) was found to be highly induced (Lang *et al.*, 2008).

**Apoptosis-related genes.** Apoptosis is an active process of cell death characterized by DNA fragmentation, nuclear chromatin condensation, membrane blebbing and cell shrinkage (Arends *et al.*, 1990). Caspases are molecules involved in apoptosis, which belong to a family of cysteine proteases located mainly in the cytosol in the form of inactive procaspase. Caspases need proteolytic cleavage for activation. Apoptosis is crucial for normal tissue physiology, and disturbed ability of apoptosis is responsible for various disorders, such as genetic and autoimmune diseases, neurodegenerative disorders and cancer. Furthermore, apoptosis is an effective process by which a virus can induce cell death, spread progeny and concomitantly reduce inflammatory and immune response (Buenz & Howe, 2006, Everett & McFadden, 2001).

RNA viruses, like the enteroviruses, replicate much more efficiently than large and slow replicating DNA viruses, and their multiplication appears to benefit from rapid initiation of cell death. Enterovirus infection can trigger either canonical cytopathic effect (CPE) or apoptosis, or both, in host cells (Buenz & Howe, 2006). Several studies have proposed anti-apoptotic response from enterovirus infection, counteracting the intrinsic apoptosis program triggered by virus-induced modifications in host cell metabolism (van

Kuppeveld *et al.*, 2005). However, full-scale apoptosis seems to be activated only at the end of enterovirus growth cycle after completed viral replication, indicating anti-apoptotic delay rather than blocking of the apoptosis pathway (van Kuppeveld *et al.*, 2005). Regardless of the short replication cycle, these viruses are also able to cause persistent infection (Buenz & Howe, 2006), affecting the apoptotic balance and escaping the immune defense. Apoptosis may also be involved in the pathogenesis of enterovirus diseases, such as myocarditis and dilated cardiomyopathy (Carthy *et al.*, 1998), as well as neurological diseases (Chen *et al.*, 2007).

Enteroviruses have been reported to either favor or inhibit apoptotic events in the cell. EV71 induced apoptosis in neuronal cells caused stimulation of c-Abi activity, which lead to the phosphorylation and activation of Cdk5 (Chen *et al.*, 2007). CBV3-induced apoptosis has been found to require activation of the MAPK pathway (Luo *et al.*, 2002). CBV3 infection is frequently the cause of virus-induced myocarditis, and a critical determinant of the severity of the disease is early onset of apoptosis (Tam, 2006, Yang *et al.*, 1999). However, CBV3 infection has also been shown to promote cell survival by degradation of p53 and downregulation of ATF3 (Hwang *et al.*, 2007). PI3K/Akt, which has been reported to play an anti-apoptotic role in numerous viral infections (Cooray, 2004), has been reported to have a role in the regulation of apoptosis during CBV3 (Esfandiarei *et al.*, 2004), PV (Autret *et al.*, 2008) and EV71 (Tung *et al.*, 2007, Wong *et al.*, 2005) infection. PV is able to prevent tumor necrosis factor (TNF)-triggered apoptosis by abolishing the cytokine receptor from the cell membrane (Neznanov *et al.*, 2001).

Depending of the phase in the PV infection cycle, the virus has been shown to promote either cell survival or apoptosis. In PV-infected cells, the amount of phosphorylated Akt increased until 30 min p.i and then decreased at 4 h p.i. to a level similar to mock infected cells (Autret *et al.*, 2008), and later (6h p.i.) apoptosis was triggered by a c-Jun NH2-terminal kinase (JNK) reaction cascade (Autret *et al.*, 2007).

## **2.7 TYPE 1 DIABETES**

Type 1 diabetes (T1D) accounts for 5-10% of all the cases of diabetes. It is characterized by progressive destruction of insulin-producing  $\beta$ -cells in the pancreatic islets (Devendra *et al.*, 2004). The destructive process can start years before the first clinical symptoms. Two distinct forms of T1D have been identified: type 1A is caused by cell-mediated autoimmune attack on  $\beta$ -cells (Devendra *et al.*, 2004), whereas type 1B is considerably less frequent, has no known cause, is characterized by varying degrees of insulin deficiency as well as by sporadic periods of ketoacidosis (Abiru *et al.*, 2002). Susceptibility to T1D is largely inherited, and over 40% of the familial clustering of T1D



can be attributed to genetic variation in the human leukocyte (HLA) region. The direct involvement of HLA class II DRB1, DQA1 and DQB1 genes is well recognized. The most predisposing DRB1-DQB1 haplotypes are DR3 (DRB1\*0301, DQA1\*0501, DQB1\*0201) and DR4 (DRB1\*0401/2/4/5, DQA1\*0301, DQB1\*0302). Of these, the most predisposing are DRB1\*04 subtypes (0401 and 0405). In addition, other allelic variation affecting susceptibility for T1D has been found in classical HLA loci, in class I and DPB1, and in recent research the region of MHC class III has been of particular interest (Valdes *et al.*, 2010). Clinical T1D starts to develop when one or more environmental triggers alter the immune function to initiate  $\beta$ -cell destruction. Several different environmental factors are thought to have a role in this process. These include viruses (e.g. enteroviruses, rubella virus, endogenous retroviruses and human cytomegalovirus) (Lammi *et al.*, 2005), bacterial toxin (bafilomycin A1) (Myers *et al.*, 2001, Myers *et al.*, 2002), environmental toxins (e.g. nitrosamines) (Helgason & Jonasson, 1981), nutrition (e.g. early exposure to cow's milk proteins, cereals or gluten) (Akerblom *et al.*, 2002, Norris *et al.*, 2003, Thorsdottir & Ramel, 2003, Vaarala *et al.*, 1999, Virtanen *et al.*, 2000), overweight (earlier onset of T1D in obese children) (Betts *et al.*, 2005) and increased hygiene (atopic disorders and T1D are more common in affluent societies than in traditional societies with a lower degree of hygiene) (Beyan *et al.*, 2003, Kaila & Taback, 2001).

The pathogenesis of T1D is associated with inflammatory response with infiltration of lymphocytes in the islet of Langerhans and production of autoantibodies against  $\beta$ -cell antigens. There are three autoantibodies that have been shown to predict clinical T1D. These include insulin autoantibodies (IAA), autoantibodies to the 65 kD isoform of glutamic acid decarboxylase (GADA), and the phosphatase-related islet antigen 2 (IA-2). In addition, recently an additional autoantigen in T1D, a zinc transporter 8 (ZnT8), was detected (Wenzlau *et al.*, 2007).

The most important group of viruses that has been associated with type 1 diabetes (T1D) are enteroviruses (Barrett-Connor, 1985, Hyöty & Taylor, 2002, Roivainen *et al.*, 1998). They replicate in various target organs including the pancreas (Kaplan *et al.*, 1983). Association with T1D and enterovirus infections has been reported in prediabetic children (Hiltunen *et al.*, 1997, Hyöty *et al.*, 1995), adults (Andreoletti *et al.*, 1997, Gamble *et al.*, 1969), and infections during pregnancy may contribute to early onset of T1D in childhood (Dahlquist *et al.*, 1995). Increased prevalence of enterovirus RNA and higher antibody levels against CBVs have been reported in individuals with recent onset of T1D (Andreoletti *et al.*, 1997, Gamble *et al.*, 1969, Lönnrot *et al.*, 2000). In a recent study, immunohistochemistry staining with enterovirus capsid protein vp1 antibody of autopsy samples showed increased enterovirus prevalence in the islets of patients with recent-onset T1D diabetes (Richardson *et al.*, 2009).

Several enteroviruses have been suggested to have a role in the onset of T1D. CBVs, especially serotype CBV4, CAV9 and several serotypes of EVs, such as EV3, 6, 9, 16, 21

and 30, have been associated with T1D (Elshebani *et al.*, 2007, Roivainen, 2006, Williams *et al.*, 2006). In fact, all enteroviruses that have been investigated in islet cell culture or in animals studies contain strains that are able to damage  $\beta$ -cells (Roivainen & Klingel, 2009). In a non-obese diabetic (NOD) mouse study, only a minority of different CBV4 strains were able to induce diabetes (Yoon *et al.*, 1986). However, there is evidence that some enteroviruses, like CBVs, are less prevalent in countries with high incidence of T1D, e.g. Finland, than in genetically similar populations with a low incidence of T1D (e.g. Russian Karelia) (Viskari *et al.*, 2005). Frequency of enterovirus infections has decreased during the 1980s and 1990s, while the incidence of type 1 diabetes has increased (Viskari *et al.*, 2004), suggesting an inverse relation between enterovirus infection and frequency of T1D. In addition, pregnant women in Finland had lower enterovirus antibody levels than those in Estonia and Karelia (Viskari *et al.*, 2005). The neutralizing antibodies from the mother protect the child from infection during the first 3 to 9 months of age. Enterovirus infection during 6-12 months of age has been shown to decrease the risk of T1D (Blom *et al.*, 1991, Gibbon *et al.*, 1997, Pundziute-Lycka *et al.*, 2000), while severe neonatal infections are a risk factor for diabetes (Anonymous, 2000, Dahlquist *et al.*, 1999). Similar results have been obtained in a study with NOD mice, where early (pre-insulinitis) caused by CBV infection, protected against T1D, while later infection after development of insulinitis could accelerate the onset of diabetes (Serreze *et al.*, 2005).

The mechanisms by which enteroviruses are able to affect T1D pathogenesis are still largely unsolved, but evidence supporting a few different alternatives exist, including direct destruction of islets, molecular mimicry, bystander destruction and viral persistence (Richer & Horwitz, 2009).

Enterovirus infection both in prediabetic individuals and individuals with newly diagnosed T1D has been associated with antibodies against T1D-related antigens, such as glutamic acid decarboxylase (GAD65) (Baekkeskov *et al.*, 1990), insulin (Palmer, 1987), tyrosine phosphatases IA-2 and IA-2beta (Notkins *et al.*, 1998) and heat shock protein 60/65 (Birk *et al.*, 1996, Elias *et al.*, 1990). In a study by Elshebani *et al.*, isolated enteroviruses replicated in human  $\beta$ -cells and caused destruction of a share of the cells. However, insulin secretion was reduced in all infected cells, suggesting that these effects on  $\beta$ -cells could lead to cellular stress, possibly triggering mechanisms that could affect the development of T1D (Elshebani *et al.*, 2007). It has been speculated that enteroviruses cause infection leading to engulfment of the infected islets and presentation of  $\beta$ -cell antigens in an inflammatory process, a mechanism that has been referred to as bystander destruction (Horwitz *et al.*, 1998). The contribution of the bystander mechanism is supported by a study where patients with newly diagnosed T1D were found to have increased levels of IFN- $\alpha$  and half of these patients were concomitantly positive for enterovirus RNA (Chehadeh *et al.*, 2000). Furthermore, local infection in non-islet cells of the pancreas might cause inflammation and cytokine-mediated  $\beta$ -cell damage and

destruction of  $\beta$ -cells, resulting in exposure of previously hidden autoantigens and stimulation of autoreactive T cells, a process referred to as the ‘‘innocent bystander’’ mechanism (Horwitz *et al.*, 1998). CBV4 and probably most of the enteroviruses can trigger production of pro-inflammatory cytokines, such as IL-1 $\beta$ , TNF- $\alpha$ , IL-2 and the type 1 interferons (Vreugdenhil *et al.*, 2000).

In addition, enterovirus infection in any tissue might induce antiviral responses that cross-react with autoantigens. This could lead to decreased tolerance to certain antigens and autoimmunity (Atkinson *et al.*, 1994, Kaufman *et al.*, 1993, Vreugdenhil *et al.*, 1998). The cross-reactivity could arise from molecular mimicry, where similar structures are shared between viral and host molecules (Maclaren & Atkinson, 1997, Oldstone, 1998). Possible immunological cross-reactivity between enteroviral proteins (2C, VP1 and VP0) and  $\beta$ -cell autoantigens (GAD-65, IA-2/IA-2beta and HSP-60) has been documented (Härkönen *et al.*, 2002, Härkönen *et al.*, 2003, Varela-Calvino & Peakman, 2003). It has been suggested that CBV4 infection could lead to activation of T lymphocytes that cross-react with pancreatic  $\beta$ -cells. In studies with CBV4, cross-reactivity has been detected between homologous regions of the virus antigens and GAD65 and IA-2/IA-2beta (Härkönen *et al.*, 2002, Kaufman *et al.*, 1992). A conserved region of the VP1 region of the virus was found to cross-react with IA-2/IA-2beta (Härkönen *et al.*, 2002). GAD65 was found to share a sequence homology with CBV4 protein and 2C protein (Kaufman *et al.*, 1992). GAD65 have been shown to be able to activate Th1 cells to secrete IFN- $\gamma$ , which seems to have a role in the pathogenesis of T1D (Karlsson & Ludvigsson, 1998). However, this hypothesis has been criticized because of the fact that T-cells do not cross-react with GAD in vitro (Denman & Rager-Zisman, 2004, Roep *et al.*, 2002). The role of GAD65 for T1D development has been tested in vivo. In a study with GAD65-deficient NOD mice, the cumulative incidence of autoimmune diabetes was not influenced by this gene (Atkinson & Leiter, 1999). Moreover, CBV infections were found to be frequently associated with immune reactions against GAD, but the reactions were transient (Cainelli *et al.*, 2000). This suggests that other environmental factors are included in the development of clinical disease. IA-2 autoantibodies have also been detected in patients after enterovirus infection, e.g. in a case of EV9 infection and acute onset of T1D (Vreugdenhil *et al.*, 2000), and in a prediabetic individual, EV3 infection induced prolonged secretion of this autoantibody (Williams *et al.*, 2006). VP1 of CAV9 has shown cross-reactivity with HSP60 (Härkönen *et al.*, 2003). However, mimicry is very common in nature, suggesting that the cause is not the phenomenon as such, but rather the crucial factor might be impaired immune regulation.

Fulminant type 1 diabetes, a subtype of type 1B diabetes is characterized by abrupt destruction of  $\beta$ -cells and onset of acute hyperglycemia and ketoacidosis (Imagawa *et al.*, 2000, Tanaka *et al.*, 2000). A recent report by Tanaka *et al.* suggested a role for enteroviruses in fulminant type 1 diabetes in three affected pancreata. They implicated that

expression of interferon- $\gamma$  and CXC chemokine ligand 10 (CXCL10) are initiated in the  $\beta$ -cells of enterovirus-infected pancreas (Tanaka *et al.*, 2009). This was in line with a former study showing that enterovirus infection of pancreatic  $\beta$ -cells induced CXCL10 expression within 1-2 days after infection (Berg *et al.*, 2006, Hultcrantz *et al.*, 2007). CXCL10, secreted from the  $\beta$ -cells, activates and enhances infiltration of T-cells and macrophages to the islet cells. These cells then release inflammatory cytokines, including interferon- $\gamma$ , simultaneously damaging the islets and further increasing CXCL10 secretion, leading to accelerated cell-mediated autoimmunity and complete  $\beta$ -cell destruction (Tanaka *et al.*, 2009). These results were further supported by the lack of induction of CXCL10 or interferon- $\gamma$  in pancreatic  $\beta$ -cells from slowly developing T1D (Tanaka *et al.*, 2009).

### **3 AIMS OF THE STUDY**

Integrins are a family of transmembrane glycoproteins that interact with the ECM in cell adhesion and migration. Altered expression of integrins in tumor cells contributes to metastasis tendency by influencing attachment to adjacent cells, migration and survival. In addition to natural ligands (such as vitronectin and collagen), viral pathogens including certain enteroviruses utilize integrins to enter host cells. Enteroviruses cause a wide spectrum of illnesses varying from common cold to myocarditis and paralysis. Several studies have suggested that enteroviruses could also be involved in the etiopathogenesis of type 1 diabetes.

#### **SPECIFIC AIMS:**

##### **1. The role of integrins in the pathogenesis of metastasis to cortical bone**

- To study if certain integrins play a role in the initial attachment of mammary carcinoma cells to bone.
- To study if collagen type 1 would be important in this attachment of tumor cells to the skeletal tissue.
- To determine whether the type and amount of integrins expressed on the cell membrane of various tumors correlates with their capability to attach to cortical bone.

##### **2. The relevance of polymorphism in enterovirus receptors in type 1 diabetes**

- To study if susceptibility to enterovirus infections and/or frequency of the occurrence of enterovirus antibodies in prediabetic and diabetic children would correlate with variation in the enterovirus receptor genes.

##### **3. Altered targeting of echovirus 1 from the lipid raft/caveolae internalization route to the clathrin pathway**

- To produce a chimeric molecular construct, in which the  $\alpha 2 I$  domain of  $\alpha 2 \beta 1$  integrin was inserted into the extracellular terminus of the transferrin receptor, which is endocytosed via the clathrin-dependent route instead of the lipid raft/caveolae internalization pathway originally used by the virus.
- To determine whether the altered receptor and entry route permits successful internalization and initiation of EV1 infection.

##### **4. Cellular gene expression during EV1 infection**

- To investigate the cellular gene expression profile induced by EV1 infection with specific emphasis on immediate early genes.

## 4 MATERIALS AND METHODS

### 4.1 Viruses (II, III)

Coxsackievirus A9 (CAV9), coxsackievirus A18 (CAV18), coxsackievirus A21 (CAV21), coxsackievirus B (CBV) 1-6, echovirus 1 (EV1), echovirus 6 (EV6), echovirus 7 (EV7), echovirus 11 (EV11), echovirus 30 (EV30), human rhinovirus 2 (HRV2), human rhinovirus 14 (HRV14) and human parechovirus 1 (HPV1) were originally obtained from the American Type Culture Collection (ATCC). The poliovirus strains used were the Sabin vaccine strains 1-3 (ATCC). These viruses were used in the neutralization assays (see below). EV1 (Farouk strain; ATCC) was propagated in green monkey kidney (GMK) cells, the infected cells and the supernatant were freeze-thawed three times and the virus was precipitated by PEG/NaCl and purified by ultracentrifugation in 5-20% sucrose gradients (Abraham & Colonno, 1984). The infectivities of the viruses were determined by plaque titration.

### 4.2 Antibodies and other reagents (I, III)

The following antibodies were used: rabbit antiserum and mouse monoclonal antibody (MAb) against caveolin-1 (Transduction Laboratories); anti-CD49b MAb (Immunotech), A211E10, recognizing the I domain of the  $\alpha 2$  integrin (a kind gift from Fedor Berditchevski, Institute of Cancer studies, Birmingham, UK); blocking MAb antibodies against  $\alpha 2$  (P1E6),  $\alpha 3$  (P1B5),  $\alpha 4$  (P4G9), and  $\alpha 5$  (P1D6) and  $\beta 1$  (P4C10) subunits of integrin receptors (GIBCO); mouse anti-human integrin  $\alpha v\beta 3$  monoclonal antibody (Chemicon); rabbit anti-bovine collagen type I polyclonal antiserum (Chemicon); rabbit antiserum against Rab11 (Zymed); rabbit antiserum against Rab4 (Abcam); rabbit antiserum against mannose 6 phosphate receptor (CI-MPR) (Marjomäki *et al.* 1990); MAb against EEA1 (Transduction Laboratories); MAb PDI (1D3; Stressgen) a rat monoclonal antibody (1D4B) against Lamp1 (the Development Hybridoma Bank, University of Iowa), mouse anti-GM130 (BD Transduction Laboratories), mouse anti-TfR (Zymed); rabbit antiserum against transferrin (Dakopatts); rabbit antiserum against the late endosome marker 6C4 (a kind gift from Jean Gruenberg, Department of Biochemistry, Geneva, Switzerland); and rabbit antiserum against purified EV1 (Marjomäki *et al.* 2002), adsorbed on SAOS- $\alpha 2\beta 1$  cells to reduce the background and subsequently filtered. Alexa Fluor (AF) 488-conjugated goat anti-rat IgG, AF488- and AF555-conjugated goat anti-mouse IgG and anti-rabbit IgG (Molecular Probes), as well as PE-conjugated rat anti-mouse IgG (BD Transduction Laboratories) were used as secondary antibodies. Human transferrin (Tf) (Sigma), AF488- and AF568-conjugated Tf

(Molecular Probes) were also used. Blocking RGDS peptide was from GIBCO. Collagenase type I, Chlorpromazine hydrochloride and nocodazole were purchased from Sigma.

### **4.3 Cell cultures (I-III) and transfections (III)**

Several different cell lines were used in the studies, including human cervical cancer cells (HeLa), human lung carcinoma A-549 cells, green monkey kidney (GMK) cells, mouse fibroblast cells (NIH3T3), Chinese hamster ovary (CHO) cells, baby hamster kidney cells (BHK-21), human osteosarcoma cells (SAOS), human breast cancer cells (MDA-MB-231), human neuroblastoma cells (SH-SY5Y), human T-cell leukemia cell line jurkat, rhabdomyosarcoma (RD) cells and prostate cancer cells (PC-3). All these cells were originally obtained from the ATCC. The SAOS- $\alpha 2\beta 1$  cell line was obtained by stable transfection of the SAOS cells, with expression of a construct encoding the  $\alpha 2$  integrin (Ivaska et al., 1999). NIH3T3, CHO, BHK-21, SAOS, SAOS- $\alpha 2\beta 1$ , MDA-MB-231, SH-SY5Y, RD and PC-3 cells were grown in DMEM. GMK cells were propagated in MEM medium. A549 cells were cultured in F12 medium. Jurkat and Hela cells were grown in RPMI-1640 culture medium. The different culture mediums were supplemented with 10% fetal calf serum (FCS), 100 IU/ml penicillin, and 100  $\mu$ g/ml streptomycin. The SAOS- $\alpha 2\beta 1$  cells were cultured in the presence of a selection antibody (200  $\mu$ g/ml of G418; Gibco). Transient transfections with the constructs pcDNA/Zeo3.1-TfR- $\alpha 2$ I and -TfR were performed in subconfluent NIH3T3, BHK-21 and CHO cells with Lipofectamine 2000 (Invitrogene) according to the manufacturer's instructions.

### **4.4 RNA and DNA purification (II)**

Confluent A-549 cells, infected with 20 MOI of EV1, were collected after 30 min, 2 h, 4 h, 6 h and 10 h. Total cellular RNA was in a guanidinium lysis buffer and frozen at  $-70^{\circ}\text{C}$ . Total RNA was purified by ultracentrifugation thiocyanate-CsCl method (Chirgwin *et al.*, 1979). Furthermore, the RNA was DNase (Sigma) treated according to the manufactures instructions. Alternatively, total RNA was purified according to the manufacturer's instructions using RNeasy Mini kit (Qiagen) supplemented with QIAshredder (Qiagen) for homogenization of cells and RNase-FreeDNase Set (Qiagen) to remove DNA completely during RNA purification.

DNA was isolated from peripheral blood mononuclear cells (PBMCs) by two methods; NucleoSpin blood kit (Macherey-Nagel), which was used according to the manufacturer's instructions, and a non-enzymatic method for purification of DNA from blood (Lahiri &

Nurnberger, 1991). In the latter method, PBMCs were lysed with Nonidet P-40 (Sigma) and centrifugated. The protein was separated from the nuclear pellet by incubation with sodium dodecyl sulfate (SDS) and NaCl precipitation. After centrifugation the DNA from the supernatant was extracted by ethanol precipitation.

#### **4.5 Design of primers, construction of the chimeric receptor and sequencing (II, III)**

Oligonucleotide primers for polymerase chain reaction (PCR) were selected from the region of receptor sequence coding for domains shown to be crucial for enterovirus binding (II, Fig 1, Table 1). The oligonucleotide primers for PVR were from exon 2. The ICAM-1 primers, amplifying receptors for the major group of HRV and some CAVs were from exon 2. The oligonucleotides for CAR were from exons 2 to 5. The oligonucleotide primer for the two integrins,  $\alpha 2\beta 1$  and  $\alpha \nu\beta 3$ , were selected from exon 7 of integrin alpha 2 I-domain and exon 4 of the  $\beta 3$  subunit. The DAF oligonucleotides spanned the SCR2, SCR3a and SCR3b regions.

For construction of a chimeric receptor consisting of TfR and  $\alpha 2I$ , oligonucleotide primers were designed for the  $\alpha 2I$  and the complete TfR. For the cloning procedure, BamHI restriction site was added to the 5' end and NotI site to the 3' end of the TfR sequence, and NotI and XbaI sites to the 5' and 3' ends of the  $\alpha 2I$  sequence.

For amplification of PVR, ICAM-1, DAF, CAR, integrin subunits  $\alpha 2$  and  $\beta 3$ , DNA purified from PBMCs was used as template for the generation of the PCR products by AmpliTaq Gold DNA-polymerase (Perkin-Elmer). pAWneo2- $\alpha 2$  construct (Riikonen *et al.*, 1995), containing the complete human integrin  $\alpha 2$  subunit and pSFV1-TfR vector (Liljestrom & Garoff, 1991) with the TfR gene were used as templates for the generation of the PCR products by Phusion High-Fidelity DNA Polymerase (Finnzymes). A-overhangs were added to the 3' end of the PCR products by DyNAzyme II DNA Polymerase (Finnzymes). The reactions were run in a thermal cycler (Perkin-Elmer Cetus). The amplicons were purified using the Qiaex II Gel Extraction Kit (Qiagen). The PCR products were first cloned in the pGEM-T Easy Vector System I (Promega) and then assembled in a mammalian cell expression vector pcDNA/Zeo3.1+ (Invitrogen) resulting in TfR- and  $\alpha 2I$ -TfR-containing constructs (III, Fig 1). The PCR amplicons and the TfR- and  $\alpha 2I$ -TfR-containing constructs were sequenced with fluorescent dye-labeled terminators using an automated DNA Sequencer (Applied Biosystems) according to the manufacturer's instructions. Primers used for PCR reactions were used in the sequencing reactions. Nucleotide sequences were analyzed with Wisconsin Package Version 10.0, Genetic Computer Group (GCG; Madison, WI).



## 4.6 RT-PCR (III)

NIH3T3 cells, which were grown on 24 well plates and transiently transfected with the TfR or TfR- $\alpha$ 2I constructs, were infected with EV1 (1 h, 4°C) and then incubated for different time periods (0 to 24 h) at 37 °C. The cells were harvested and stored at -80 °C until tested. The cell pellet was suspended in PBS and subjected to automated nucleic acid extraction (Nuclisens easyMag, BioMerieux) with an elution volume of 55  $\mu$ l. RNA (10  $\mu$ l) was reverse-transcribed in two separate reactions with either antisense (4-) or sense (3+) primer from the 5'-noncoding region of picornaviruses as described earlier (Santti *et al.*, 1997). EV1 RNA from purified virions with spectrophotometrically determined copy number was used as the quantitative standard. PCR was performed in a RotorGene 3000 instrument (Corbett Life Sciences) in 25  $\mu$ l reactions containing QuantiTect SYBR Green PCR mix (Qiagen, Hilden), 600 nM of 4+ and 3- primers, and 5  $\mu$ l of the RT-reaction product. Amplification steps were: 95°C for 15 min followed by 45 cycles at 95°C for 15 min, at 65–55°C for 30 s (touch-down 1°C/cycle for first 10 cycles) and at 72°C for 40 s.

## 4.7 HLA typing (II)

The informative HLA-DQB1-DQA1 and DRB1 alleles as genetic risk factors for T1D were defined using a typing method based on PCR amplification of the gene segments and hybridization with a panel of lanthanide-labeled sequence-specific oligonucleotide probes (Nejentsev *et al.*, 1999).

## 4.8 Cell adhesion assay measuring attachment to cortical bone (I)

Bovine cortical long bones were obtained from a local slaughterhouse and stored at -20 °C. The femoral cortical shaft was cleaned from soft tissue and bone marrow. The bone was cut and shaped on a lathe to round rods with a diameter of 6 mm, which were further cut by a diamond wafering saw blade into 200  $\mu$ m thin disks. The bone slices were placed into 96 well microplates (Greiner GmbH, Frickenhausen) and treated with 1% bovine serum albumin (BSA) in RPMI 1640 medium for 15 min at RT. MDA-MB-231 cells were loaded with acetoxymethyl ester of 2', 7'-bis-(2-carboxyethyl)-5(6)-carboxyfluorescein (BCECF-AM) (Molecular Probes) for 15 min at 37 °C in RPMI 1640 medium before adding to bone disks. The plates were then centrifuged for 3 min at 800 rpm. The cells were washed with a Na<sup>+</sup>-solution (140 mM NaCl, 1mM CaCl<sub>2</sub>, and 20 mM Hepes (pH 7,2) and re-suspended in K<sup>+</sup>-solution (pH 8), 140 mM KCl, 1mM CaCl<sub>2</sub>, and 20 mM

Hepes (pH 7.2) containing 10  $\mu$ M nigericin (Sigma). The fluorescence from cells attached to bone was measured in the Fluoroscan II microplate fluorometer (Labsystem).

#### **4.9 FACS analysis (I, III)**

MDA-MB-231 and CHO cells, transfected with pcDNA/Zeo3.1-TfR and pcDNA/Zeo3.1-TfR- $\alpha$ 2I constructs were detached with EDTA. The MDA-MB-231 cells were incubated for 45 min at 4°C in 1:100 dilutions with blocking MAb antibodies against  $\alpha$ 2 (P1E6),  $\alpha$ 3 (P1B5),  $\alpha$ 4 (P4G9),  $\alpha$ 5 (P1D6) and  $\beta$ 1 (P4C10) subunits of integrin receptors (GIBCO), and integrin  $\alpha$ v $\beta$ 3 (Chemicon). The cells were washed with PBS and treated with FITC conjugated rabbit anti-mouse Ig (Boehringer Mannheim) for 45 min at 4°C. CHO cells, transfected with the pcDNA/Zeo3.1-TfR or pcDNA/Zeo3.1-TfR- $\alpha$ 2I constructs, were incubated for 1 h with 100  $\mu$ g/ml of Tf, washed with PBS and incubated with MAb against Tf (Dakopatts) and  $\alpha$ 2I (A211E10). AF488-conjugated goatanti-rabbit and PE-conjugated ratanti-mouse were used as secondary antibodies. The transfected CHO cells were fixed with 4 % formaldehyde for 20 min. Fluorescence intensity was measured by FACSCalibur flow cytometer (BD Biosciences, San Jose, CA) and CellQuest Pro software (BD Biosciences, San Jose, CA). Raw data was further analyzed with WinMDI 2.9 software (J. Trotter, Scripps Research Institute, La Jolla, CA). The MDA-MB-231 cells were analyzed on FACScan cytometer (Becton Dickson, Mountain View, CA, USA).

#### **4.10 Immunofluorescence and confocal microscopy (III)**

During a 1h incubation period at 4 °C EV1 was allowed to bind to the NIH3T3, BHK-21 or CHO cells transfected with pcDNA/Zeo3.1-TfR or pcDNA/Zeo3.1-TfR- $\alpha$ 2I constructs. Unbound virus was removed from the cells before further incubation at 37 °C. Human holo-Tf, AF488- or AF568-conjugated Tf was added to virus- and mock-infected NIH3T3 cells transfected with pcDNA/Zeo3.1-TfR or pcDNA/Zeo3.1-TfR- $\alpha$ 2I constructs and incubated at 37 °C. Alternatively, the transfected NIH3T3 cells were incubated for 15 min in the presence of holo-Tf, AF488- or AF568-conjugated Tf prior to infection. The cells were fixed with 4 % formaldehyde (Sigma) for 20 min, quenched with 50 mM NH<sub>4</sub>Cl for 10 min and permeabilized with 0.3 % Triton-X 100 (BDH) in PBS if not otherwise mentioned and stained with primary and secondary antibodies. The cells were studied with an axiovert confocal microscope Leica TCS SP2 with HCX PL APO 63x/1.32-0.6 oil objective or with Olympus Fluoview 1000 confocal setup. Images were acquired using Fluotar 60x objective (60 x 1.25, oil) with digital resolution of 512 x 512. False

colocalization signals were avoided by scanning fluorescence from different excitation wavelengths separately. The images were analyzed with Leica (LCS-Lite) or Olympus (FV10-ASW 1.4) software and then converted further to JPEG or TIFF format for additional processing in Photoshop (Adobe systems). For quantitative confocal microscopy, samples of EV1 infected NIH3T3 cells, transfected with the pcDNA/Zeo3.1-TfR- $\alpha$ 2I construct, were collected at different time points and immunostained with antibodies against EV1 and  $\alpha$ 2I, followed by secondary antibodies (AF488-conjugated goat anti-mouse and AF555-conjugated goat anti-rabbit). The samples were examined by confocal microscopy, and Z-section images were taken from the upper surface to the bottom of each cell. Colocalization of  $\alpha$ 2I and EV1 in 15 to 20 cells from each time point was analysed with BioimageXD (2007).

#### **4.11 Infectivity assays with drugs (III)**

SAOS-  $\alpha$ 2 and NIH3T3 cells, transfected with pcDNA/Zeo3.1-TfR or pcDNA/Zeo3.1-TfR- $\alpha$ 2I constructs, were preincubated in 33 $\mu$ M chlorpromazine hydrochloride (Sigma) or 25  $\mu$ M nocodazole (Sigma) for 30 min at 37 °C before addition of EV1 for 1 h at 4 °C. Unbound virus was removed and the cells were further incubated at 37 °C for 2min to 6h. After fixation, the cells were stained with antibodies against EV1,  $\alpha$ 2I and EE1, and the virus localization in the cell was studied with confocal microscopy.

#### **4.12 Determination of neutralizing antibody levels (II)**

Serum specimens were diluted serially at 2-fold steps (1:8-65 536) on microtiter plates (Nunclon Microtest plates, 96-well). Pretitrated virus solution corresponding to 100 TCID<sub>50</sub> units was added to each well. The viruses that were used included CAV-9,-18, -21, CBV1-6, EV-1, -6, -7, -11, HRV-1,-14, and HPV1, all obtained from ATTC, and PV were Sabin vaccine strains. The mixtures were incubated for 2h at 36 °C and left overnight at RT. 30 000 cells were added to each well. GMK cells were used for CAV9, CBV1-6, PV1-3 and EV11. HeLa cells were used for HRV-2 and -14 and CAV-18 and -21, while A-549 cells were used for EV-1,-6-7, -30 and HPV1. The plates were incubated at 36°C for 6 days before staining with crystal violet.

### **4.13 Infectivity titration (III)**

For the determination of the viral replication cycle, the NIH3T3 cells transfected with pcDNA/Zeo3.1, pcDNA/Zeo3.1-TfR or pcDNA/Zeo3.1-TfR- $\alpha$ 2I constructs, SAOS- $\alpha$ 2 cells and A549 cells were infected by EV1 and collected after different time points of infection. SAOS- $\alpha$ 2 cells were used as positive controls for the transfected NIH3T3 cells. After three freeze-thaw cycles, the amount of intracellular virus was determined in dilutions of  $10^{-1}$  to  $10^{-8}$  in GMK cells by plaque titration.

### **4.14 Human cDNA U133A arrays and clustering**

The Affymetrix Human Genome U133A Array (Affymetrix, Santa Clara, CA, USA) that contains 22215 human gene cDNA probe sets representing  $\sim 19,000$  genes (*i.e.*, each gene may be represented by more than one probe set), were used to perform gene expression analysis. The arrays were scanned and the fluorescence intensities measured by Microarray Suite 5.0 software (Affymetrix). The data was transferred to DNA-Chip Analyzer software (Affymetrix) for normalization and model-based analysis (Li & Wong, 2001). For each probe set a detection p-value was calculated, and any probe sets with  $p < 0.04$  were obtained as “present”, showing that the gene transcript was reliably detected (Affymetrix, 2001). Differently expressed genes were identified by Affymetrix dCHIP software ([www.dCHIP.org](http://www.dCHIP.org)). Alterations exceeding 1.5 were considered significant in genes where either of the values was more than 40. To analyze the networks of protein-protein interactions, the STRING 8.2 database was used (Jensen *et al.*, 2009).

## 5 RESULTS AND DISCUSSION

### 5.1 THE ROLE OF INTEGRINS IN BREAST CANCER METASTASIS TO THE SKELETON (I)

Breast cancer cells frequently metastasize to the skeleton. Preferential attachment of breast cancer cells to bone-specific molecules may facilitate favored metastasis to the skeleton. A requirement for metastatic spread is the capability of the tumor cell to reorganize the cytoskeleton to increase cellular motility. Integrin-mediated adhesion is crucial for the regulation of tissue integrity and function of mammalian tissue. Integrins have been implicated in the multi-step process of metastasis from breast tumor to bone tissue, including detachment and escape from primary organ, invasion through ECM and survival in circulation, capture to a distant endothelium, extravasation across the endothelium, migration through ECM and establishment of secondary tumor through cross-talk with osteoclast and osteoblast (Peyruchaud, 2007, White & Muller, 2007). This frequently leads to osteolytic (bone destructive) lesion, osteoblastic (bone formation) or mixed lytic and blastic lesion can also occur (Kozlow & Guise, 2005). In this study, the role of integrins in the initial attachment of mammary carcinomas to bone was analyzed by an in vitro microplate attachment assay, measuring the binding of MDA-MB-231 breast cancer cells to bovine cortical bone disks. In addition, the correlation between integrin surface expression and tumor's capability to attach to cortical bone was investigated.

#### 5.1.1 High surface expression of $\alpha 2\beta 1$ and $\alpha 3\beta 1$ integrins on human breast cancer MDA-MB-231 facilitates attachment to cortical bone matrix

The expression of integrin molecules on the human breast cancer cell line MDA-MD-231 was determined by FACS analysis. The majority of the cells strongly reacted with the monoclonal antibodies against  $\beta 1$ ,  $\alpha 2$  and  $\alpha 3$  integrin subunits, confirming the presence of  $\alpha 2\beta 1$  and  $\alpha 3\beta 1$  collagen receptors (I, Fig. 1 and Table 1). In addition, antibodies against the  $\alpha 5$  integrin subunit stained the cells, while antibodies directed against the  $\alpha 4$  integrin subunit or the  $\alpha v\beta 3$  integrin gave very weak staining. These results were in line with previous studies showing similar patterns of surface integrin expression on these cells (Boissier *et al.*, 1997, Morini *et al.*, 2000, van der Pluijm *et al.*, 1997).

MDA-MB-231 cells have been shown to be able to rapidly attach to cortical bone disks (Nordström *et al.*, 1999). To study the relative contribution of the various integrin receptors in the rapid attachment process, the MDA-MB-231 cells were pretreated with function-blocking monoclonal antibodies against various subunits in the integrins before

use in the attachment assay. Pre-treatment of the cells with monoclonal antibodies against the  $\beta 1$  or  $\alpha 2$  integrin subunit inhibited the MDA-MB-231 cell attachment to cortical bone by 75 % and 76 % respectively (I, Fig. 2). Cells pretreated with antibody against the  $\alpha 3$  subunit inhibited attachment by 26 %, while antibodies against the  $\alpha 5$  inhibited attachment by 8%. Antibodies to  $\alpha 4$  did not inhibit, as expected, since  $\alpha 4$  was not expressed on the MDA-MB-231 cells. Cells pretreated with an antibody against the  $\alpha v\beta 3$  integrin (vitronectin receptor) had no inhibitory effect on the cell attachment. In line with this, a tetrapeptide containing the RGD recognition sequence had no inhibitory effect on the binding to cortical bone (data not shown). Collagen type I is the major protein present in cortical bone (~90% of total protein) (Carter & Spengler, 1978). To further analyze the role of this protein in the attachment process, MDA-MB-231 breast cancer cell surface collagen receptors were saturated by preincubation with soluble collagen type I. This reduced the binding of cell to bone matrix by 85%. The blocking of rapid attachment of cancer cells by using inhibiting antibodies against the  $\alpha 2$  and  $\beta 1$  integrin subunits or by using soluble collagen type I was very close to the 90 % inhibition obtained by pretreating the cells with a mouse antiserum raised against the MDA-MB-231 cell line (data not shown). The results thus implicate that rapid attachment of MDA-MB-231 breast cancer cells to bone matrix mainly involves the  $\alpha 2\beta 1$  and  $\alpha 3\beta 1$  collagen receptors and collagen type I. The stronger inhibition of attachment of cancer cells to cortical bone disks by antibodies against the  $\alpha 2\beta 1$  integrin, compared with those against the  $\alpha 3\beta 1$ , is consistent with the reports implicating the integrin  $\alpha 2\beta 1$  to be the major cell surface collagen type I receptor (Kirchhofer *et al.*, 1990, Vihinen *et al.*, 1996).

Furthermore, incubating cortical bone disks with collagenase type 1 for 30 min at 37 °C or polyclonal antiserum against bovine collagen type I also had a blocking effect on the attachment by over 40%. However, the much higher inhibition achieved by incubating cells with  $\alpha 2$  and  $\beta 1$  integrin antibodies or soluble collagen type I may be explained by the fact that  $\alpha 2\beta 1$  and  $\alpha 3\beta 1$  collagen receptors are also able to attach to other bone matrix proteins, such as laminin and fibronectin.

In animal models the collagen/laminin receptor  $\alpha 2\beta 1$  and the fibronectin receptor  $\alpha 4\beta 1$  have been shown to be responsible for selective metastasis of cancer cells to the skeleton (Chan *et al.*, 1991, Matsuura *et al.*, 1996). Prostate cancer is another tumor that preferentially metastasizes to the skeleton. The attachment to bone of two pancreatic cancer cell lines LNCAPcol obtained by serial passage on type I collagen and C4-2B was observed to be dependent on the  $\alpha 2\beta 1$  integrin and its ability to stimulate RhoC GTPase activity (Hall *et al.*, 2006, Hall *et al.*, 2008). RhoC GTPase has been found to be associated with the progression of many cancers, including breast, melanoma and pancreas (Clark *et al.*, 2000, Suwa *et al.*, 1998, van Golen *et al.*, 2002). RhoC GTPase is associated with poor prognosis in breast and lung cancers (Ikoma *et al.*, 2004, Pille *et al.*, 2005).

The mechanism for MDA-MB-231 cells' attachment to cortical bone (van der Pluijm *et al.*, 1997), basement membrane (Morini *et al.*, 2000) and vitronectin has been investigated in the past (Wong *et al.*, 1998). In line with our results  $\alpha 3\beta 1$  was reported to be crucial for MDA-MB-231 cells' invasion and migration in in vitro cell migration assay. Furthermore, the expression of the  $\alpha 3\beta 1$  integrin was determined to be higher in breast cancer metastases than in primary tumors (Morini *et al.*, 2000). In contrast to reports by Pluijm *et al.*, where the cells were kept in contact with bone surface for 3h at 37 °C (van der Pluijm *et al.*, 1997), we did not see any inhibition with antibodies against the vitronectin receptor  $\alpha v\beta 3$  integrin. Moreover, Wong *et al.* reported that the  $\alpha v\beta 3$  integrin did not support the binding of MDA-MB-231 cells to vitronectin (Wong *et al.*, 1998). In their experiments they used a vitronectin cell adhesion assay, where cells were allowed to adhere for 30 min at 37 °C and a cell migration assay, where cells were allowed to traverse a vitronectin-coated membrane. In contrast, they suggested the  $\alpha v\beta 1$  integrin receptor to be crucial for MDA-MB-231 cells' attachment to vitronectin, since the binding was inhibited by both RGD peptide and antibody against  $\beta 1$  (Wong *et al.*, 1998). In our experiments the cells were not allowed to be in contact with the bone surface for more than 5 min. Consequently, the short time did not allow the cells to spread and form adhesion sites, and microscopic examination of the attached cells clearly showed that they had a round morphology. However, if the cells were attached to bone surface for longer time, they began to spread and acquired a flattened morphology. During longer attachment periods, the cells themselves might secrete adhesion proteins, such as vitronectin, fibronectin and osteopontin, or upregulate new cell surface receptors. The cell spreading started about 30-45 min after their initial attachment (data not shown). This might explain why our results and the ones published by Wong *et al.* (Wong *et al.*, 1998) are different from those published by Pluijm *et al.* (van der Pluijm *et al.*, 1997).

In conclusion, our results suggest an important role for the  $\alpha 2\beta 1$  and  $\alpha 3\beta 1$  integrin receptors in the initial anchoring of MDA-MB-231 breast cancer cells to cortical bone matrix.

### **5.1.2 Correlation between surface expression of $\alpha 2\beta 1$ and $\alpha 3\beta 1$ integrins on tumor cells and their tendency to anchor to cortical bone matrix**

To further study the roles of  $\alpha 2\beta 1$  and  $\alpha 3\beta 1$  collagen receptors in cancer cell attachment to cortical bone, the integrin surface expression on three additional human cell lines that included a prostate cancer cell line PC-3, T-cell leukemia line Jurkat and the neuroblastoma cell line SH-SY5Y were studied. PC-3 cells have been reported to preferentially metastasize to the skeleton in nude mice models (Shevrin *et al.*, 1988, Shevrin *et al.*, 1991) and easily adhere to cortical bone disks (Nordström *et al.*, 1999, van

der Pluijm *et al.*, 1996a, van der Pluijm *et al.*, 1996b). PC-3 expressed high levels of the  $\alpha 2\beta 1$  and  $\alpha 3\beta 1$  integrin receptors (I, table 1) and was also able to rapidly attach to cortical bone matrix.

In contrast, the human Jurkat and SH-SY5Y cells, which only modestly attached to cortical bone, showed very low expression of these integrins (I, Table 1, Fig. 4). Surface expression of the  $\alpha 4$  integrin on Jurkat cells did not support rapid attachment to bone matrix, although in a former study the  $\alpha 4\beta 1$  integrin has been suggested to be one candidate that specifically localizes cancer cells to the skeleton through adhesion to VCAM-1 (Matsuura *et al.*, 1996).

Together these results implicate a close connection between  $\alpha 2\beta 1$  and  $\alpha 3\beta 1$  integrin receptor expression and the ability of different cancer cell types to attach to cortical bone.

## **5.2 VARIATION IN ENTEROVIRUS RECEPTOR GENES (II)**

Enteroviruses are believed to contribute to the pathogenesis of type 1 diabetes (T1D). Higher antibody levels against CBVs and presence of enterovirus RNA have been reported in individuals with recent onset of T1D (Andreoletti *et al.*, 1997, Gamble *et al.*, 1969) and in prediabetic children (Hiltunen *et al.*, 1997, Hyöty *et al.*, 1995). Moreover, in autopsy patients with recent-onset T1D showed higher prevalence for vp1 in pancreas compared with a control group (Richardson *et al.*, 2009).

It is possible that sensitivity to enterovirus infections might correlate with individual variation in enterovirus receptor genes. To investigate this possibility, sequence analysis of the domains known to be critical for virus binding in the major enterovirus receptors (CAR, DAF, ICAM-1, PVR, and  $\alpha 2$ - and  $\beta 3$  integrin subunits) were performed from human blood samples collected from healthy individuals and children with type 1 diabetes. In parallel, virus-specific neutralizing antibodies and type 1 diabetes risk-associated HLA-alleles were analyzed.

### **5.2.1 Sequence analysis of enterovirus receptor genes and HLA types**

PCR and sequence analysis were carried out for the enterovirus receptor genes CAR, DAF, ICAM-1, PVR, and  $\alpha 2$ - and  $\beta 3$  integrin subunits for the regions reported to be important for virus binding. DNA samples were acquired from a group of children with T1D (21 individuals) and a control group of healthy adults (20 individuals). Ten additional samples from diabetic children and five samples of healthy children from Estonia were analyzed to clarify the frequency of the variation found in the PVR gene. These samples were also used as additional controls in serological studies.



A heterozygote single nucleotide polymorphism (SNP) was detected in the V-domain (exon 2) of the PVR at Ala 67(GCG)→Thr (ACG) in 4 individuals of the 31 children with T1D (12.5%), but it was not found in the healthy control group. This variation in the variable domain of PVR is placed in the virus binding region and may thus inhibit cellular binding of all three PV serotypes. Heterozygotic polymorphism of this gene was recently suggested to be a risk factor for the development of vaccine-associated or paralytic poliomyelitis associated with wild-type virus (Kindberg *et al.*, 2009). Moreover, this variation has been found to be more frequent among individuals with the motor neuron disease Amyotrophic lateral sclerosis (ALS) than controls (Saunderson *et al.*, 2004). In former studies enteroviruses have been suggested to be implicated in the development of this disease (Berger *et al.*, 2000, Woodall & Graham, 2004). This variation in the PVR genome has been shown to reduce the infection rate of PV by 50%, increase resistance to cell lysis (Pavio *et al.*, 2000) and reduce apoptosis (Gosselin *et al.*, 2003) in human neuroblastoma cells. The delayed course of poliovirus-induced catalysis could therefore be connected to persistent infection in the CNS (Kindberg *et al.*, 2009). Persistent infection has been suggested to be a possible mechanism in the development of T1D. This could be due to improper immune response to enterovirus infection, leading to viral persistence and increased pancreatic  $\beta$ -cell damage (Richer & Horwitz, 2009). Persistent CBV4 infection in pancreas has been associated with diabetic-like syndrome in mice (Zhou & Li, 2008), and association of persistent infection in gut mucosa and in pancreas has been reported in T1D (Richardson *et al.*, 2009). Although former results indicate no relationship between vaccination and T1D (Hviid *et al.*, 2004), one could still speculate that oral polio vaccination (OPV) could be a risk factor for T1D in those individuals possessing this genetic variation. However, since the OPV vaccinations have not been used for over a decade in Finland, this could not be the case for those diabetic children included in this study. Therefore, serum samples from Estonian children who had been vaccinated with live poliovirus vaccine were studied. One of the children had no serum antibodies for any of the PV serotypes and one did not have antibodies for the PV3. These children did not, however, have the SNP found in the first part of the study in diabetic children. Moreover, one could speculate that a possible mechanism in the pathogenesis of T1D for those possessing this variation in PVR could be connected with impaired immune response. In a number of studies, PVR has been shown to serve as an important ligand for cell surface receptors expressed on lymphocytes, monocytes and dendritic cells. PVR attaches to DNAX accessory molecule 1 (DNAM-1;CD226) (Bottino *et al.*, 2003, Tahara-Hanaoka *et al.*, 2004) and Tactile (CD96) (Fuchs *et al.*, 2004, Seth *et al.*, 2007), which are expressed on NK cells, CD8<sup>+</sup> T cells and CD4<sup>+</sup> T cells. DNAM-1 regulates monocyte extravasation via its interaction with PVR expressed at endothelial junctions (Reymond *et al.*, 2004). In the tissue monocytes can differentiate into dendritic cells and macrophages to elicit an immune response. In addition a recent study showed a novel interaction between PVR and

a novel immunoreceptor, called T cell immunoreceptor with Ig and ITIM domains (TIGIT) (Boles *et al.*, 2009), which is expressed on human follicular B helper T cells (TFH).

A heterozygous SNP was also found in the first Ig-like domain (exon 2) of ICAM-1 at Lys56 (AAG)→Met (ATG) in one individual in both the control and the diabetes group. The individual from the diabetes group also had the heterozygous variation found in PVR. ICAM-1 is a receptor for the major receptor group human rhinovirus (Greve *et al.*, 1989, Staunton *et al.*, 1989) and has also been shown to be used by coxsackievirus A13, A15, A18, A20 and A21 (Colonno, 1986, Pulli *et al.*, 1995, Shafren *et al.*, 1997b). The SNP found in this study is in the sequence of the first 159 amino acids (domain 1) of ICAM-1 required for human rhinovirus binding (Staunton *et al.*, 1990).

The same variation was earlier reported to be associated with increased risk of cerebral malaria and named ICAM-1<sup>Kilifi</sup> (Fernandez-Reyes *et al.*, 1997). However, a later study by A. E. Fry *et al.* using larger case groups did not support this association (Fry *et al.*, 2008). In a later report ICAM-1<sup>Kilifi</sup> was shown to reduce immune responsiveness since it decreases the avidity to lymphocyte function-associated antigen-1 (LFA-1) and abolishes binding to soluble fibrinogen (Craig *et al.*, 2000). Furthermore, ICAM-1<sup>Kilifi</sup> was observed to prevent HRV16 binding (Xiao *et al.*, 2004), and in crystal structure studies the binding of CVA21 to ICAM-1<sup>Kilifi</sup> was suggested to possibly be weaker than its binding to ICAM-1 (Xiao *et al.*, 2005).

Silent SNP variations, both as homozygotic or heterozygotic, were frequently found in both groups from the  $\alpha 2$  integrin I domain subunit at Phe43(TTT)→Phe(TTC), and a silent heterozygous SNP in the glutamine codon 111 (CAA→CAG) from CAR exon 2 was also seen in one individual in the diabetes group.

HLA-DR4-DQ8, which is associated with increased risk of type 1 diabetes, was found in 74% of children with type 1 diabetes and in 10 % of the adult control group. Three diabetic children with the SNP in the PVR gene, who were HLA typed, were all positive for HLA-DR4-DQ8. In general, no significant correlation between neutralizing antibodies and the HLA alleles could be seen. HLA genotypes among cases and controls were expected. HLA-DR4-DQ8 was significantly increased and DR2-DQ6 decreased among the children with type 1 diabetes (data not shown).

Taken together, the study shows individual variation in some genes coding for enterovirus receptors. In the PVR, SNP causing amino acid change in a region critical for efficient binding and infection of PV were detected in the first group of individuals with T1D. Interestingly, three of the diabetic children with the SNP in PVR gene, who were HLA typed, were all positive for HLA-DR4-DQ8. However, its direct connection to T1D should be analyzed with a larger number of individuals to obtain statistically sustainable results. Genetic variation was found in ICAM-1 in one individual in both the diabetic and the control group. In contrast, no variation leading to amino acid change occurred in genes

coding for the CAR and DAF, which are the receptors for coxsackie B viruses and echoviruses, showing most frequent association with T1D. However, since only the virus-binding regions of the receptor sequence were studied, it is still possible that other parts of the receptor molecules (e.g. the ones involved in endocytosis and signaling events) may enclose genetic variation that could influence enterovirus infection.

### **5.2.2 Serological markers of enterovirus infection**

Serum antibody levels against a collection of human enteroviruses and human parechovirus 1 were measured by microneutralization assay from the plasma of 21 children with type 1 diabetes, 20 matched control children, and 20 healthy adults. In addition, serum antibodies against poliovirus 1-3 were studied in a group of 43 OPV-vaccinated children from Estonia to search for seronegative individuals possessing the genetic variation found in PVR.

Several enteroviruses have been suspected to be involved as environmental triggers of T1D. Especially the involvement of CBVs and echoviruses has been implicated in the onset of T1D (Roivainen, 2006). In our study, the levels of neutralizing antibody titers against the enteroviruses were higher in the adults than in the children, except for poliovirus 1-3 and human parechovirus 1. In general, no clear difference was detected between serum antibody levels against most of the enteroviruses between the groups of diabetic and control children. Low levels of serum antibodies against EV 1, 6, 7 and 11 were seen in both adults and children, while the vast majority of the children lacked antibodies against CBV 1-6, and no significant differences between the groups of children were observed. These results can partly be explained by the relatively low level of CBV and echovirus infections during the years 1998-2001 compared with the previous three-year period (Register of the Public Health Institute, Finland). Furthermore, CAV18, A21, and HRV2 and 14 antibodies, studied to correlate the findings to the variation in the ICAM-1 gene, were generally low, and no direct conclusions could be made (data not shown).

Seropositivity for CAV9 was found in only two healthy control children, but high individual antibody levels against CAV9 were observed in six diabetic children. However, the difference was not statistically significant (II, Fig. 3). CAV9 infection has been associated with increased production of islet cell autoantibodies in prediabetic children (Roivainen *et al.*, 1998). In *in vitro* studies, the virus was observed to cause persistent infection in human pancreatic islet cells, occasionally accompanied by minor morphological changes associated with impaired functional properties of insulin-producing  $\beta$ -cells (Roivainen *et al.*, 2000).

The levels of neutralizing antibodies against EV30 were significantly lower in the children with newly diagnosed T1D when compared with healthy children ( $P < 0.0003$ ) (II, Fig. 2 and 3). EV30 has been shown to be islet cell destructive in in vitro studies (Paananen *et al.*, 2007, Roivainen *et al.*, 2002) and to sometimes generate a humoral response to homologous regions in islet cell autoantigenes such as IA-2/IA-2beta and HSP-60 (Härkönen *et al.*, 2003). However, in a recent study with a group of 100 diabetic children and non-diabetic controls did not support our finding of lower antibody levels in diabetic children, as no difference in antibody levels against EV30 was observed (Paananen *et al.*, 2007). EV30, which binds to the SCR1 domain of DAF, was reduced by 21% in rhabdomyosarcoma (RD) cells (data not shown) with monoclonal antibodies against this domain, while monoclonal antibodies recognizing domains two and three had no effect (data not shown). This incomplete inhibition of virus binding could be explained by a result in a recent report by Ylipaasto *et al.*, suggesting that  $\alpha\beta 3$  integrin functions as a cellular receptor for EV30 (Ylipaasto *et al.*, 2009).

No significant difference in the levels of neutralization antibodies to PV1-3, induced by the inactivated vaccine used in Finland, was found among patients with T1D and healthy children, although slightly higher levels of antibodies to PV2 were observed in healthy children ( $P = 0.056$ ) (II, Fig. 2 and 3). In both groups, a small group of children had low neutralization antibody levels or no antibodies against PV3. Interestingly, three of these children with T1D carried the heterozygotic SNP in the V-domain region of PVR (II, Fig. 2, Table 2). Of the serum samples obtained from Estonia, one was seronegative for all three poliovirus serotypes and one lacked antibodies against PV3. However, the samples in question did not contain the SNP in PVR found in the first group of diabetic children.

In conclusion, the results showed no remarkable difference in the levels of neutralizing antibodies against enteroviruses and rhinoviruses among the groups studied. Higher antibody levels against CAV9 were observed in the T1D group, although the difference was not statistically significant. Interestingly, the level of neutralization antibody against EV30 was significantly lower in the group of diabetic children compared with the group of healthy children.

### **5.3 ALTERED TARGETING OF EV1 TO CLATHRIN-DEPENDENT PATHWAY (III)**

Some picornavirus serotypes, including CBV3, FMDV and EV6, have been shown to be able to use both lipid raft/caveolin- and clathrin-dependent host cell endocytosis, depending on cell type or genetic differences in the virus genome (Chung *et al.*, 2005, Coyne *et al.*, 2007b, Leveque *et al.*, 2007, Wang *et al.*, 1993). Echovirus (EV1) has been reported to enter host cells from lipid rafts, through caveolae (Marjomäki *et al.*, 2002,

Pietiäinen *et al.*, 2004) or by macropinocytosis (Karjalainen *et al.*, 2008). The aim of the study was to investigate if EV1 could be directed to the clathrin-dependent entry pathway by a chimeric receptor and would be able to initiate productive infection in host cell.

### **5.3.1 Colocalization of EV1 and $\alpha$ 2I with human transferrin in cells expressing a chimeric TfR- $\alpha$ 2I receptor**

In order to study whether attachment of EV1 to a receptor mediating clathrin-dependent pathway could lead to successful internalization of the virus, a chimeric molecule was constructed: The  $\alpha$ 2I domain from human  $\alpha$ 2 integrin subunit, known to bind EV1, was inserted into the extracellular terminus of human TfR, which normally transports transferrin-bound iron through clathrin-dependent endocytosis (III, Fig. 2). Some animal parvoviruses, including CPV, use TfR as a receptor in clathrin-directed endocytosis (Hueffer *et al.*, 2003, Palermo *et al.*, 2003). The chimeric TfR- $\alpha$ 2I and human TfR were transiently expressed in NIH3T3 and CHO cells. Normally, EV1 does not bind to mouse NIH3T3 cells or hamster CHO cells due to dissimilarities between mouse, hamster and human  $\alpha$ 2 integrin sequences.

The expression of the receptors in transiently transfected NIH3T3 and CHO cells was analyzed by IF microscopy and flow cytometry (FACS). In IF microscopy using antibodies against  $\alpha$ 2I and fluorescent Tf, the receptors were seen to be expressed in both cell lines. In flow cytometry (FACS) analysis, CHO cells were first incubated with human Tf at 4 °C, and the receptors were detected by antibodies against  $\alpha$ 2I and Tf. Both TfR- and TfR- $\alpha$ 2I-transfected cells bound human Tf (III, Fig. 2A and B). In addition, nontransfected cells also bound Tf, but more efficient binding was seen in the transfected cell lines (data not shown). Double-labeled cells showed that the same population of TfR- $\alpha$ 2I transfected cells was positive for both Tf and  $\alpha$ 2I (III, Fig. 2 C). This data indicated that the chimeric receptor can function as a receptor for Tf.

To identify whether EV1 could enter by clathrin-directed endocytosis into NIH3T3 cells, transiently transfected with the TfR- $\alpha$ 2I and TfR receptor constructs, colocalization between Tf,  $\alpha$ 2I and EV1 was analyzed by confocal microscopy (III, Fig. 3). EV1 was first attached to the cells for 1 h at 4°C (indicated as 0 h p.i.). Then the cells were incubated with Tf at 37°C or, alternatively, the cells were first incubated with Tf for 15 min at 37°C before attaching of virus to the cells. Colocalization between Tf and  $\alpha$ 2I (III, Fig. 3A) and partial colocalization of Tf and EV1 was seen from 15 min (III, Fig. 3 B) to 2 h p.i.

These results showed that both the TfR and the chimeric receptor are functional Tf receptors and the chimeric construct can act as an internalization receptor for EV1. In addition, these results indicate that EV1 is endocytosed through a clathrin-directed pathway and colocalizes with Tf in recycling endosomes.

### **5.3.2 EV1 attaches and enters host cells expressing TfR- $\alpha$ 2I chimeric receptor**

To further study the interaction between EV1 with the TfR- $\alpha$ 2I chimeric receptor, EV1 was attached to TfR- $\alpha$ 2I-transfected NIH3T3 cells. The virus and the receptor were detected by antibodies against  $\alpha$ 2I and EV1 and studied by confocal microscopy. EV1 bound to the TfR- $\alpha$ 2I chimeric receptor on the cell surface, and 30 min p.i., colocalization between  $\alpha$ 2I and EV1 in vesicular structures was detected near the cell membrane (III, Fig. 4A). EV1 mainly remained in intracellular structures 2 h p.i., while the receptor was recycled to the plasma membrane, typical for TfR. This differs from canine parvovirus (CPV) entry, where the virus remains attached to TFR for several hours (Parker *et al.*, 2001). EV1 could not attach to or enter NIH3T3 cells, transfected with TfR (III, Fig. 4B). Furthermore, the colocalization of the virus and chimeric receptor was studied by quantitative confocal microscopy. Z-sections were obtained from EV1-infected NIH3T3 cells, transfected with the chimeric receptor and analysed with BioimageXD software. The colocalization between  $\alpha$ 2I and EV1 diminished during a time period spanning from 0 h p.i. to 30 min p.i., indicating gradual detaching of the virus from the receptor.

### **5.3.3 Colocalization of EV1 and the chimera receptor with cellular markers**

Clathrin-mediated transport is crucial for several cellular processes, including nutrient uptake, uptake of iron-loaded transferrin that binds to TfR, synaptic vesicle recycling and selective endocytosis of receptor-bound ligands (Conner & Schmid, 2003, Simonsen *et al.*, 2001). Receptor-bound ligands are transported from clathrin-coated vesicles to early endosomes (EEs), which possess a slightly acidic milieu, causing dissociation of some viruses from the receptor and release of the genome to cytoplasm (Mukherjee *et al.*, 1999). The endocytic pathway of EV1 in TfR- $\alpha$ 2I-transfected cells was studied using different antibodies against intracellular organelle markers in confocal microscopy. Cellular markers for EE included the early endosome antigen 1 (EEA-1) and Rab4, a small GTPase. EV1- infected BHK-21 cells, double-stained for EV1 and EEA-1, showed partial colocalization 2 min p.i. (III, Fig. 5A) that disappeared already 5 min p.i. The BHK-21 cells that are normally not infected by EV1 were used because of a stronger fluorescence signal of EEA-1 compared with the NIH3T3 cells. In EV1-infected, TfR- $\alpha$ 2I-transfected NIH3T3 cells, clear colocalization between  $\alpha$ 2I and Rab4 was seen 2 min p.i. (III, Fig. 5B).

The cargo from EE can be transported to RE. The iron-Tf-TfR complex is rapidly endocytosed into clathrin-coated pits (Mellman, 1996) and further transported to early or sorting endosome. In the endosomal acidic milieu, iron is released from Tf and the resultant apo-Tf-TfR is recycled to the plasma membrane by fast endosome-directed

transport dependent on Rab4 or through a slower process via perinuclear recycling compartments, dependent on Rab11 (Hao & Maxfield, 2000, Morgan, 1996, Qian *et al.*, 1997, Sheff *et al.*, 1999). Furthermore, the ligand-receptor complex can be transported from EE to LE, possessing a more acidic milieu for instance during endocytosis of the CPV-TfR complex (Parker *et al.*, 2001). Alternatively, CPV is transported from EE shortly after cell entry to perinuclear recycling endosomes (PNRE) where the virus has been shown to colocalize with endocytosed transferrin, suggesting a similar recycling pathway as in Tf transport (Parker & Parrish, 2000, Suikkanen *et al.*, 2002). CPV is released into the cytosol through a mechanism that has been suggested to be transient or to include limited pore formation of the endosomal membrane (Harbison *et al.*, 2008). In EV1-infected cells, partial colocalization between EV1 and Rab11, a marker for RE, was seen from 5 min to 30 min p.i. This result suggested that EV1 is transported in TfR- $\alpha$ 2I-transfected NIH3T3 cells from EE to RE in a process resembling that of iron transport and also partly in a manner similar to the early infection steps in CPV endocytosis, although CPV remains bound to TfR for several hours (Parker *et al.*, 2001).

Other markers used for endocytotic cellular organelles (caveolae/caveosomes and LE/lysosomes) showed no colocalization between either  $\alpha$ 2I or EV1 in infected cells transfected with a TfR- $\alpha$ 2I construct. The markers included caveolin-1, the endoplasmic reticulum marker (PDI) and a Golgi marker (Gm130). For some markers, BHK-21 cells were used because a better fluorescence signal was obtained. CI-MPR, a LE marker, Lamp1, a late endosome and lysosome marker, detected by 1D4B antibody, and another LE marker 6C4 (30 min to 1 h p.i.) showed no colocalization with  $\alpha$ 2I or EV1.

These results suggested that EV1 probably remains in the early and recycling endosomes and is not transported further to the late endosomes, lysosomes, Golgi or endoplasmic reticulum.

### **5.3.4 EV1 replication is initiated in TfR- $\alpha$ 2I-transfected NIH3T3 cells**

After showing that EV1 was able to enter transiently transfected NIH3T3-TfR- $\alpha$ 2I cells, the next focus of interest was to investigate if the virus would be able to initiate productive infection in those cells. In EV1-infected host cells the viral genomic (+)RNA is copied by viral 3D into complementary (-)RNAs, which serve as template for the synthesis of new genomes. RNA replication was measured in infected, TfR- $\alpha$ 2I-transfected NIH3T3 cells and Saos- $\alpha$ 2 cells by quantitative RT-PCR detecting positive (III, Fig 6 A) or negative (III, Fig. 6 B) strand of viral RNA. In Saos- $\alpha$ 2 a considerable increase in (-)RNA copy number was detected (III, Fig. 6 A), as well as a minor increase of (+)RNA (III, Fig. 7 B). This was in line with former studies, where the EV1 RNA synthesis was detected 3 h p.i. and production of new virus started 4h p.i. in the cells (e.g. CV-1 cell line), susceptible to EV1

infection (Pietiäinen *et al.*, 2004). In the TfR- $\alpha$ 2I-transfected NIH3T3 cells, the increase of both viral (+)RNA and (-)RNA was seen later, first 6 h p.i., thus indicating a slower initiation of replication compared with cells possessing the human  $\alpha$ 2 $\beta$ 1 integrin. The increase of copy number of both (+)RNA and (-)RNA in Saos- $\alpha$ 2 cells 12 h p.i, compared with 2 h p.i., was significantly higher compared with TfR- $\alpha$ 2I-transfected NIH3T3 cells. Furthermore, in plaque assay experiments, infected TfR- $\alpha$ 2I-transfected NIH3T3 cells were shown to produce infectious virus, although in low quantity. Enterovirus replication starts upon release of viral genomic RNA into the cytoplasm, and since the EV1 infection in TfR- $\alpha$ 2I-transfected NIH3T3 cells caused production of new viruses, the virus was released from the vesicular structures in the cell. A low pH step is crucial for replication of CPV. In CV-1 cells, EV1 is found in caveosomes 30 min p.i., and viral capsid proteins and RNA can be detected in these structures for 4 h p.i. (Pietiäinen *et al.*, 2004). Moreover, in a recent study with Saos- $\alpha$ 2 $\beta$ 1 cells, caveolin-1 negative tubulovesicular endosomes, containing EV1, were found to fuse with internalized caveolae or caveosomal structure maturing into multivesicular structures, a process that started 15 min p.i and continued for 3 h (Karjalainen *et al.*, 2008). Genome release of picornaviruses from intracellular vesicles includes rupture of endosomes by the major rhinovirus receptor group (Schober *et al.*, 1998) and pore formation in endosomes by the minor rhinovirus receptor group (Brabec *et al.*, 2005). Release of the EV1 genome in transfected NIH3T3-TfR- $\alpha$ 2I cells could proceed by rupture of vesicles containing viruses, or alternatively more specific mechanisms could be involved.

Some chimeric receptors have earlier been used in picornavirus studies. For instance, a chimera made of PVR and ICAM-1 or CD4 receptor (Selinka *et al.*, 1991) has been shown to be a functional poliovirus receptor (Selinka *et al.*, 1992), and expression of a single-chain antibody, recognizing FMDV and inserted to ICAM-1, made cells susceptible to infection (Rieder *et al.*, 1996). Together these results show that EV1 initiates productive infection in TfR- $\alpha$ 2I-transfected NIH3T3 cells, although the efficiency is reduced.

## **5.4 HOST GENE EXPRESSION DURING EV1 INFECTION**

Previous studies have shown that certain immediate early genes (IEGs) are activated in response to 5-10 h of EV1 infection. The aim was to use cDNA array technique to clarify how the EV1 and  $\alpha$ 2 $\beta$ 1 integrin interaction, signaling and virus endocytosis influence on cellular host gene expression. Host gene RNA expression was studied in human A549 lung carcinoma cells at 30 min, 2 h and 6 h post infection (p.i.).

Picornaviruses may regulate the cells' transcriptional machinery to gain advantage over the host cell in the competition for translational components and ribosomes. At a late stage of enterovirus replication, the infection can be detected by CPE that is characterized



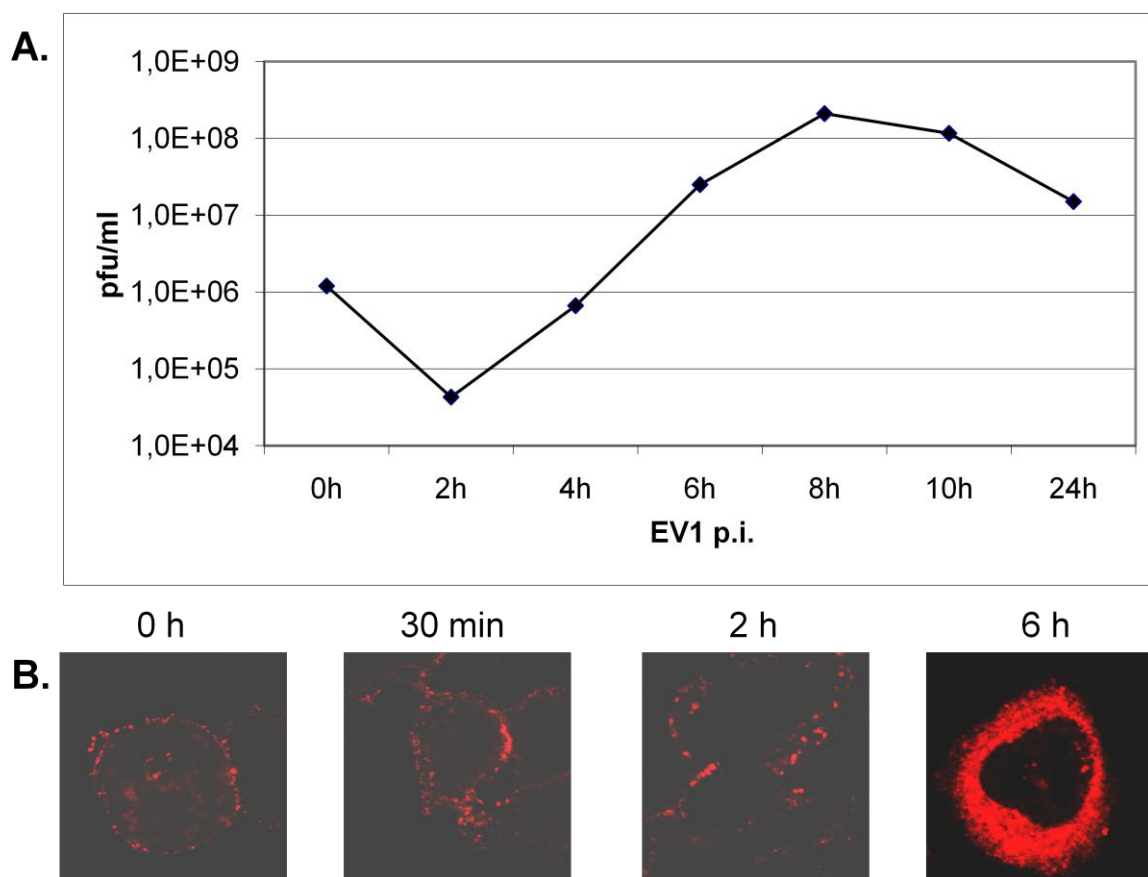
by morphology changes in cell, such as cell rounding and detachment and finally cell lyses (Racaniello, 2001). Picornaviruses lack a 5'-cap structure in their mRNA (Belsham & Sonenberg, 1996, Sachs *et al.*, 1997) needed for normal cellular gene expression. Some picornaviruses can inhibit cellular transcription and protein synthesis (shut-off) by preventing the translation of 5'-capped mRNAs (Knipe *et al.*, 2001, Lamphear & Rhoads, 1996). The translation of viral genes is not affected due to the internal ribosome entry site (IRES) in the picornavirus genome (Dorner *et al.*, 1984, Pelletier & Sonenberg, 1989) that can also be found in some cellular mRNAs.

Confluent A549 (ATCC) cells were infected with EV1 (Farouk strain; ATCC) and the multiplication of the virus was studied by plaque titration (Fig. 1). For RNA purification, the cells were collected after 30 min, 2 h, and 6 h incubation in a guanidinium lysis buffer and frozen at -70°C. Total RNA was purified by ultracentrifugation in CsCl gradients, followed by ethanol precipitation. The preparations were then treated with DNase (Sigma). Alternatively, total RNA was purified according to the manufacturer's instructions using RNeasy Mini kit (Qiagen), supplemented with QIAshredder (Qiagen) for homogenization of cells and RNase-FreeDNase Set (Qiagen) to remove DNA completely during RNA purification. Activation and downregulation of cellular genes was studied by using the Affymetrix Human Genome U133A Array (Affymetrix), that contains 22 215 human cDNA probe sets, representing approximately 19 000 genes. The arrays were scanned, and the fluorescence intensities were measured by Microarray Suite 5.0 software (Affymetrix). The data was transferred to DNA-Chip Analyzer software (Affymetrix) for normalization and model-based analysis (Li *et al.*, 2001). For each probe set, a detection p-value was calculated and sets with  $p < 0.04$  were considered to be present, indicating that the gene transcript was reliably detected. Each microarray experiment was repeated. Differently expressed genes were identified by Affymetrix dCHIP software ([www.dCHIP.org](http://www.dCHIP.org)). Alterations exceeding 1.5 were considered significant in genes where either of the values was greater than 40. To analyze the networks of protein-protein interactions, the STRING 8.2 database was used (Jensen *et al.*, 2009).

In EV1-infected A549 cells, no difference in the amount of RNA in EV1-infected cells, compared with mock-infected cells, was observed at 6 h p.i., although a clear CPE effect in the cells was detected (result not shown). However, at 10 h p.i. the RNA content was significantly decreased in the EV1-infected sample, compared with the mock-infected sample. This could be due to the fact that the CPE in cells decrease the number of viable cells, and/or to virally caused shut-off, although former studies have shown that EV1 causes CPE but does not cause shut-off (Zhang & Racaniello, 1997), or the shut-off is inefficient (Pietiäinen *et al.*, 2000). During early stages of EV1 infection at 30 min p.i. and 2 h p.i., only a few host gene expressions were altered. At 6h EV1 p.i., the virus replication had already started and one hundred genes were found to be differently expressed. At this time about 50 % the genes showed decreased expression.

In the early phase of EV1 infection (30 min and 2 h p.i.), the virus is first bound to its cellular receptor, the  $\alpha 2\beta 1$  integrin, and subsequently found in vesicular structures. It is possible that the events occurring during virus endocytosis do not require specific alteration of host cell gene expression to enhance initiation of infection. This could explain why only a few genes were differently expressed during these early infection events.

Differently expressed genes at 30 min p.i. in EV1 infected cells possessed functional features, such as actin cytoskeleton, transcription, catalytic activity, cell surface receptors, cell communication and others, including genes with unknown function. Six genes were induced and nine were downregulated. Three of the induced genes in infected cells, including phosphatidylinositol-4-phosphate 5-kinase, type 1C (PIP5K1C), integrin  $\alpha 6$  subunit (ITGA6) and receptor-associated coactivator 3 (RAC3) were all shown to be involved in the entry processes of virus. However, their role in EV1 infection requires further studies. STRING 8.2 interactions of the genes did not show connections between the differently expressed genes, except for a strong acetyl-Coenzyme A acetyltransferase 2 (ACAT2)-acetyl-Coenzyme A acyltransferase 1 (ACAA1) association.



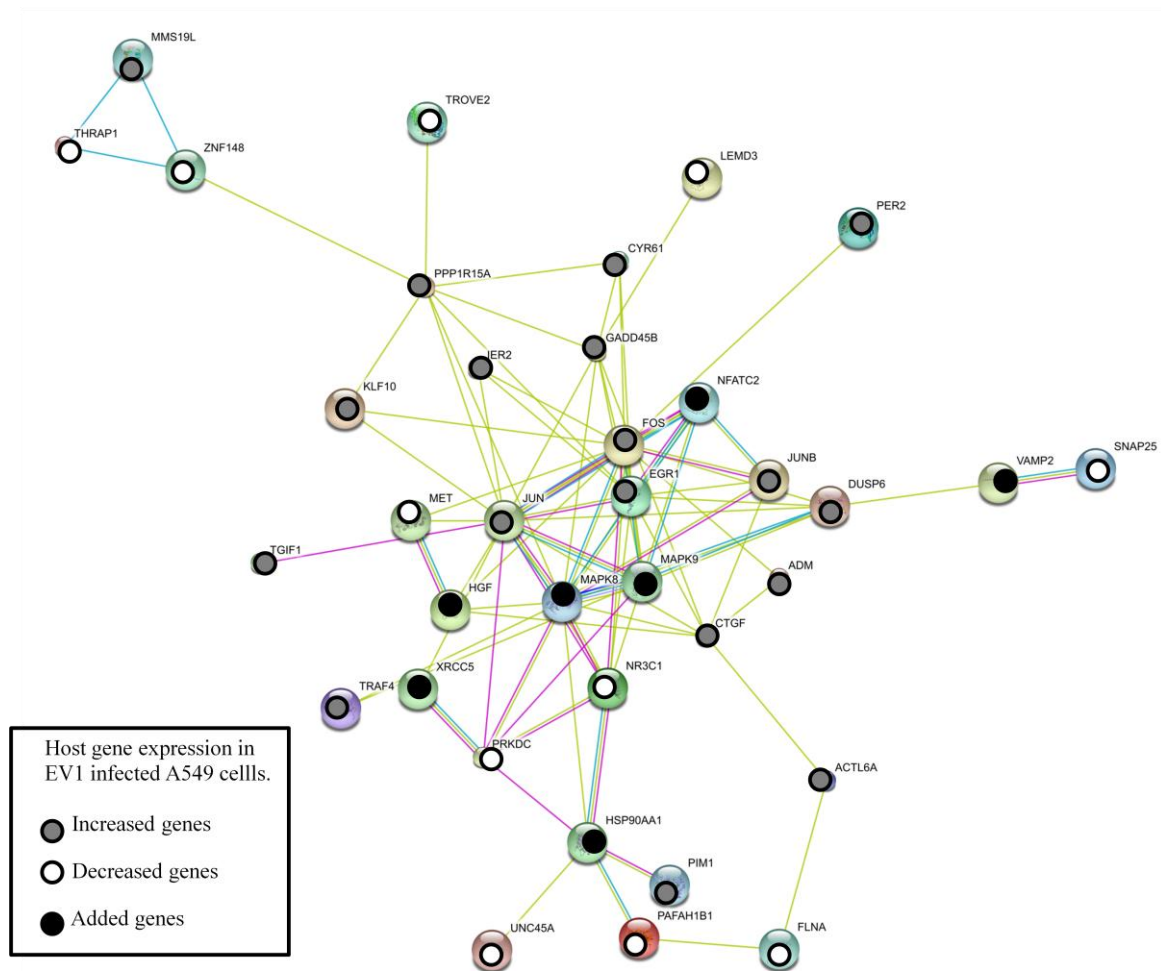
**Figure 1.** A. The replication cycle of EV1 in A549 cells. The amount of virus was determined by a plaque titration assay. B. IF labelling of EV1 by rabbit antiserum against EV1 in A549 cells at 0 h, 30 min, 2 h and 6 h p.i.

At 2h EV1 p.i., altered expressed genes included genes involved in cell communication, GTPase activity, JNK cascade, peptidase activity, transcription, anti-apoptosis and others. STRING 8.2 did not show a connection between these genes, but some of these genes, including MAP2K4, CAPN1, IL13RA1 and BCL2A1, could potentially have a role in early infection events and possibly have a role in defense against the virus. However, further investigation into the matter is required.

At 30 min and 2h EV1 p.i., the proteasome subunit beta type 2 (PSMB2) was induced twofold in infected cells, compared to mock-infected cells. PSMB2 is a part of the 20 S proteasome, which is a multicatalytic complex. The 20S proteasome forms a catalytic core in 26S proteasomes. The catalytic core is capped at one or both ends by 19S regulatory particle(s) (Rechsteiner *et al.*, 1993, Voges *et al.*, 1999). 19S caps structures recognize ubiquitinated proteins, and the substrate is further processed in the catalytic site of the 20S proteasome (Schlax *et al.*, 2007). The proteasome is involved in several cellular processes, including stress response (Finley *et al.*, 1987) and coordinated protein synthesis regulation, and it generally has an inhibitory effect on translation of cellular mRNA. Proteasome ubiquitination has been shown to be important in the pathogenesis of the enteroviruses CBV3 and PV. CBV3 infection enhances protein ubiquitination, and the ubiquitin-proteasome pathway is needed for optimal replication of the virus (Si *et al.*, 2008). The proteasome activity could possibly be involved in host cell stress response to the virus or be part of virus regulation of cellular translation.

In conclusion, the fact that only few genes expression were altered indicate that the virus attachment to receptor and endocytosis cause only minor effects on host cell transcriptional machinery. These results are in line with previous results showing no effect on EV1 expression in HOSp $\alpha$ 2AW cells at 1h or 3h p.i. in a human cDNA array containing almost 600 genes (Pietiäinen *et al.*, 2000).

At 6h EV1 p.i, the differently expressed genes included several different functional classes, such as genes involved in transcription, regulation of translation, apoptosis, defend respond, cell-cell adhesion, cell cytoskeleton, motility, catalytic activity, cell signaling, IEGs and others, including several genes whose function is not known yet. Analysis of the interactions of the differently expressed genes by STRING 8.2 database (Jensen *et al.*, 2009) showed a main cluster of IEGs connected to several other functional genes (Fig 2.). IEGs are a class of genes that show rapid and usually transient activation in the absence of the novo protein synthesis (Platenik *et al.*, 2000), in response to a wide variety of cellular stimuli.



**Figure 2.** Altered gene products associated with IEGs 6 h after EV1 infection. Induced genes are marked with a grey sphere, decreased genes with a white sphere and associated genes, added based on the STRING 8.2 database, are marked with a black sphere.

No difference in IEG gene expression was observed before 6 h EV1 p.i. Although  $\alpha\beta1$  integrin-mediated cell adhesion to type I collagen is known to induce certain IEGs, the activation of IEGs transcription in EV1 infected cells has been shown to require viral replication (Huttunen *et al.*, 1997). EV1 6h p.i. in A549 cells induced the expression of several IEGs, including cysteine-rich, angiogenic inducer, 61 (CYR61), JUNB, JUN, immediate early response 2 (IER2), pim-1 oncogene (pim-1), Krueppel-like factor 10 (KLF10), connective tissue growth factor (CTGF) and Polo-like kinase 2 (PLK2) (Table 1). Furthermore, two additional IEGS, early growth response 1 (EGR1) and FOS, were induced during EV1 infection, though they were expressed at low expression values that were slightly under the chosen cut-off level. In former studies many of these IEGs have been reported to be differently expressed during enterovirus infection (Huttunen *et al.*, 1997, Huttunen *et al.*, 1998, Johannes *et al.*, 1999, Kim *et al.*, 2004, Lang *et al.*, 2008, Pietiäinen *et al.*, 2000).

**Table 1.** Examples of significantly altered gene expression in EV1-infected cells 6 h p.i. The ratios represent values of infected cells (EV1)/uninfected cells (C).

Induced/downregulated gene	Accession No.	EV1	C	Ratio
Murine osteosarcoma viral oncogene homolog (FOS)	NM_005252.2	33	7	+4,8
Early growth response 1 (EGR1)	NM_001964.1	38	11	+3,5
Hairy and enhancer of split 1 (Drosophila) (HES-1)	NM_005524.2	57	19	+3,0
Meningioma expressed antigen 5 (hyaluronidase) (MGEA5)	NM_012215	112	41	+2,7
Protein phosphatase 1, regulatory subunit 15A (PPP1R15A)	NM_014330.2	92	38	+2,4
PIM1 oncogene	NM_002648.1	95	41	+2,3
Actin-like 6A (ACTL6A)	NM_004301.1	55	23	+2,3
Growth arrest and DNA-damage-inducible, beta (GADD45B)	NM_015675.1	82	37	+2,2
Dual specificity phosphatase 6 (DUSP6)	BC003143.1	85	40	+2,1
RNA binding motif protein 5 (RBM5)	NM_005778.1	77	37	+2,1
CDC-like kinase1 (CLK1)	AI251890	45	21	+2,1
Rab geranylgeranyltransferase, beta subunit (RABGGTB)	U49245.1	305	151	+2,0
JUN	NM_002228.2	86	43	+2,0
Vacuolar protein sorting 13 homolog C ( <i>S. cerevisiae</i> ) (VPS13C)	NM_017684.1	21	57	-2,7
LEM domain containing 3 (LEMD3)	NM_014319.2	18	48	-2,7
Quinoid dihydropteridine reductase (QDPR)	NM_000320.1	57	151	-2,6
Clone RP5-1121G12 on chromosome 20; C20orf104 and SCAND1	AL109965	35	80	-2,2
Chromosome 8 open reading frame 4 (C8ORF4)	NM_020130.1	47	98	-2,1
cDNA DKFZp566I043	AA160522	40	84	-2,1
Chromosome 8 open reading frame 4 (C8ORF4)	NM_020130.1	47	98	-2,0
Cadherin 2, type 1, N-cadherin (neuronal) (CDH2)	NM_001792.1	38	76	-2,0

Cysteine-rich, angiogenic inducer, 61 (CYR61) and connective tissue growth factor (CTGF) both belong to the CCN family of integrin-binding matrix signaling modulators (Moussad & Brigstock, 2000). CYR61 regulates cell proliferation, differentiation, apoptosis, adhesion, migration, apoptosis and extracellular matrix production. Cyr61 expression has been shown to increase during PV infection and CBV3 infection (Johannes *et al.*, 1999). Cyr61 could potentially enhance EV1 replication in host cell, since it has been shown to have a positive effect on both CBV3 (Kim *et al.*, 2004) and herpes simplex virus 1 (HSV-1) replication (Kurozumi *et al.*, 2008), and CYR61 siRNA introduced into Hela cells was able to reduce the CBV3 infection titer (Kim *et al.*, 2004). Furthermore, CYR61 is suggested to trigger apoptosis in CBV3-infected Hela cells (Kim *et al.*, 2004). CTGF promotes endothelial cell growth, migration, adhesion, and cell survival (Moussad & Brigstock, 2000). In a murine model of chronic CBV3 myocarditis, CTGF was found to be strongly induced (Lang *et al.*, 2008). Moreover, in a signaling cascade that has been implicated to be part of diabetic neuropathy, CTGF enhanced the TGF $\beta$ /Smad signaling

pathway by transcriptional suppression of Smad7, an antagonist for TGF $\beta$ . This was followed by an induction of the transcriptional factor Krueppel-like factor 10 (KLF10) (Wahab *et al.*, 2005), an IEG found to be induced in this study. KLF10 was reported to be crucial for the CTGF-mediated downregulation of Smad 7 (Wahab *et al.*, 2005). Overexpression of KLF10 has been shown to induce p53 mitochondrial apoptosis, and the level of suppression of this gene is associated with the invasive pattern of breast cancer (Subramaniam *et al.*, 1998). Moreover, the expression of KLF10 has been reported to be induced during CBV3 infection in Hela cells (Kim *et al.*, 2004) and in EV1 infection 10h p.i. in HOS pa2AW cells (Pietiäinen *et al.*, 2000).

Furthermore, CTGF has also been described to be activated by JUN/AP-1 (Yu *et al.*, 2009). JUN and JUNB genes are components of the dimeric AP-1 transcription factor that regulates a wide range of cellular processes, such as cell proliferation, death survival and differentiation (Shaulian & Karin, 2002). The transcription of both JUN and JUNB, increased during EV1 replication in this study, and has previously been shown to increase during EV1 and EV7 infection 5-10 h p.i. (Huttunen *et al.*, 1997, Huttunen *et al.*, 1998, Pietiäinen *et al.*, 2000). The EV1 activated stress-related p38 mitogen activated protein kinase (MAPK) and increased the expression of JUNB (Huttunen *et al.*, 1998). All or some of the IEGs CYR61, CTGF, KLF10, JUN and JUNB could possibly be involved in the signaling pathway induced by EV1 infection as described above. Some of these genes could also be involved in virus regulation of host genome replication and/or cell survival.

PV infections have been shown to induce both Pim-1 (Johannes *et al.*, 1999, Pietiäinen *et al.*, 2000) and Polo-like kinase 2 (PLK2) (Johannes *et al.*, 1999) expression in host cell. Both PLK2 and Pim-1 could facilitate cell survival in EV1 infection, since they have been shown to activate antiapoptotic pathways in cells (Matsumoto *et al.*, 2009), although PLK2 can also function as a tumor suppressor inducing apoptosis (Syed *et al.*, 2006).

The only IEG induced by EV1 infection in this study that to our knowledge has not previously been reported to be differently expressed during enterovirus infection was the immediate early response 2 (IER2) gene. IER2 is suggested to act as a putative transcriptional factor. A possible link to IER2 cell death-inducing potential represents the gene of protein phosphatase 1 and the regulatory (inhibitor) subunit 15A (PPP1R15A) (Kruger *et al.*, 2006), the expression of which induced over 2-fold in EV1-infected cells. PPP1R15A is a DNA damage-response gene able to induce apoptosis (Grishin *et al.*, 2001). ETR2 has also been found to increase the expression of early growth response 1 (EGR1) in rat fibroblast (Shin *et al.*, 2002). EGR1 induced by genotoxic stress was reported to stimulate the expression of growth arrest and DNA-damage-inducible, alpha (GADD45A) and GADD45B and mediate epidermal cell death (Thyss *et al.*, 2005).

**Table 2.** IEG-associated genes listed by function altered during EV1-infection used in the analysis by the STRING 8.2- database (see Fig.2).

<b>Induced/downregulated gene</b>	<b>Accession No.</b>	<b>EV1</b>	<b>C</b>	<b>Ratio</b>
<b>Transcription</b>				
Murine osteosarcoma viral oncogene homolog (FOS)	NM_005252.2	33	7	+4,8
Early growth response 1 (EGR1)	NM_001964.1	38	11	+3,5
JUN	NM_002228.2	86	43	+2,0
Immediate early response 2 (IER2)	NM_004907.1	566	299	+1,9
Period homolog 2 (Drosophila) (PER2)	NM_022817.1	86	48	+1,8
Homeobox protein TGIF1 (5'-TG-3'-interacting factor 1) (TGIF1)	NM_003244.1	314	194	+1,6
jun B proto-oncogene (JUNB)	NM_002229.1	103	62	+1,6
MMS19-like (MET18 homolog, <i>S. cerevisiae</i> ) (MMS19L)	NM_022362.1	76	46	+1,6
Kruppel-like factor 10 (KLF10)	NM_005655.1	201	134	+1,5
Zinc finger protein 148 (ZNF148)	NM_021964.1	28	47	-1,6
TROVE domain family, member 2 (TROVE2)	M25077.1	129	217	-1,7
nuclear receptor subfamily 3, group C, member 1 (NR3C1)	X03348.1	115	188	-1,6
THRAP1 - Thyroid hormone receptor-associated protein complex	NM_005121.1	66	102	-1,5
<b>Apoptosis</b>				
Protein phosphatase 1, regulatory (inhibitor) subunit 15A (PPP1R15A)	NM_014330.2	92	38	+2,4
TNF receptor-associated factor 4 (TRAF4)	NM_004295.1	65	39	+1,7
Growth arrest and DNA-damage-inducible, beta (GADD45B)	NM_015675.1	82	37	+2,2
Dual specificity phosphatase 6 (DUSP6)	BC003143.1	85	40	+2,1
<b>Defence respond</b>				
FOS - FBJ murine osteosarcoma viral oncogene homolog	NM_005252.2	33	7	+4,8
Nuclear receptor subfamily 3, group C, member 1 (NR3C1)	X03348.1	115	187	-1,6
Zinc finger protein 148 (ZNF148)	NM_021964.1	28	47	-1,6
<b>Catalytic activity</b>				
<b>Protein kinase activity</b>				
Pim-1 oncogene	NM_002648.1	95	41	+2,3
Polo-like kinase 2 (Drosophila) (PLK2)	NM_006622.1	209	116	+1,8
MMS19-like (MET18 homolog, <i>S. cerevisiae</i> ) (MMS19L)	NM_022362.1	76	46	+1,6
Met proto-oncogene (MET) (hepatocyte growth factor receptor)	U19348.1	77	132	-1,7
Protein kinase, DNA-activated, catalytic polypeptide(PRKDC)	NM_006904.5	115	184	-1,6
<b>Other genes possessing catalytic activity</b>				
Dual specificity phosphatase 6 (DUSP6)	BC003143.1	85	40	+2,1
Platelet-activating factor acetylhydrolase, isoform Ib, subunit 1 (45kDa) (PAFAH1B1)	NM_000430	71	129	-1,8
<b>cytoskeleton/motility</b>				
Actin-like 6A (ACTL6A)	NM_004301.1	55	23	+2,3
Connective tissue growth factor (CTGF)	M92934.1	66	34	+1,9
Platelet-activating factor acetylhydrolase, isoform Ib, alpha subunit 45kDa (PAFAH1B1)	NM_000430	71	130	-1,8
Filamin A, alpha (actin-binding protein-280) (FLNA)	NM_001456	139	252	-1,8
<b>IEGs</b>				
FOS - FBJ murine osteosarcoma viral oncogene homolog	NM_005252.2	33	7	+4,8
Early growth response 1 (EGR1)	NM_001964.1	38	11	+3,5
Pim-1 oncogene (Pim-1)	NM_002648.1	95	41	+2,3
JUN	NM_002228.2	86	43	+2,0
Immediate early response 2 (IER2)	NM_004907.1	566	299	+1,9

Connective tissue growth factor (CTGF)	M92934.1	66	34	+1,9
Polo-like kinase 2 (PLK2)	NM_006622.1	209	116	+1,8
Cysteine-rich, angiogenic inducer, 61 (CYR61)	NM_001554.1	125	79	+1,6
jun B proto-oncogene (JUNB)	NM_002229.1	103	62	+1,6
Kruppel-like factor 10 (KLF10)	NM_005655.1	201	134	+1,5
<b>Other</b>				
Adrenomedullin (ADM)	NM_001124.1	583	346	+1,7
Ribosomal RNA processing 7 homolog A (S. cerevisiae) (RRP7A)	NM_015703.1	128	82	+1,6
LEM domain containing 3 (LEMD3)	NM_014319.2	18	48	-2,7
Synaptosomal-associated protein, 25kD (SNAP25)	NM_003081.1	60	109	-1,8

GADD45B was induced by EV1-infected A549 cells, and both GADD45A and GADD45B genes activate cell death in cells failing in DNA repair. In a former study, EGR1 expression increased at 6 h p.i. in EV1-infected HOS p $\alpha$ 2AW, and the induction was increased over two-fold at 10h p.i. Furthermore, at this time point the GADD45A gene was also induced (Pietiäinen *et al.*, 2000). This represents two possible pathways by which EV1 could regulate cell survival by activating the ETR2 gene. In addition, further examples of mechanisms by which EV1 could possibly control cell survival included cell regulation mechanisms of some altered genes reported to either suppress or induce apoptosis. In EV1-infected cells the expression of the genes RNA binding motif protein 5 (RBM5) and dual specificity phosphatase 6 (DUSP6), of which both have been reported to activate apoptosis, were over 2-fold increased (Table 2). In a former study, upregulation of cellular expression of RBM5 in A549 cells was shown to suppress cell proliferation by increasing apoptosis and inducing the cell cycle arrest in G<sub>1</sub> (Oh *et al.*, 2006). Together these implicated some possible mechanisms by which EV1 could regulate the host cell survival of A549 cells. However, this needs to be analyzed in further studies. A study by Huttunen *et al.* suggested that a minor part of the HOS p $\alpha$ 2AW cells undergo apoptosis during infection by EV1 at 12 h p.i. or by Semliki Forrest virus at 24 h p.i. (Huttunen *et al.*, 1998), a virus shown to induce apoptosis in several cell lines (Glasgow *et al.*, 1997, Scallan *et al.*, 1997).

Our study also suggested possible roles for genes involved in cytoskeleton and motility during EV1 infection in A549 cells. This involved platelet-activating factor acetylhydrolase, isoform Ib, alpha subunit 45kDa (PAFAH1B1), and filamin A (FLNA) linked to IEGs by predicted interaction pathway by STRING 8.2 database (Jensen *et al.*, 2009) (Fig. 2).

In a study by Kondratova *et al.*, PV 3A protein was described to inhibit the action of PAFAH1B1 by blocking PAFAH1B1-containing complexes on the cytoplasmic surface of the ER and the Golgi, thereby blocking the vesicular transport from ER to Golgi. This event leads to prompt disappearance of short-living receptors from plasma membrane and loss of cell sensitivity to TNF and interferon (Kondratova *et al.*, 2005). A possible role of



PAFAH1B1 in neuronal disease caused by PV infection has also been suggested, since neurons are most sensitive to defiance of PAFAH1B1 protein activity and decrease of PAFAH1B1 concentration (Fogli *et al.*, 1999). PAFAH1B1 may also protect EV1 from host defence by a mechanism similar to the one reported for PV, and it could be speculated whether this gene could also play a role in EV1 neuronal infections.

In conclusion, several IEGs were expressed in a similar pattern in EV1 infected A549 cells as reported in earlier studies for EV1 and also for other enteroviruses (Huttunen *et al.*, 1997, Huttunen *et al.*, 1998, Johannes *et al.*, 1999, Kim *et al.*, 2004, Lang *et al.*, 2008, Pietiäinen *et al.*, 2000). Together these results suggest a central role for certain IEGs in signaling pathways induced by EV1 replication. During the EV1 replication pattern several differently expressed genes, known to play a role in apoptosis, seemed to favor apoptosis over cell survival, although some specific gene expressions also suggested the possibility of antiapoptotic events in the cell. Furthermore, differently expressed genes involved in cytoskeleton and motility could possibly affect the host cell by negatively affecting the structural integrity of the cell, and thus lead to growth arrest and hamper host cell defense. However, further studies are needed to clarify the role of these genes in EV1 replication.

## 6 CONCLUSIONS

Integrins are a family of cell adhesion receptors that mainly recognize ECM ligands and cell-surface ligands, but some soluble ligands have also been reported. Integrins have been implicated in various diseases and disease processes, including inflammation, atherosclerosis and cancer. Moreover, several viral pathogens, including enteroviruses, use integrins as cellular receptors. Enteroviruses have also been suggested to be involved in the etiopathogenesis of type 1 diabetes. The thesis focused on studying the role of integrins in the pathogenesis of metastasis to cortical bone, type 1 diabetes and echovirus 1 infection.

Favored adherence of breast cancer cells to bone-specific factors may facilitate preferential metastasis to the skeleton. The most important integrins in the initial attachment of breast cancer cells to bone were studied in an in vitro microplate attachment assay, measuring the binding of MDA-MD-231 breast cancer cells to bovine cortical bone disks. The results suggest  $\alpha 2\beta 1$  and  $\alpha 3\beta 1$  to be the key receptors in the initial anchoring of breast cancer cells to cortical bone matrix.

Enterovirus infection has been suggested to be associated with the pathogenesis of T1D. Increased prevalence and higher enterovirus antibody levels, as well as presence of enterovirus RNA in blood, have been reported in individuals with recent onset T1D. The possibility that sensitivity to enterovirus infections could correlate with individual variation in enterovirus receptor genes, including some integrins, was investigated by sequence analysis. The predicted polypeptide domains known to be critical for virus binding in the major enterovirus receptors were determined. In the PVR, an SNP causing an amino acid change was detected in four individuals with T1D. The patients also had a lower level of neutralizing antibody against echovirus 30, compared to healthy children. However, the findings of direct connection to T1D should be analyzed in a larger cohort to obtain statistically sustainable results.

Echovirus 1 (EV1) binds to the  $\alpha 2$  I domain ( $\alpha 2$ I) of the human  $\alpha 2\beta 1$  integrin. EV1 has been reported to enter a host cell either via lipid rafts, by macropinocytosis or, through caveolae. To determine if EV1 could initiate productive infection by using clathrin-directed entry, a chimeric receptor was constructed by inserting  $\alpha 2$ I into the extracellular terminus of transferrin receptor (TfR), responsible for transport of transferrin-bound iron through clathrin-dependent endocytosis. In immunofluorescence and confocal microscopy studies, the TfR- $\alpha 2$ I chimeric receptor when transfected into non-permissive cells, was localized to the cell surface and also in vesicular structures in the cytoplasm. EV1 was able to bind the chimeric receptor and, consequently, the chimeric virus receptor complex was internalized through the clathrin-mediated endocytosis to the early endosomes and recycling endosomes. After 1 h, the chimeric receptor was completely separated from the

virus as it was recycled to the plasma membrane, whereas the virus remained in intracellular vesicles. Based on quantitative RT-PCR detecting both positive and negative strand viral RNA, the replication cycle of EV1 was initiated in the cells carrying the chimeric receptor. Furthermore, in plaque assay experiments infected TfR- $\alpha$ 2I-transfected NIH3T3 cells were shown to produce infectious virus, although in low quantities. The results indicate that the natural entry route is not an absolute requirement for EV1 replication; instead, the virus can adapt to use alternative internalization mechanisms.

Previous studies have shown that certain immediate early genes (IEGs) are activated in response to EV1 infection. To elucidate the effect of EV1 and  $\alpha$ 2 $\beta$ 1 integrin interaction, virus endocytosis and replication in human A549 lung carcinoma cells, cDNA microarray analysis was performed. In samples collected during virus endocytosis (30 min and 2h p.i.) only a few genes were differently expressed. Six hours after initiation of the infection, a cytopathic effect was observed in the cells and approximately 100 genes (0.53%) of those investigated were differently expressed, including IEGs, genes affecting the host cell immune response and apoptosis. Several of the induced IEGs, such as CYR61, JUNB, JUN, PIM1, KLF10, CTGF and PLK2, have been reported to be expressed during infection of other enteroviruses. STRING-analysis of this gene pattern detected cluster, consisting mainly of IEGs, suggested IEGs to be primarily associated with EV1 replication in host cell.

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