

# Thesis Title

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# **Erklärung**

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# Nomenclature

AAV	Adeno-associated virus
AMDV	Aleutian mink disease virus
B19V	Human parvovirus B19
Bp	Base pair
BPV	Bovine parvovirus
ChPV	Chicken parvovirus
CPV	Canine parvovirus
Da	Dalton
DMEM	Dulbecco modified Eagle's medium
DNA	Deoxyribonucleic acid
DPV	Duck parvovirus
dsDNA	Double stranded DNA
EPC	Erythroid progenitor cell
FCS	Fetal calf serum
FPV	Feline parvovirus
GFAV	Gray fox amdovirus
GmDNV	Galleria mellonella densovirus
GPV	Goose parvovirus
HBoV	Human Bocavirus
HBV	Hepatitis B virus
HCV	Hepatitis C virus
HIV	Human immunodeficiency virus
IF	Immunofluorescence
IP	Immunoprecipitation
ITR	Inverted terminal repeat
Kb	Kilo base
kDa	Kilodalton
KRV	Kilham rat virus
mAb	Monoclonal antibody
MVM	Minute virus of mice
MVMi	Immunosuppressive strain of MVM

MVMp	Prototype strain of MVM
NIH	National institutes of health
Nt	Nucleotide
ORF	Open reading frame
PARV4	Parvovirus 4
PCR	Polymerase chain reaction
PEC	Poult enteritis complex
PEMS	Poult enteritis mortality syndrome
PLA2	Phospholipase A2
PPV	Porcine parvovirus
PstDNV	Penaeus stylirostris densovirus
qPCR	Quantitative PCR
RNA	Ribonucleic acid
RSS	Runting-stunting syndrome
SN	Supernatant
ssDNA	Single stranded DNA
SV40	Simian vacuolating virus 40 or Simian virus 40
TuPV	Turkey parvovirus
VP1u	VP1 unique region

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## **Part I**

# **Introduction**





# 1 Introduction

## 1.1 Morphology

Parvoviruses belong to the smallest of isometric viruses. A linear single-stranded DNA genome of about 5 kb is packaged into the virus capsid [1, 2, 3]. They are non-enveloped and their diameters range from 215 Å (Penaeus stylirostris densovirus, PstDNV) to 255 Å (CPV). The icosahedral nature of parvoviruses was shown unambiguously by X-ray crystallography. The capsid surface of some, particularly invertebrate, parvoviruses appears to be smooth (Galleria mellonella densovirus, GmDNV) whereas others (Adeno-associated virus-2, AAV-2) are spiky at the 3- or 5-fold symmetry axes [4, 5].

## 1.2 Physicochemical properties

Infectious parvovirus virions are composed of about 75 % protein and 25 % DNA. Their molecular weight is approximately  $5.5\text{--}6.2 \times 10^6$ . The virion buoyant density is 1.39 to 1.43 gcm<sup>-3</sup>, measured in CsCl gradients [6, 7]. Since parvoviruses are devoid of a lipid envelope, mature virions are stable in the presence of lipid solvents. In particular, animal parvoviruses show considerable heat resistance. Most species remain stable and infectious on exposure to pH 7-9 or incubation at 56 °C for 60 min [8, 9, 10, 11]. Only harsh conditions, such as treatment with formalin,  $\beta$ -propiolactone, hydroxylamine, ultraviolet light, and oxidizing agents as for example sodium hypochlorite ensure effective virus inactivation [12, 13, 14, 15].

## 1.3 Taxonomy

The classification of the *Parvoviridae* family is based on morphological and functional characteristics. Parvoviruses are ubiquitous animal and insect pathogens that belong to the smallest DNA-containing viruses. Hence the prefix "parvum" which means small in Latin. The name "parvovirus" was first introduced to the literature by Carlos Brailovsky, in an early attempt to establish a latinized binomial taxonomy system for viruses, in 1966 [16]. The age of the *Parvoviridae* family may exceed 40 to 50 million years [17]. Apart from their ancient history, the genomes of parvoviruses were affirmed to display

similar high mutation rates as RNA viruses [18, 19, 20]. Such high mutation rates in conjunction with the long history might be a reason for the vast genetic divergence and high diversity of the family *Parvoviridae*. The *Parvoviridae* family comprises all non-enveloped, isometric, small DNA viruses that contain linear single-stranded genomes. Indeed, parvoviruses are the only viruses in the known biosphere that have both single-stranded and linear DNA genomes. The encapsidated single genomic molecule is 4-6 kb in length and terminates in palindromic duplex hairpin telomers. In general, there are two large open reading frames, ORF1 and ORF2, encoding for the non-structural protein(s) and the capsid protein(s), respectively. In some cases, an additional ORF3 has been identified that encodes an accessory protein, such as NP1, a non-structural protein only found in members of the genus *Bocaparvovirus* and in PPV4 a member of the genus *Copiparvovirus* [21, 22, 23]. As a consequence of such a simple genome, parvoviruses are highly dependent on their host for diverse functions in their reproduction [4, 24]. The terminal hairpins are fundamental for the unique replication strategy of the *Parvoviridae* family and hence serve as an invariant hallmark for classification. Members of the family *Parvoviridae* infect a wide variety of hosts, ranging from insects to primates. Depending on their host range, the *Parvoviridae* are subdivided into *Parvovirinae* infecting vertebrates and *Densovirinae* infecting insects and other arthropods, respectively. The *Parvovirinae* subfamily is further subdivided into eight genera: *Amdoparvovirus*, *Aveparvovirus*, *Bocaparvovirus*, *Copiparvovirus*, *Dependoparvovirus*, *Erythroparvovirus*, *Protoparvovirus* and *Tetraparvovirus* [25]. The subdivision into the eight genera is based on differences in transcription maps, organization of the ITRs, the ability to replicate efficiently either autonomously or with helper virus, the sense of the ssDNA that is packaged in separate virions, and sequence homology amongst the *Parvovirinae* subfamily [26, 5].

### 1.3.1 The *Parvovirinae* subfamily

#### ***Amdoparvovirus***

Mature virions exclusively contain negative strand genomic DNA of approximately 4.8 kb in length harbouring dissimilar palindromic sequences at each end [27, 28]. A single promoter located at map unit 3 at the left end of the genome generates all mRNA transcripts of AMDV. Polyadenylation may occur at either the proximal site or at the distal site of the genome. Thus, the transcription profile of the genus *Amdoparvovirus* most closely resembles that of the genus *Erythroparvovirus* []. Only two distant species have been reported. Firstly, *Carnivore amdoparvovirus 1*, which comprises only Aleutian mink disease virus (AMDV) and secondly, *Carnivore amdoparvovirus 2*, which encompasses solely gray fox amdovirus (GFAV) [29]. Permissive replication is tightly restricted

to Crandell feline kidney cells. The virion surface displays three mounds elevated around the threefold icosahedral axis of symmetry. Several structure features were ascertained to be similar to those found in B19V, CPV, FPV, and MVM. Such appearance is comparable to those observed for the genus *Dependoparvovirus* [30]. Remarkably, there is no evidence of a phospholipase 2A enzymatic core within the naturally truncated N-VP1 terminus of members belonging to the genus *Amdoparvovirus* as it is common to the other genera of the subfamily *Parvovirinae* [5].

### ***Aveparvovirus***

*Aveparvovirus* is a new genus within the *Parvovirinae* subfamily that comprises of the species chicken parvovirus and turkey parvovirus. The name *Aveparvovirus* is derived from avian parvoviruses, referring to the hosts from which the members were isolated. Although these viruses were identified for years in the intestinal tracts of poultry [31, 32, 33], analysis of the complete nucleotide sequence has been reported only recently. Phylogenetic study of the genomic sequences revealed that interestingly, ChPV and TuPV do not group phylogenetically with GPV and DPV, that are members of the genus *Dependoparvovirus*. It was clearly demonstrated that ChPV, along with the closely related TuPV, represents the prototype of a novel genus within the *Parvovirinae* subfamily [34, 35]. Identical direct repeat sequences flank the genome at both the 3' and the 5' end. Each of which contains a 39 nt ITR that is predicted to form a hairpin structure. ChPV and TuPV feature an overall genome organization similar to that of members of the genus *Bocaparvovirus* [36]. Although it has been demonstrated that ChPV can induce clinical signs in broiler chickens that show characteristics of the runting-stunting syndrome (RSS) [37], the role of avian parvoviruses in the aetiology of enteric diseases in poultry still remains to be demonstrated. RSS, also referred to as malabsorption syndrome, is characterized by significantly decreased egg hatchability, poorly developed hatched chickens, serious growth retardation, diarrhoea, enteritis, disturbed feathering, low vitality, and bone disorders [38, 39, 40]. Currently, the pathogenicity of TuPV has not been investigated yet. The predominant enteric diseases in turkeys are known as poult enteritis complex (PEC) [41] or the more drastic poult enteritis mortality syndrome (PEMS) [42]. Understanding the role of avian parvoviruses in PEMS, PEC, and RSS is of great interest due to the economic losses resulting from enteric diseases in poultry. [35].

### ***Bocaparvovirus***

The name of the genus is derived from bovine and canine, referring to the two hosts of the first identified members of this genus. The genomes of members of the genus

*Bocaparvovirus* are quite distinct from all other viruses in the subfamily *Parvovirinae*. As the members of the genera *Protoparvovirus* and *Amdoparvovirus* they contain non-identical imperfect palindromic sequences at both ends of their 5.5 kb genome. Mature virions contain mainly, but not exclusively, negative strand ssDNA [43, 44]. All RNA transcripts are generated from a single P4 promoter at the left-hand end of the genome. The transcripts are alternatively spliced and polyadenylated either at an internal site or at the 3'-end of the genome [45]. Noteworthy, bovine parvovirus (BPV), the main representative, encodes a 22.5 kDa nuclear phosphoprotein, NP1, whose function still remains unknown. This protein is distinct from any other parvovirus-encoded polypeptide [21]. A human bocavirus was first described in 2005, when it was detected in nasopharyngeal aspirates of young children with respiratory tract infection [46, 47]. More recently, HBoV has been identified in diarrheal feces of children with gastroenteritis [48]. HBoV infection is associated with acute respiratory symptoms and is usually detected in children under 2 years of age [49, 50, 51]. HBoV infections have been reported world-wide and HBoV was often isolated in respiratory samples of diseased as well as asymptomatic patients sometimes long after the primary infection. Therefore, it can be frequently detected even though it is not likely acting as a pathogen, thus complicating the use of PCR in diagnostics. Furthermore, long-term persistence may explain that HBoV infection among adults was predominantly reported in association with immunosuppression or immunodeficiency [51, 52].

### ***Copiparvovirus***

Based on phylogenetic analysis, the genus *Copiparvovirus* encompasses PPV4 and BPV2. PPV4 was identified in clinical samples from swine herds [23, 53, 54] and represents a distinct branch together with BPV2 [46]. The name *Copiparvovirus* refers to cows and pigs, the hosts from which members of that genus were isolated. PPV4 is unique in that it is phylogenetically most closely related to BPV2 but the coding capacity and genome organization resemble more those of viruses of the genus *Bocaparvovirus*. Whereas the ORF3 encoded proteins of bocaviruses share significant identity among themselves, the PPV4 ORF3 encoded protein does not display homology with any protein in the GenBank database [23, 53]. Recently, two novel porcine parvoviruses, PPV5 and PPV6, were discovered [55, 56]. Characterization of their nucleotide sequences revealed that their full-length genomes are approximately 6 kb in length. As a consequence of this capacious genome size, especially their capsid protein encoding genes are exceptionally large. Interestingly, the genomic organization of PPV5 and PPV6 is different from PPV4 in that they lack the extra ORF3 in the middle of the genome. Moreover, PPV5 as well as PPV6 possess the conserved putative secretory PLA2 motif which is present in the capsid

protein of most parvoviruses but is lacking in PPV4. In spite of considerable differences in the genomic organization between BPV2, PPV5, and PPV6 on one hand and PPV4 on the other hand, phylogenetic analysis revealed a close evolutionary relationship of these viruses, suggesting that they share the same immediate ancestor [57, 56]. Since members of the genus *Copiparvovirus* were discovered quite recently, their biological characteristics, relatedness to disease, and potential clinical manifestations are still not fully understood [23, 53, 57, 56]. Especially, porcine parvovirus Kresse belonging to the genus *Protoparvovirus* is known to be an important pathogen responsible for embryonic and fetal death in swine, resulting in considerable losses in the pig industry worldwide [58, 59, 60, 61]. In order to clarify the precise role of the latest discovered members of the genus *Copiparvovirus* as causal agents for reproductive failure in breeding animals, more comprehensive epidemiologic studies are required in the future [56].

### ***Dependoparvovirus***

Positive and negative strand ssDNA is distributed indifferently among mature virions belonging to the genus *Dependoparvovirus* [62, 2]. The 4.7 kb DNA molecule contains identical ITRs of 145 nt, the first 125 nt of which form a palindromic sequence [63]. Three mRNA promoters that are located at map units 5, 19, and 40 initiate transcription that can be terminated in two polyadenylation sites located at the right-hand end or alternatively, in the middle of the genome [64, 65]. Common for all currently accepted replication-defective members of the genus *Dependoparvovirus* is their strict dependence upon helper adenoviruses or herpesviruses [66, 67, 68]. Therefore, their host range tropism strongly depends on the one of the helper virus. The only exceptions are the autonomously replicating duck and goose parvoviruses which are also comprised within the *Dependoparvovirus* genus based on phylogenetic analysis [5]. The most important members of this genus are the adeno-associated viruses (AAV). They attracted considerable interests since at least one of them, AAV-2, has been reported to integrate site-specifically into human chromosome 19 [69, 70, 71, 72]. This characteristic makes AAV a promising candidate for creating viral vectors for gene therapy [73, 74]. As a well characterized member of the *Dependoparvoviruses* AAV-2 represents the model virus among this genus.

### ***Erythroparvovirus***

Equivalent numbers of positive and negative sense ssDNA are packaged into infectious virions of the genus *Erythroparvovirus*. As in the case with the genus *Dependoparvovirus*, the 5.5 kb ssDNA molecule contains identical ITRs of 383 nt in length at both the 3' and the 5' end. The first 365 nt of those secondary elements form palindromic sequences

[75]. Transcription is regulated by a single mRNA promoter located at map unit 6 [76]. A distal polyadenylation site for use in termination of RNA synthesis is located at the far right side. Additionally, transcripts may be terminated at an unusual internal polyadenylation site in the middle of the genome [77]. Viruses belonging to this genus are highly erythrotropic, meaning that efficient replication only occurs in rapidly dividing erythroid progenitor cells (EPCs) such as erythroblasts and megakaryocytes present in the bone marrow. B19V, a widespread human pathogen that causes fifth disease, polyarthropathia, anemic crises in children with underlying hematological diseases (e.g. sickle cell anemia or thalassemia) and intrauterine infections (with hydrops fetalis in some cases) [78] represents the model virus among the genus *Erythroparvovirus*.

### ***Protoparvovirus***

Kilham Rat virus (KRV), a member of the genus *Protoparvoviruses* was the first member of the subfamily *Parvovirinae* to be discovered in 1959 [79]. Some members of the genus contain positive strand DNA in variable proportions up to 50 % [80]. However, in mature virions of most members, virtually only negative strand DNA occurs. What they have in common are their hairpin structures at both the 5' and 3' ends of the linear 5 kb ssDNA molecule that differ in both sequence and predicted structure [81]. Transcription of the genome is regulated by two mRNA promoters at map units 4 and 39 [82]. There is only one polyadenylation site at the 3' end. Viral replication provokes characteristic cytopathic effects in cell culture. Many species display hemagglutination with erythrocytes of one or several species, but not enforcedly of their natural host [83]. The genus *Protoparvovirus* is primarily represented by MVM [5, 24].

### ***Tetraparvovirus***

The genus *Tetraparvovirus* is a new genus that arose recently. To date, six species have been discovered, which were isolated from humans [84], chimpanzees, baboons [85], cows, pigs [86, 87, 88], as well as sheep [89]. RNA transcripts that encode the NS-proteins or the VP-proteins are generated from two promoters that are located at map units 6 and 38, respectively. Transcription can be terminated in two polyadenylation sites located at the right-hand end of the genome or alternatively, at an internal polyadenylation site. Since the full-length genome has not been sequenced yet, information of the terminal repeats is still lacking [90]. Analysis of the NS1 protein revealed a G2/M cell cycle arrest induced in NS1-expressing hematopoietic stem cells that clearly involved the predicted helicase motifs [91, 92, 93] of NS1. To date, no PLA2-like activity of expressed VP1u polypeptides has been demonstrated for any member of the genus *Tetraparvovirus* [90]. PARV4 is one of the only four groups of parvoviruses that is known to infect humans besides B19V,

HBoV, and AAV. It was first reported in an intravenous drug user who was positive for HBV infection in 2005. The patient suffered from arthralgia, confusion, diarrhea, fatigue, neck stiffness, night sweat, pharyngitis, and vomiting. PARV4 represents a phylogenetic deeply rooted lineage between avian dependoviruses and bovine parvovirus type 3 [84]. So far, most evidence about PARV4 transmission comes from patients who had engaged in high risk behaviour for blood borne viral infections, where PARV4 infection basically was observed to be strongly associated with HCV and HIV infection [94, 95, 96]. However, there are several reports of parenteral transmission in the absence of HIV, HBC, or HCV. PARV4 IgG has been documented independently from other blood borne viruses among injecting drug users [97], in haemophilia patients [98], and in patients who were subjected to intra-muscular injections in the past [99]. Currently, no definitive clinical syndrome was associated with PARV4 infection and there is no evidence for a potential pathogenicity of related members of the genus *Tetraparvovirus* in animals [86]. PARV4 viraemia appears to be asymptomatic [100] and co-existing blood borne viruses do not increase severity [95].



Table 1.1: The type species for each genus is indicated in bold type. [25]

Genus	Species	Virus or virus variants	Abbr.	ACNO <sup>1</sup>
<i>Amdoparvovirus</i>	<b><i>Carnivore amdoparvovirus 1</i></b>	Aleutian mink disease virus	AMDV	JN040434
	<i>Carnivore amdoparvovirus 2</i>	Gray fox amdovirus	GFAV	JN202450
<i>Aveparvovirus</i>	<b><i>Galliform aveparvovirus 1</i></b>	Chicken parvovirus	ChPV	GU214704
		Turkey parvovirus	TuPV	GU214706
<i>Bocaparvovirus</i>	<i>Carnivore bocaparvovirus 1</i>	Canine minute virus	CnMV	FJ214110
	<i>Carnivore bocaparvovirus 2</i>	Canine bocavirus 1	CBoV	JN648103
	<i>Carnivore bocaparvovirus 3</i>	Feline bocavirus	FBoV	JQ692585
	<i>Pinniped bocaparvovirus 1</i>	California sea lion bocavirus 1	CslBoV1	JN420361
		California sea lion bocavirus 2	CslBoV2	JN420366
	<i>Pinniped bocaparvovirus 2</i>	California sea lion bocavirus 3	CslBoV3	JN420365
	<i>Primate bocaparvovirus 1</i>	Human bocavirus 1	HBoV1	JQ923422
		Human bocavirus 3	HBoV3	EU918736
		Gorilla bocavirus	GBoV	HM145750
	<i>Primate bocaparvovirus 2</i>	Human bocavirus 2a	HBoV2a	FJ973558
		Human bocavirus 2b	HBoV2b	FJ973560
		Human bocavirus 2c	HBoV2c	FJ170278
		Human bocavirus 4	HBoV4	FJ973561
	<b><i>Ungulate bocaparvovirus 1</i></b>	Bovine parvovirus	BPV	DQ335247
	<i>Ungulate bocaparvovirus 2</i>	Porcine bocavirus 1	PBoV1	HM053693
		Porcine bocavirus 2	PBoV2	HM053694
		Porcine bocavirus 6	PBoV6	HQ291309
	<i>Ungulate bocaparvovirus 3</i>	Porcine bocavirus 5	PBoV5	HQ223038
	<i>Ungulate bocaparvovirus 4</i>	Porcine bocavirus 7	PBoV7	HQ291308
	<i>Ungulate bocaparvovirus 5</i>	Porcine bocavirus 3	PBoV3	JF429834
		Porcine bocavirus 4-1	PBoV4-1	JF429835
		Porcine bocavirus 4-2	PBoV4-2	JF429836
<i>Copiparvovirus</i>	<b><i>Ungulate copiparvovirus 1</i></b>	Bovine parvovirus 2	BPV2	AF406966
	<i>Ungulate copiparvovirus 2</i>	Porcine parvovirus 4	PPV4	GQ387499
<i>Dependoparvovirus</i>	<b><i>Adeno-associated dependoparvovirus A</i></b>	Adeno-associated virus-1	AAV1	AF063497
		Adeno-associated virus-2	AAV2	AF043303
		Adeno-associated virus-3	AAV3	AF028705
		Adeno-associated virus-4	AAV4	U89790
		Adeno-associated virus-6	AAV6	AF028704
		Adeno-associated virus-7	AAV7	AF513851
		Adeno-associated virus-8	AAV8	AF513852
		Adeno-associated virus-9	AAV9	AX753250
		Adeno-associated virus-10	AAV10	AY631965
		Adeno-associated virus-11	AAV11	AY631966
		Adeno-associated virus-12	AAV12	DQ813647
		Adeno-associated virus-13	AAV13	EU285562
		Adeno-associated virus-S17	AAVS17	AY695376
	<i>Adeno-associated dependovirus B</i>	Adeno-associated virus-5	AAV5	AF085716
		Bovine adeno-associated virus	BAAV	AY388617
		Caprine adeno-associated virus	CapAAV	DQ335246
	<i>Anseriform dependoparvovirus 1</i>	Duck parvovirus	DPV	U22967
		Goose parvovirus-PT	GPV2	JF926695
		Goose parvovirus	GPV	U25749
	<i>Avian dependovirus 1</i>	Avian adeno-associated virus	AAAV	AY186198
	<i>Chiropteran dependoparvovirus 1</i>	Bat adeno-associated virus	BtAAV	GU226971
	<i>Pinniped dependoparvovirus 1</i>	California sea lion adeno-associated virus	CslAAV	JN420372
	<i>Squamate dependoparvovirus 1</i>	Snake adeno-associated virus	SAAV	AY349010
<i>Erythroparvovirus</i>	<b><i>Primate erythroparvovirus 1</i></b>	Human parvovirus B19-Au	B19V-Au	M13178
		Human parvovirus B19-J35	B19V-J35	AY386330
		Human parvovirus B19-Wi	B19V-Wi	M24682
		Human parvovirus B19-A6	B19V-A6	AY064475
		Human parvovirus B19-Lali	B19V-Lali	AY044266
		Human parvovirus B19-V9	B19V-V9	AJ249437
		Human parvovirus B19-D91	B19V-D91	AY083234
	<i>Primate erythroparvovirus 2</i>	Simian parvovirus	SPV	U26342
	<i>Primate erythroparvovirus 3</i>	Rhesus macaque parvovirus	RhMPV	AF221122
	<i>Primate erythroparvovirus 4</i>	Pig-tailed macaque parvovirus	PtMPV	AF221123
	<i>Rodent erythroparvovirus 1</i>	Chipmunk parvovirus	ChpPV	GQ200736
	<i>Ungulate erythroparvovirus 1</i>	Bovine parvovirus 3	BPV3	AF406967
<i>Protoparvovirus</i>	<i>Carnivore protoparvovirus 1</i>	Feline parvovirus	FPV	EU659111
		Canine parvovirus	CPV	M19296
		Mink enteritis virus	MEV	D00765
		Raccoon parvovirus	RaPV	JN867610

Table 1.1: The type species for each genus is indicated in bold type. [25]

Genus	Species	Virus or virus variants	Abbr.	ACNO <sup>1</sup>
	<i>Primate protoparvovirus 1</i>	Bufavirus 1a	BuPV1a	JX027296
		Bufavirus 1b	BuPV1b	JX027295
		Bufavirus 2	BuPV2	JX027297
	<i>Rodent protoparvovirus 1</i>	H-1 parvovirus	H1	X01457
		Kilham rat virus	KRV	AF321230
		LuIII virus	LuIII	M81888
		Minute virus of mice (prototype)	MVMp	J02275
		Minute virus of mice (immunosuppressive)	MVMi	M12032
		Minute virus of mice (Missouri)	MVMm	DQ196317
		Minute virus of mice (Cutter)	MVMc	U34256
		Mouse parvovirus 1	MPV1	U12469
		Mouse parvovirus 2	MPV2	DQ196319
		Mouse parvovirus 3	MPV3	DQ199631
		Mouse parvovirus 4	MPV4	FJ440683
		Mouse parvovirus 5	MPV5	FJ441297
		Hamster parvovirus	HaPV	U34255
		Tumor virus X	TVX	In preparation
		Rat minute virus 1	RMV1	AF332882
		Rat parvovirus 1	RPV1	AF036710
		Porcine parvovirus Kresse	PPV-Kr	U44978
		Porcine parvovirus NADL-2	PPV-NADL2	L23427
<i>Tetraparvovirus</i>	<i>Chiropteran tetraparvovirus 1</i>	Eidolon Helvum (bat) parvovirus	Ba-PARV4	JQ037753
	<i>Primate tetraparvovirus 1</i>	Human parvovirus 4 G1	PARV4G1	AY622943
		Human parv4 G2	PARV4G2	DQ873391
		Human parv4 G3	PARV4G3	EU874248
		Chipmanzee parv4	Ch-PARV4	HQ113143
	<i>Ungulate tetraparvovirus 1</i>	Bovine hokovirus 1	B-PARV4-1	EU200669
		Bovine hokovirus 2	B-PARV4-2	JF504697
	<i>Ungulate tetraparvovirus 2</i>	Porcine hokovirus	P-PARV4	EU200677
	<i>Ungulate tetraparvovirus 3</i>	Porcine Cn virus	CnP-PARV4	GU938300
		Ovine hokovirus	O-PARV4	JF504699

## 1.4 Tropism

Most parvoviruses, such as MVM, CPV and FPV, show specific host ranges and tissue tropisms. The majority of the parvoviruses are members of those tightly controlled viruses. However, some parvoviruses, as for example many of the AAVs, infect many hosts and a variety of tissues. Understanding controls of these properties for autonomous parvoviruses show great promise for the therapeutic delivery to be controlled or modified in gene therapy applications [101].

To date, two independent strains of the parvovirus MVM have been described to occur in mice. Both strains display disparate *in vitro* tropism and *in vivo* pathogenicity

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<sup>1</sup>NIH GenBank accession number

despite differing by only 14 amino acids in their capsid proteins. First, MVMp, the prototype strain, was originally isolated from a contaminated murine adenovirus stock and was shown to replicate efficiently in mouse fibroblasts [102]. Secondly, MVMi, the immunosuppressive strain, was recovered from an infected EL-4 T-cell lymphoma culture [103]. Although MVMi infection may result in pathology of infected mice, it has been shown that the infection more likely interferes with numerous T-cell functions *in vitro*. The infection rather causes problems for the ongoing study the mice are being used for as the immune system will be activated, the activity of T-lymphocytes or B-lymphocytes will be altered and tumor formation may be suppressed [104, 105, 106].

As above-mentioned, it has been shown that the allotropic MVM strains, MVMi and MVMp, differ in their target cell tropism. In order to map the viral sequences responsible for that difference, chimeric viral genomes were constructed *in vitro* from infectious genomic clones of both strains. The differences in the cell tropism between MVMi and MVMp have been mapped to the capsid gene, in particular to the VP2 residues 317 and 321. Both residues are located at the base of the threefold spike of the virion and are involved in controlling the cell tropism of the two distinct MVM strains [107, 108, 109]. Interestingly, residue 321 aligns with residue 323 of CPV, that itself is a critical determinant for CPV host range tropism. Further residues (VP2 residues 399, 553 and 558) were identified in MVMi to be able to confer fibrotropism to single site-directed mutants. Those residues cluster around the twofold dimple-like depression [110].

In general, tissue tropism determining amino acids were found to be located on, or near, the viral surface, mainly by raised structural elements around the threefold axes of symmetry. Differences in tropism and pathogenicity have also been mapped to the capsid proteins of Aleutian mink disease parvovirus [111], porcine parvovirus (PPV) [112], CPV [113, 114], and FPV [115] in a capsid region analogous to that observed for MVM. Although the same structural element of viruses is involved in mediating host and tissue tropisms, each appears to be affecting a different mechanism. Host ranges of CPV and FPV are controlled by receptor binding, whereas the cell tropisms of MVM appear to be due to restrictions of interactions with intracellular factors [110, 101].

## 1.5 Structure

### 1.5.1 Parvoviruses in general

Parvovirus capsids are devoid of a lipid envelope and have an average diameter of 18 to 26 nm. The viral capsid is made up of 60 copies of between two and four structural proteins that overlap each other. For each virus there is one major capsid protein present in the capsid structure. Minor proteins form the same core structure, but differ in the

sequence length on their amino termini. The capsid proteins display a T=1 icosahedral symmetry and are variously designated VP1-VP4. Thus, the capsid has a 5-3-2 point group symmetry containing 31 rotational symmetry elements that intersect at the center: six fivefolds, ten threefolds, and fifteen twofolds. Despite the differences in protein forms and the low homology between some of the viruses, several structural elements on the capsid surface are common to most parvoviruses. These include raised cylindrical channels at the fivefold axes surrounded by depressed, canyon-like regions. Further shared surface characteristics are protrusions at the threefold axes, termed as spikes or peaks, and dimple-like depressions at the icosahedral twofold axes. A common feature of parvoviruses is their high resistance to physicochemical challenges. This stability provides an effective protection to the fragile, condensed genome in the extracellular environment ensuring transmission between their hosts. The ssDNA genome consists of approximately 5000 bases, packed as either a positive or, more usually, as a negative sense strand. At the 5' and 3' ends, the genome harbors palindromic sequences of about 120 to 250 nucleotides, that form secondary hairpin structures which are essential for the initiation of viral genome replication [116, 117, 118, 110, 119, 120, 101].

### 1.5.2 MVM

Both DNA-containing full and empty particles were crystallized in the monoclinic space group C2. Following data processing and refinement, the resulting electron density map was interpreted with respect to the amino acid sequence of MVMi. The known CPV structure was used as a phasing model since 52 % of the 578 amino acids in VP2 of MVM are identical to CPV. The polypeptide chain of the major structural protein, VP2, could be traced from residue 39 to residue 587 at the C-terminus [121]. The common c-terminal part of the structural proteins has an eight-stranded antiparallel  $\beta$ -barrel topology, frequently found in viral capsid proteins [122]. Large loops between the  $\beta$ -strands of the  $\beta$ -barrel that form the principal surface features, particularly the threefold spikes, and determine host-range tropism were found to be quite dissimilar in MVM and CPV. The first 37 amino acids are not visible in the electron density map. Since the N-VP2 terminal part contains a predominantly poly-glycine conserved sequence, it might be highly flexible. There is density extending along the fivefold channels of the MVMi capsid that was modeled as the glycine-rich N-terminal region [123, 124]. *In vitro*, trypsin digestion of full MVM virions results in a truncated VP3 polypeptide that still contains the glycine-rich sequence. In this way, most VP2 N-termini can be cleaved. These findings suggest that there is a dynamic situation at the fivefold channel. In one model, one in five amino termini are externalized along the

fivefold axes and are accessible for cleavage. Newly created, cleaved N-VP3 termini could withdraw into the virion and be replaced at the surface by an uncleaved N-VP2 terminus. [125, 110]. A substantial amount of internal electron density could be related to 10 DNA nucleotides that were previously found in the analysis of the structure of CPV [126, 127]. For MVM, 19 additional DNA nucleotides were identified in a difference electron-density map with respect to the data of empty particles. Thus, 29 ordered, or partially ordered, nucleotides per icosahedral asymmetric unit imply that approximately 34 % of the total genome display icosahedral symmetry. This finding, and the conservation of base-binding sites between MVMi and CPV, identifies a DNA-recognition site on the parvoviral capsid interior [110].

## **1.6 Nucleic Acid**

### **1.6.1 Genome organization**

### **1.6.2 Transcriptome**

## **1.7 Viral proteins**

### **1.7.1 Structural Proteins**

Three capsid proteins (LRV) [128] Three capsid proteins (AAV) [129, 130]

### **1.7.2 Non-structural proteins**

## **1.8**

### **1.8.1**

### **1.8.2**

## 2 Methods

### 2.1 Cell Cultures

A9 ouab<sup>r</sup>11 cells, a derivative from the original HGPRT<sup>-</sup> L-cell line A9 represent a clone resistant to 10<sup>-3</sup> M ouabain after nitrosoguanidine mutagenesis [131]. NB324K cells are a clone of SV40-transformed human newborn kidney cells [132]. The SV40 large T antigen was detected by immunofluorescent staining with monoclonal antibodies [133]. However, NB324K cells do not produce infectious SV40 spontaneously. Both cell lines, A9 mouse fibroblasts and NB324K cells, were routinely propagated under a minimal number of passages in DMEM supplemented with 5 % of heat inactivated fetal bovine serum at 37 °C in 5 % CO<sub>2</sub> atmosphere.

#### 2.1.1 Freezing and thawing of cells

Before use the A9 mouse fibroblasts or NB324K cells were thawed at 37 °C and cultured in 5 mL of pre-warmed DMEM supplemented with 5 % FCS. The medium was replaced every 3 to 4 days. In order to freeze the cells for long storage in liquid nitrogen they were passed the day before, to ensure exponential growth. Subsequently, 7.5 % DMSO was added and the cells were frozen slowly at -70 °C over night before transfer to liquid nitrogen.

### 2.2 Virus Stocks

Stocks of MVM without detectable levels of VP3 were propagated on A9 mouse fibroblast monolayers. As soon as the cytopathic effect became evident, the supernatant was collected and pre-cleared from cell debris by low-speed centrifugation. Thereby, intracellular, VP3 rich capsids were discarded. In order to remove low-molecular contaminants, virus containing SN was pelleted through 20 % sucrose cushion in PBS by ultra-centrifugation. Virus titers were determined by qPCR as DNA-packaged particles per microliter.

### 2.2.1 Separation of empty and full capsids

Sucrose purified capsids were prepared as previously described in section 2.2, page 15. The virus pellet was resuspended in 10 mL PBS. Caesium chloride was added to a density of 1.38 g/mL adjusted by refractometry ( $\eta=1.371$ ) at 4 °C. The gradient was centrifuged to equilibrium for 24 h at 41000 rpm and 4 °C in a Beckmann SW-41 Ti rotor. Gradients were fractionated and tested for intact capsids by dot blot analysis using B7 mAb. CsCl was depleted from the corresponding fractions by size-exclusion chromatography through PD-10 desalting columns and concentrated by ultra-centrifugation when required.

## 2.3 Freezing bacteria stocks in glycerol

Bacteria were frozen in dry ice. A volume of 700  $\mu$ L of the bacteria culture that was grown over night in LB-medium was mixed with 300  $\mu$ L of 50 % glycerol in a cryotube. In order to mix well the glycerol the cryotube was vortexed intensively. Following snap-freeze in dry ice the bacteria were stored at -70 °C.

## 2.4 Anion-exchange chromatography

A Mono Q HR 5/5 (Pharmacia) column (5 x 50 mm) was used to analyse viral samples. The Mono Q column was connected to the ÄKTAmicro chromatography system (GE Healthcare) that was operated by the UNICORN control software. The Mono Q column was equilibrated with six column volumes (CV) starting buffer (20 mM Tris-HCl, 1 mM EDTA, pH 7.2). Samples (1 mL) containing at least  $10^{10}$  virus particles in 10 mM Tris-HCl, 1 mM EDTA, pH 8 were applied to the Mono Q column through a 2 mL loop. After eluting the protein, which did not bind to the column in the starting buffer, a linear salt gradient (0-2 M NaCl) in 20 mM Tris-HCl, 1 mM EDTA, pH 7.2, was applied. Fractions of 0.185 mL were collected in 96-well plates. Viral genomes in each fraction were quantified by qPCR. All buffers were filtered and degassed before application to the Mono Q column.

## 2.5 Quantitative PCR

Amplification of MVM DNA and real-time detection of PCR products were performed by using BioRad CFX96 technology with SYBR green supermix. PCR was carried out by using the hot-start iTaq<sup>TM</sup> DNA polymerase (Bio-Rad Laboratories) following the manufacturer's guide-lines. Viral DNA was isolated using DNeasy blood and tissue kit. Elution of the purified vDNA was carried out using 100  $\mu$ L elution buffer. As templates

2  $\mu\text{L}$  of the isolated viral DNA were used for the PCR reaction and were added to the following master mix:

Component	Amount	Final concentration
dH <sub>2</sub> O, PCR grade	6 $\mu\text{L}$	-
Forward primer, 10 pM	1 $\mu\text{L}$	0.5 pM
Reverse primer, 10 pM	1 $\mu\text{L}$	0.5 pM
2x IQ <sup>TM</sup> SYBR <sup>®</sup> Green Supermix	10 $\mu\text{L}$	1x
<b>Total volume</b>	<b>18 <math>\mu\text{L}</math></b>	

Table 2.1: Master mix for quantitative PCR. In order to minimize pipetting errors a master mix was prepared. Following preparation the master mix was distributed across the 96 well plates. The master mix contains all the ingredients which are required for the DNA amplification except the initial DNA template that differs among the samples.

To ensure accurate quantification, the 96-well plates containing master mix and template DNA were shortly spun and transferred into the BioRad CFX96 unit. The following PCR program was used for quantification of viral DNA:

Cycles	Step	Temperature	Time
1x	Initial denaturation	95 °C	300 s
40x	Denaturation	95 °C	15 s
	Annealing	61 °C	15 s
	Extension	72 °C	15 s
1x	Final denaturation	95 °C	60 s
1x	Melting curve	65 °C up to 95 °C	0.1 °C/s

Table 2.2: PCR conditions for the amplification and real-time detection of MVM DNA.

To provide standards for sample quantification, serially diluted plasmids containing the entire MVM genomic DNA were used. For cell number variations that may exist between the samples, the number of applied cells per PCR reaction needed to be quantified for normalization as well. For this purpose quantification of cellular  $\beta$ -actin gene was performed. After normalization, direct comparison of the results is possible.  $\beta$ -actin quantification was carried out with the same PCR conditions outlined in table 2.2, 17.

## 2.6 Immunoprecipitation

Either *in vitro* treated viruses or viruses from cell extracts were transferred to LoBind tubes that were pre-blocked with PBS containing 1 % bovine serum albumin (PBSA 1 %). The volume was adjusted to 200  $\mu\text{L}$  with PBSA 1 %. The antibody was added in excess



and incubated with the viral capsids for 1 h at 4 °C on a rotary shaker. Subsequently, 20  $\mu$ L protein G-agarose beads were added. Following overnight incubation at 4 °C and centrifugation at 2500 rpm for 5 min the supernatant was discarded. The beads were washed 4 times with PBSA 1 %. To remove the BSA an additional wash step was carried out with PBS. Finally, the beads were frozen at -20 °C until further use or immediately processed.

## **2.7 Chymotrypsin treatment**

Virus particles were incubated with 0.5 mg/mL chymotrypsin (Sigma) in PBS for 1.5 h at 37 °C. The reaction was stopped by adding 100  $\mu$ M chymostatin (Sigma). Negative controls were incubated in the same buffer for the same time.

### **2.7.1**

## **2.8**

### **2.8.1**

### **2.8.2**

## **Part II**

# **Publication**



# **1 Wolfisberg et al., Journal of Virological Methods, 2013**

**Impaired genome encapsidation restricts the *in vitro* propagation of human parvovirus B19.**

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# Impaired genome encapsidation restricts the *in vitro* propagation of human parvovirus B19



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## ABSTRACT

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The lack of a permissive cell culture system hampers the study of human parvovirus B19 (B19V). UT7/Epo is one of the few established cell lines that can be infected with B19V but generates none or few infectious progeny. Recently, hypoxic conditions or the use of primary CD36+ erythroid progenitor cells (CD36+ EPCs) have been shown to improve the infection. These novel approaches were evaluated in infection and transfection experiments. Hypoxic conditions or the use of CD36+ EPCs resulted in a significant acceleration of the infection/transfection and a modest increase in the yield of capsid progeny. However, under all tested conditions, genome encapsidation was impaired seriously. Further analysis of the cell culture virus progeny revealed that differently to the wild-type virus, the VP1 unique region (VP1u) was exposed partially and was unable to become further externalized upon heat treatment. The fivefold axes pore, which is used for VP1u externalization and genome encapsidation, might be constricted by the atypical VP1u conformation explaining the packaging failure. Although CD36+ EPCs and hypoxia facilitate B19V infection, large quantities of infectious progeny cannot be generated due to a failure in genome encapsidation, which arises as a major limiting factor for the *in vitro* propagation of B19V.

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## 1. Introduction

Human parvovirus B19 (B19V) is spread worldwide and typically causes a mild self-limiting infection in children known as *erythema infectiosum*. B19V has also been associated to myocarditis, acute and chronic arthropathies in adults, transient aplastic crisis and chronic anemia in individuals with altered immunologic or hematologic conditions, hydrops fetalis and intrauterine fetal death (Heegaard and Hornsleth, 1995; Heegaard and Brown, 2002; Servey et al., 2007).

Considering its worldwide distribution, prevalence and associated disorders, B19V is regarded as a prominent human pathogen and the only parvovirus undoubtedly linked to human disease. However, the experimental research with B19V is hampered seriously due to the lack of an appropriate and sufficiently permissive cell system to propagate the virus and study its biology. The reason for this is the rigorous replication requirements of the virus. B19V has an extraordinary tropism for erythroid progenitor cells in the bone marrow at a particular differentiation stage corresponding to BFU-E and CFU-E (Takahashi et al., 1990; Ozawa et al.,

1986, 1987). The narrow tropism of B19V is mediated, at least in part, by its particular uptake mechanism. B19V utilizes globoside (Gb4Cer) as a primary attachment receptor, which is expressed in few cell types (Brown et al., 1993) and a co-receptor (Weigel-Kelley et al., 2003) to initiate the internalization process. However, cells expressing the required receptors and co-receptors are not always permissive, suggesting that the selective replication of B19V is determined by additional intracellular factors restricted to erythroid cells (Pallier et al., 1997; Brunstein et al., 2000; Gallinella et al., 2000; Guan et al., 2008; Chen et al., 2010; Luo et al., 2011). The high viremia that is typically associated to B19V acute infections, exceeding occasionally  $10^{13}$  genome equivalents (geq) per ml of plasma (Kooistra et al., 2011), suggests that the virus can replicate efficiently in the target cells when all the required elements are present. However, despite continuous efforts, the specific cellular factors that control B19V infection in the natural target cells have not yet been reproduced adequately in an established cell line. Some erythropoietin-dependent leukemic cell lines, notably UT7/Epo (Shimomura et al., 1992) and KU812Ep6 (Miyagawa et al., 1999), have been shown to be semi-permissive to B19V infection, producing in general none or minor amounts of infectious progeny. The permissivity of non-erythroid cells, such as HepG2 cells has produced contradictory results (Caillet-Fauquet et al., 2004a; Bonvicini et al., 2008). Considering all these limitations, highly viremic donors without B19V neutralizing antibodies remain the only source of infectious B19V. Thus, the need to develop

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a cell culture method capable of producing large amounts of infectious B19V remains a major challenge.

Recently, the use of cells cultured under hypoxic conditions has been described as a promising method to produce high quantities of infectious particles (Caillet-Fauquet et al., 2004b; Pillet et al., 2004; Chen et al., 2011). Similarly, the use of *ex vivo* expanded CD36+ primary human erythroid progenitor cells (CD36+ EPCs), previous CD34+ *in vitro* preselection (Pillet et al., 2008; Wong et al., 2008), has also been described as a highly permissive system, based on the expression of B19V non-structural and capsid proteins. A simplified approach to generate CD36+ EPCs directly from ordinary blood samples, without *ex vivo* stem cell mobilization has been reported (Filippone et al., 2010). The combination of both approaches, primary CD36+ EPCs cultured under hypoxic conditions, has been shown to enhance remarkably B19V infection (Chen et al., 2011). Hypoxia, which mimics the oxygen microenvironment in the bone marrow, seems to promote B19V infection by the direct stimulating effect of HIF1 $\alpha$  on the B19V p6 promoter (Pillet et al., 2004). However, an alternative HIF1 $\alpha$ -independent mechanism based on STAT5A and MEK signaling has been proposed recently (Chen et al., 2011).

These novel approaches based on hypoxia and primary CD36+ EPCs have been compared systematically in infection and transfection experiments with the established erythroid cell line UT7/Epo. In all cases, a substantial amount of capsid progeny was obtained. The use of the novel approaches resulted in a significant acceleration of the infection and the augmentation in the number of infected cells resulting in a modest but noticeable increase in virus progeny production. However, in all tested cells and under all conditions genome encapsidation was impaired seriously generating an empty non-infectious virus progeny. Differently to the wild-type virus, the VP1 unique region (VP1u) of the virus progeny was exposed partially and upon heat treatment did not undergo the expected conformational change that renders VP1u fully externalized. The abnormal configuration and rigidity of VP1u, which utilizes the genome encapsidation portal for its externalization, might constrict the fivefold axes channel impeding the translocation of the viral genome into the pre-assembled capsid.

## 2. Materials and methods

### 2.1. Cells and viruses

UT7/Epo cells were maintained in Eagle's minimum essential medium (MEM) supplemented with 5% heat-inactivated fetal calf serum (FCS) and 2 U/ml of recombinant human erythropoietin (Epo; Janssen-Cilag, Midrand, South Africa) at 37 °C with 5% CO<sub>2</sub>. For hypoxic conditions the oxygen tension was lowered to 1%. Cells with adherent phenotype were selected by removing the non-adherent cells in every passage. CD36+ erythroid progenitor cells (CD36+ EPCs) were obtained from ordinary blood samples and cultured as described previously (Filippone et al., 2010). A B19V-infected plasma sample (Genotype 1; CSL Behring AG, Charlotte, NC), without detectable B19V-specific IgM or IgG antibodies, was used as a source of native infectious virus. The virus was pelleted by ultracentrifugation through 20% (w/v) sucrose and the concentration of virions was determined by quantitative PCR (qPCR).

### 2.2. Antibodies and chemicals

Two human monoclonal antibodies (mAb), one directed to a conformational epitope in the major capsid protein VP2 (mAb 860-55D), which detects exclusively intact capsids, and the other against the N-terminal region of VP1, also known as VP1 unique region (VP1u) (mAb 1418), were provided by S. Modrow

(Regensburg, Germany). These antibodies were produced from peripheral blood mononuclear cells of normal, healthy individuals with high titers of serum antibodies against B19 virus proteins (Gigler et al., 1999). A rabbit antibody against the C-terminal region of VP1u was described earlier (Bönsch et al., 2008). A mouse mAb against B19V capsids (mAb 521-5D) was purchased from Millipore (Billerica, MA). A globoside-specific mouse IgM mAb (AME-2) was provided by J. de Jong (The Netherlands Red Cross, Amsterdam, Netherlands). Mouse IgG mAb against Ku80 and CD49e were purchased from BD Biosciences (San Jose, CA). A mouse antibody against B19V proteins was obtained from US biologicals (Swampscott, MA). Chloroquine diphosphate (CQ) was purchased from Sigma (St. Louis, MO) and dissolved in water.

### 2.3. Flow cytometry

The presence of B19V receptors and co-receptors on the cell surface of UT7/Epo cells was analyzed quantitatively by flow cytometry. UT7/Epo cells were incubated with either an anti-Ku80 or an anti-Gb4Cer antibody at 4 °C for 1 h in PBS containing 2% fetal calf serum, followed by incubation with fluorescein isothiocyanate (FITC)-conjugated rat anti-mouse IgG or IgM, respectively (BD Biosciences). Additionally, UT7/Epo cells were stained with R-phycoerythrin conjugated anti-human CD49e (BD Biosciences). The cells were analyzed on a BD FACSanto II (Becton Dickinson, San Jose, CA). Data acquisition and analysis were conducted with a software (BD FACSdiva, BD Biosciences).

### 2.4. Infection

UT7/Epo and primary CD36+ EPCs ( $3 \times 10^5$ ) cultured under normoxia or hypoxia (1% O<sub>2</sub>) during 2 days, were infected with B19V at  $10^4$  geq per cell for 1 h at 4 °C. The cells were washed to remove unbound viruses and further incubated at 37 °C. At different post-infection (p.i.) times, cells and supernatants were collected. The cells were washed and processed for immunofluorescence (IF), immunoprecipitation (IP), as well as DNA and RNA extraction. The supernatant was used for IP and DNA extraction.

### 2.5. Transfection

A total of  $5 \times 10^6$  UT7/Epo cells, cultured under normoxia or hypoxia (1% O<sub>2</sub>) during 2 days, were transfected using the AMAXA nucleofector™ II device (Lonza, Cologne, Germany) following the manufacturer's instructions. Transfection was carried out with 5  $\mu$ g of the B19V genome excised from a B19V infectious clone (pB19-M20) (Zhi et al., 2004) or with 2  $\mu$ g of a GFP-control plasmid, using the T-20 program. As a transfection reagent, AMAXA™ Cell Line Nucleofector™ Kit R (Lonza) was used. After transfection, the cells were maintained in 20 ml of pre-warmed culture medium. A volume of 5 ml of fresh MEM culture medium supplemented with 5% FCS and Epo (2 U/ml) was added to the cells 24 h post-transfection (p.t.). At increasing times p.t., the cells and supernatant were collected for further analysis.

### 2.6. Quantitation of B19V DNA and NS1 mRNA

Total DNA was extracted from cells or from the supernatant by using the DNeasy blood and tissue kit (Qiagen, Valencia, CA). For the isolation of total mRNA, cells were transferred to RNase-free tubes (Safe-Lock Tubes 1.5 ml, Eppendorf Biopur) and washed twice with PBS. Total poly-A-mRNA was isolated with the Dynabeads mRNA direct kit (Roche Diagnostics, Mannheim, Germany). The RNA preparations were used for reverse transcription as described previously (Bönsch et al., 2010a). Amplification of DNA or cDNA and real-time detection of PCR products were performed by qPCR

with the iQ SYBR Green Supermix and the CFX96 device (Bio-Rad, Cressier, Switzerland). Primers used for amplification were described elsewhere (Bönsch et al., 2010a).

### 2.7. Immunoprecipitation of B19V particles and quantitation of virions

Viral particles were immunoprecipitated from cell extracts or from the supernatant of infected cells with a human mAb against intact capsids (860-55D) (Gigler et al., 1999). As reference control, a known amount of virions was added to the uninfected cell extracts or to the supernatant. After overnight incubation at 4 °C in the presence of 20 µl of protein G agarose beads (Santa Cruz Biotechnology, Heidelberg, Germany) the supernatant was discarded and the beads were washed four times with PBSA. Immunoprecipitated viral capsids were detected by SDS-PAGE. To verify the presence of the viral genome, DNA was extracted from the immunoprecipitated virions by using the DNeasy blood and tissue kit (Qiagen) and quantified as specified above.

### 2.8. Immunofluorescence

Cells or purified viruses were fixed on coverslips by using acetone/methanol (1:1 [v/v]) solution at –20 °C for 4 min. Following blocking with goat serum diluted in PBS (20% [v/v]), the samples were incubated with the primary antibodies in PBS containing 2% goat serum for 1 h at room temperature (RT). The samples were washed and the appropriate fluorescently labeled secondary antibody in 2% goat serum was added for 1 h at RT. Nuclei was stained with 4',6-diamidino-2-phenylindole (DAPI). Mowiol supplemented with 2.5% 1,4-Diazabicyclo[2.2.2]octan (DABCO) was used to maintain the fluorescent signal. Samples were examined by confocal laser scanning microscopy (Axiovert 200M, Carl Zeiss A.G., Feldbach, Switzerland).

### 2.9. Fluorescence *in situ* DNA hybridization

The presence of newly replicated viral genomes in the infected cells was examined by fluorescence *in situ* DNA hybridization (FISH). Biotinylated probes specific for B19V DNA were generated from PCR products by nick translation (Roche), according to the manufacturer's instructions. The size of the hybridization probes was 200–500 nucleotides in length, as confirmed by agarose gel electrophoresis. Cells were fixed and immunostained with mAb 860-55D against capsids and incubated in a humid chamber at 37 °C for 18 h with a volume of 20 µl hybridization mix (5 ng/µl biotinylated probe in 60% deionised formamide, 300 mM NaCl, 20 mM sodium citrate, 10 mM EDTA, 25 mM NaH<sub>2</sub>PO<sub>4</sub> pH 7.4, 5% dextran sulfate and 250 ng/µl sheared salmon sperm DNA). Subsequently, the cells were washed (50% deionised formamide, 25 mM NaCl and 2.5 mM sodium citrate pH 7.4) three times for 5 min at RT and once at 37 °C. The samples were blocked for 30 min with 1% blocking solution (Roche) in 150 mM NaCl, 100 mM Tris–HCl pH 7.4. Biotin was detected with avidin-rhodamine (Roche) 1:500 in blocking solution for 45 min. Finally, the cells were washed three times 10 min (200 mM Tris–HCl pH 7.4, 1.5 M NaCl and 0.05% Tween-20), mounted with mowiol supplemented with DABCO and examined by confocal laser scanning microscopy.

## 3. Results

### 3.1. General profile of B19V infection in UT7/Epo cells

UT7/Epo cells have been used extensively to study B19V infection. However, intracellular factors restrict severely the infection of B19V in these and other cells, resulting in the production of

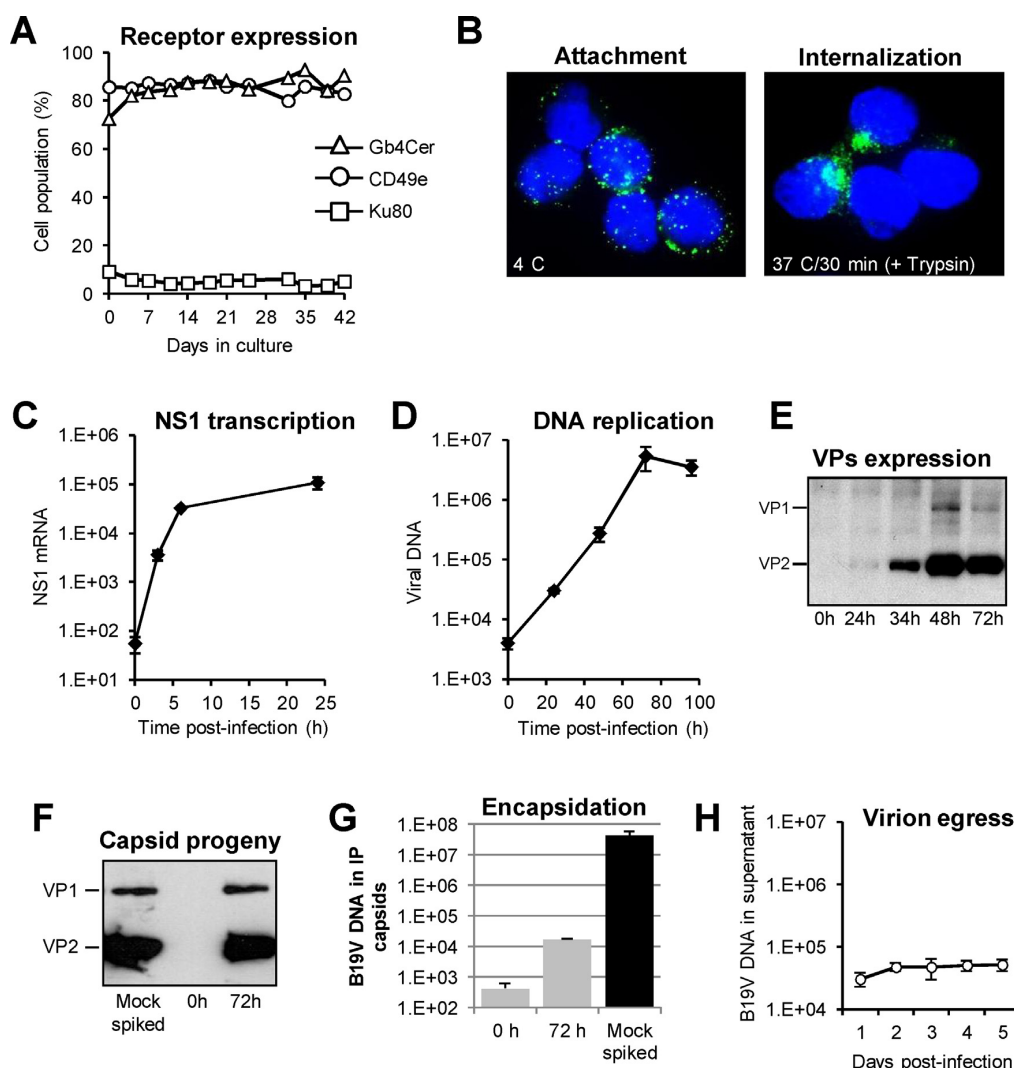
none or few infectious progeny (Pallier et al., 1997; Brunstein et al., 2000; Gallinella et al., 2000; Guan et al., 2008). In order to better identify which steps of the infection are deficient, different parameters of B19V infection in UT7/Epo cells have been analyzed. Analysis of the expression profile of B19V receptor and co-receptors over a period of six weeks showed a high and stable expression of Gb4Cer and CD49e along the specified period. In contrast, expression of Ku80, which may have a similar role to Gb4Cer in certain cells (Munakata et al., 2005), was not significant (Fig. 1A). IF microscopy examination of infected cells confirmed that B19V can attach and internalize cells, adopting the typical intracellular distribution around the microtubule organizing center (MTOC) observed in other parvovirus infections (Fig. 1B). The kinetics of viral transcription and replication were analyzed quantitatively. The synthesis of viral RNA (NS1 mRNA) was already detectable by 3 h p.i. and reached a plateau by 24 h p.i. (Fig. 1C). Viral replication started later and reached a plateau by the third day p.i. (Fig. 1D). Expression of viral proteins became detectable after 24 h and reached a plateau after 2 days (Fig. 1E). Immunoprecipitation at 3 days p.i. with an antibody against intact viral particles (mAb 860-55D) (Gigler et al., 1999) demonstrated that virus assembly occurred and that a significant amount of capsid progeny was produced (Fig. 1F). Quantitative determination of the viral DNA from the immunoprecipitated capsids revealed that the virus progeny was essentially empty (Fig. 1G). Mature virion progeny was not either detected in the supernatant of the infected cells (Fig. 1H). These results together indicate that despite the substantial amount of capsid progeny produced, deficiencies in genome packaging and capsid egress limit the progression of B19V infection in UT7/Epo cells.

### 3.2. B19V infection of UT7/Epo cells, under normoxia or hypoxia, generates mostly empty capsids

Infected cells were collected at progressive days, washed and lysed. Viral particles were immunoprecipitated from the cell lysate with the antibody 860-55D, against assembled capsids. The results confirmed that under hypoxic conditions, the capsid progeny was more abundant but also appeared earlier (after 48 h p.i. under normoxia and after 24 h p.i. under hypoxia) (Fig. 2A and B). These results confirmed previous observations indicating that hypoxia enhances B19V infection (Cailliet-Fauquet et al., 2004b; Pillet et al., 2004; Chen et al., 2011). The virus progeny generated under hypoxic or normoxic conditions was further characterized. The amount of viral genomes in the immunoprecipitated viral particles from the experiment shown in Fig. 2A and B was analyzed quantitatively. The results revealed that independently of the oxygen environment, a limited number of progeny capsids (<1% of the reference control) contained the viral DNA (Fig. 2C and D). Quantitation of the viral DNA in the supernatant of the infected cells showed no increase over the background signal (day 0 p.i.) under normoxia and modestly under hypoxic conditions (Fig. 2E and F). Capsid proteins in the supernatant were undetectable by IP and Western blot (data not shown). These results indicate that although hypoxic conditions result in the acceleration of the infection and an augmented capsid production, the improvement of the genome encapsidation step was not significant.

### 3.3. Hypoxia enhances significantly the transfection efficiency, however genome packaging and egress remained restricted

In a control transfection experiment in UT7/Epo cells, the oxygen level did not influence the transfection efficiency with a control plasmid expressing green fluorescent protein (GFP) (Fig. 3A). However, the transfection efficiency increased drastically under hypoxic conditions with an infectious clone of B19V (pB19-M20)



**Fig. 1.** Characterization of B19V infection in UT7/Epo cells. (A) Expression of B19V-related receptors in UT7/Epo cells. The presence of B19V receptors and co-receptors on the cell surface of UT7/Epo cells was quantitatively analyzed by flow cytometry during a period of 6 weeks. (B) Binding and internalization of B19V in UT7/Epo cells. B19V was added to the cells at 4 °C for 2 h, washed, fixed and stained with an antibody against intact capsids. For internalization, the cells were further incubated for 30 min at 37 °C, washed and trypsinized to remove uninternalized particles. (C) Kinetics of NS1 mRNA synthesis in infected cells. At increasing times p.i., total mRNA was isolated and NS1 mRNA quantified. Samples taken 10 min p.i. served as background controls. (D) Kinetics of viral DNA replication. At increasing times p.i., total DNA was isolated and viral DNA quantified. Samples taken prior to virus internalization served as background controls. (E) Kinetics of B19V capsid proteins expression. (F) Production of assembled capsid progeny in UT7/Epo cells. B19V capsids were immunoprecipitated from cell extracts with mAb 860-55D against intact capsids. As a reference control, B19V ( $4 \times 10^{10}$ ) was added to mock-infected cell extracts. (G) B19V capsids were immunoprecipitated and B19V DNA was quantified. As a reference control, B19V ( $4 \times 10^{10}$  virions) was added to mock-infected cell extracts. (H) Quantitation of virus egress. B19V DNA was quantified from the supernatant of the infected cells.

(Fig. 3B). Immunoprecipitation experiments confirmed that assembled capsids were generated (Fig. 3C) and similarly to the infection experiments, progeny capsids were slightly more abundant and appeared earlier under hypoxic conditions.

As shown in Fig. 3D, at progressive times p.t. no viral DNA above the input signal was detected in the immunoprecipitated capsids. Additionally, virions were not detectable in the supernatant of the transfected cells (Fig. 3E).

### 3.4. Chloroquine enhances B19V infection in UT7/Epo cells but has no influence in genome encapsidation and egress

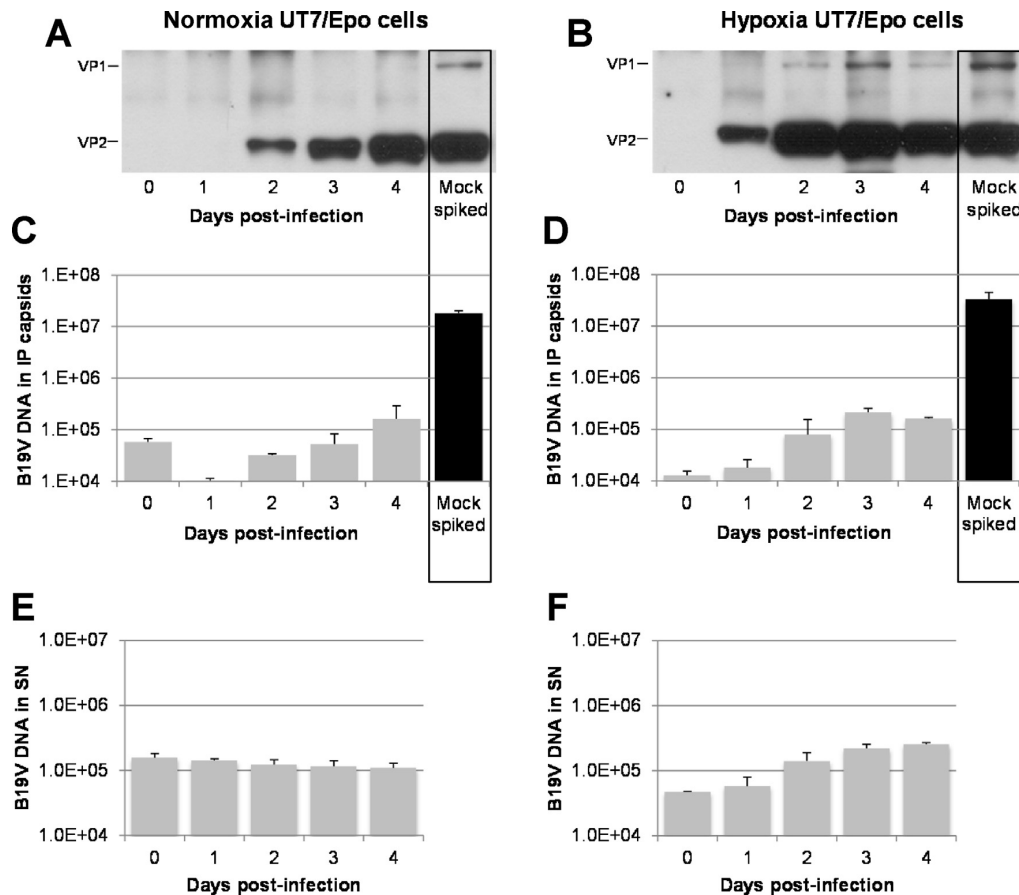
It has been shown previously that chloroquine (CQ) enhances B19V infection. In the presence of CQ, an increased production of

viral DNA, RNA and proteins was observed and the infection was accelerated (Bönsch et al., 2010b). The production of mature virions in CQ-treated UT7/Epo cells was examined. The results confirmed, that in the presence of CQ, an increased amount of assembled capsids was produced (Fig. 4A). However, similar to untreated cells, most of the progeny capsids remained empty (Fig. 4B). Viral DNA or capsid proteins were not detected in the supernatant of infected cells (data not shown).

### 3.5. B19V infection is enhanced in CD36+ EPCs, in particular under hypoxia, but genome encapsidation remains restricted

Immunofluorescence microscopy examination of infected primary CD36+ EPCs confirmed that B19V can attach and internalize





**Fig. 2.** Capsid progeny and quantitation of virions in UT7/Epo cells. Cells ( $3 \times 10^5$ ) were infected with B19V under normoxia or hypoxia. At progressive times p.i., the supernatant was collected and the cells were lysed. (A and B) B19V capsids were immunoprecipitated from the cell extracts with mAb 860-55D. As a reference control, B19V ( $4 \times 10^{10}$ ) was added to mock-infected cell extracts. (C and D) B19V DNA was quantified from the immunoprecipitated capsids. As a reference control, B19V ( $4 \times 10^{10}$  virions) was added to mock-infected cell extracts. (E and F) B19V DNA was quantified from the supernatant of the infected cells. Data are the mean  $\pm$  SD of two independent experiments.

EPCs without noticeable differences to UT7/Epo cells or between normoxic and hypoxic conditions (Fig. 5A). However, the oxygen environment had an important influence in the number of cells infected by B19V. By 2 days p.i., the number of UT7/Epo cells with detectable capsid progeny was 1–5% and 15–20% under normoxia and hypoxia, respectively. In CD36+ EPCs, the number of infected cells increased to approximately 25% under normoxia and above 70% under hypoxic conditions (Fig. 5B).

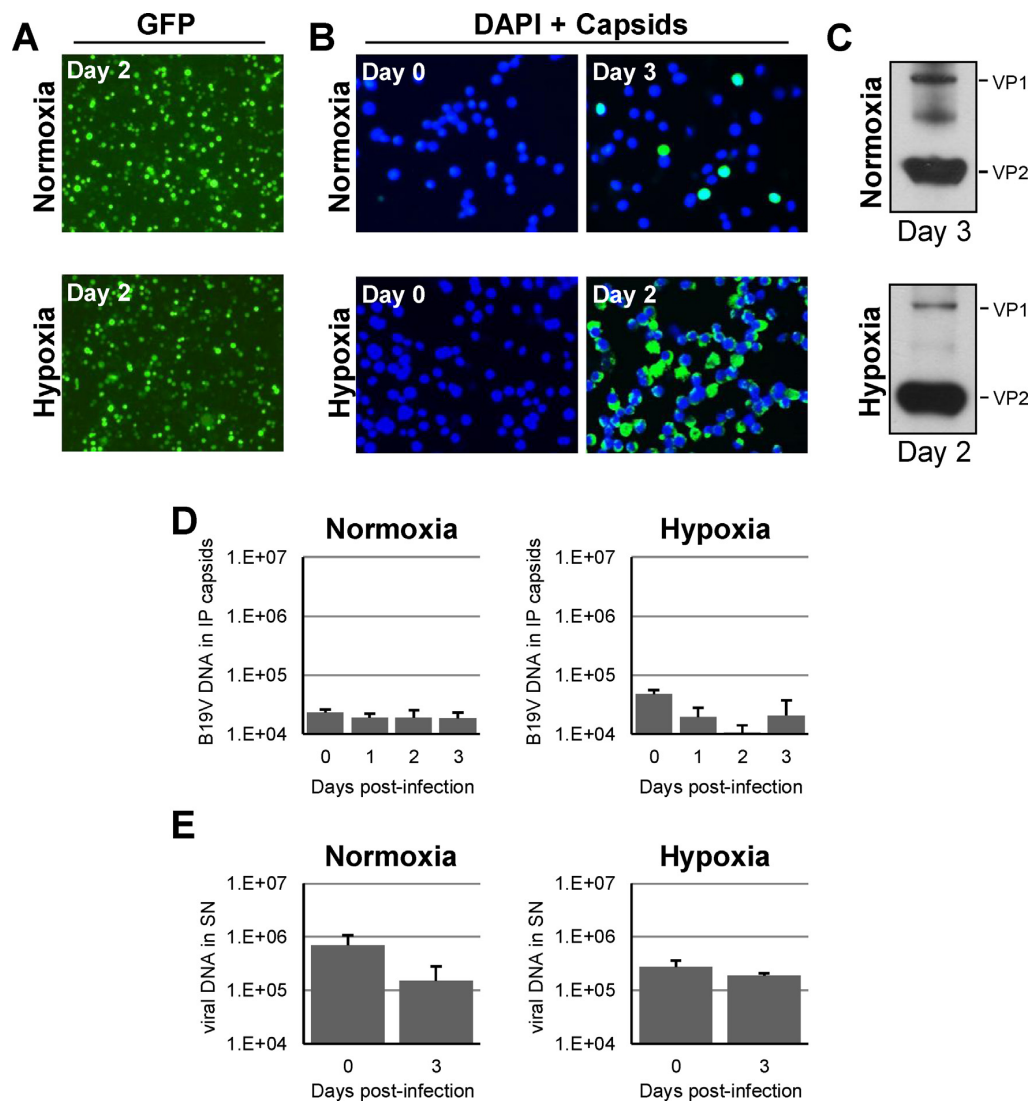
Immunoprecipitation experiments with the antibody 860-55D (against intact capsids) at progressive days p.i. showed, that regardless the oxygen conditions, progeny capsids appeared earlier in CD36+ EPCs than in UT7/Epo cells. While in UT7/Epo cells, capsid progeny production reached a plateau on day 4 under normoxia and on day 2–3 under hypoxia, in CD36+ EPCs, maximal capsid progeny was observed already after 24 h p.i. (compare Fig. 6A and B and Fig. 2A and B). The amount of viral DNA in the immunoprecipitated samples from the experiment shown in Fig. 6A and B was analyzed quantitatively. The results revealed that a limited number of capsids containing the viral DNA were produced after 24 h p.i. and did not increase subsequently (Fig. 6C and D). The presence of viral DNA in the supernatant increased and reached similarly a plateau already after 24 h p.i. (Fig. 6E and F).

Capsid progeny was detectable in the supernatant of infected EPCs, in particular under hypoxic conditions (Fig. 7A and B).

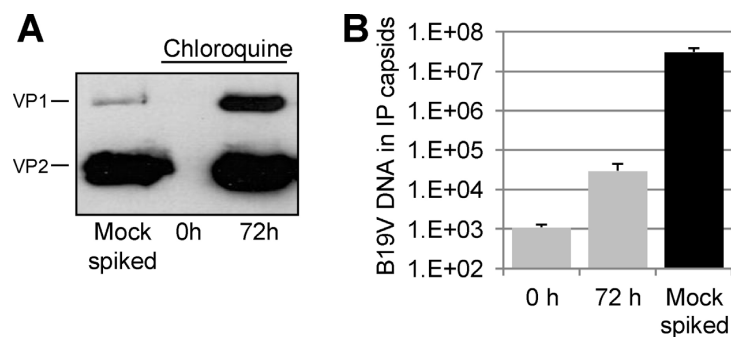
However, quantitation of their DNA content and comparison with the reference control revealed that only a modest proportion of the particles represented mature infectious virions (Fig. 7C and D). The IP of capsid-associated DNA increased and reached a plateau by 24 h p.i. At this time, the capsid progeny was undetectable under normoxia and hardly detectable under hypoxia (Fig. 7A and B). Therefore, the increase of capsid progeny observed in the following days represented essentially empty particles. These results indicate that despite the augmented and earlier production of virus progeny, the deficient packaging step remains the limiting factor for the propagation of B19V in CD36+ EPCs.

### 3.6. Intracellular distribution of viral genomes and capsids

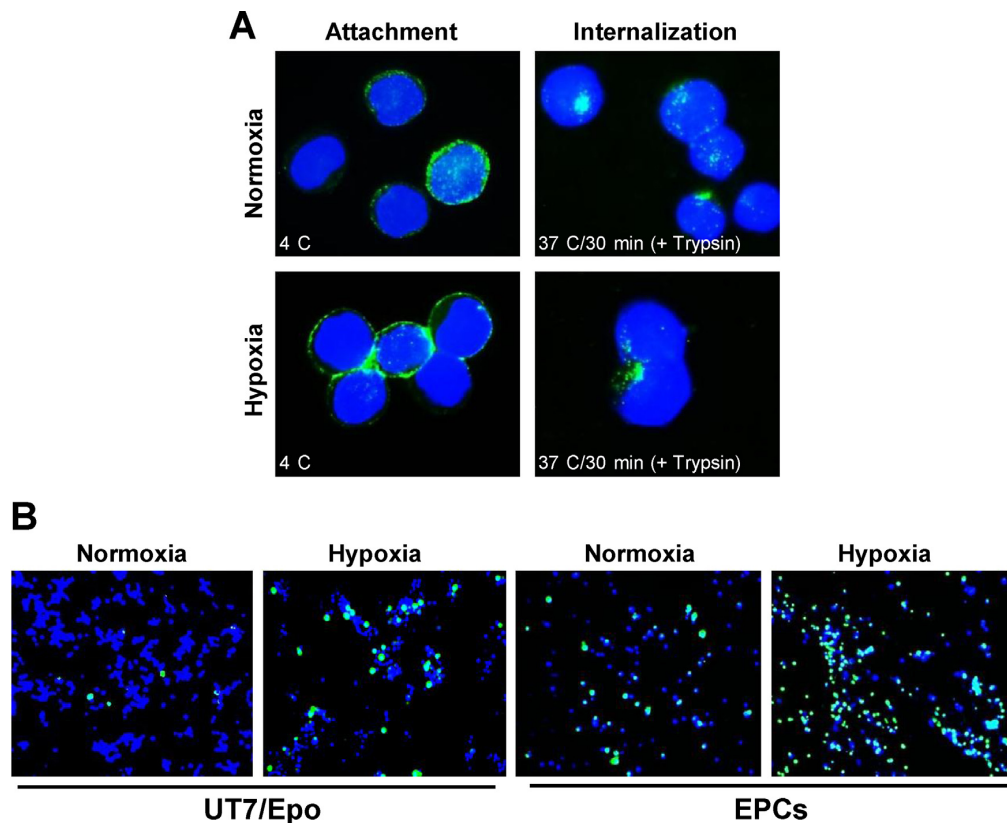
The presence and distribution of the viral genomes and capsids in the infected UT7/Epo cells was examined by FISH. In some cells, assembled capsids and viral genomes colocalized within large intranuclear clusters (Fig. 8A, panel i) resembling the nuclear compartments described earlier in AAV, containing non-structural proteins, capsids, and viral genomes and where presumably encapsidation takes place (Hunter and Samulski, 1992; Wistuba et al., 1997). However, in a larger proportion of cells the viral genomes appeared isolated in the nucleus, while the assembled capsids were detected in the cytoplasm (Fig. 8A, panel ii).



**Fig. 3.** Transfection of UT7/Epo cells with a B19V infectious clone under normoxia and hypoxia. (A) Transfection of UT7/Epo cells with a control plasmid expressing GFP is not influenced by normoxia or hypoxia. (B) Detection of B19V capsids by IF following transfection with a B19V infectious clone (pB19-M20). (C) Detection of B19V capsids by IP with mAb 860-55D from pB19-M20 transfected cells. (D) At progressive days p.i. B19V capsids were immunoprecipitated from cell lysates and B19V DNA was quantified. (E) B19V DNA was quantified from the supernatant of the infected cells. Data are the mean  $\pm$  SD for two independent experiments.



**Fig. 4.** Effect of chloroquine (CQ) in B19V infection in UT7/Epo cells. (A) Production of capsid progeny in UT7/Epo cells treated with CQ (25  $\mu$ M). B19V capsids were immunoprecipitated from the cell extracts with mAb 860-55D. As a reference control, B19V ( $4 \times 10^{10}$ ) was added to mock-infected cell extracts. The production of capsid progeny in untreated UT7/Epo cells is shown in Fig. 1F. (B) B19V DNA was quantified from the immunoprecipitated capsids. As a reference control, B19V ( $4 \times 10^{10}$  virions) was added to mock-infected cell extracts. Data are the mean  $\pm$  SD for two independent experiments.



**Fig. 5.** Attachment, internalization and infection of B19V in EPCs under normoxia and hypoxia. Cells ( $3 \times 10^5$ ) were infected with B19V under normoxia or hypoxia. (A) Binding and internalization of B19V in EPCs. B19V was added to the cells at 4 °C for 1 h, washed, fixed and stained with an antibody against intact capsids. For internalization, the cells were further incubated for 30 min at 37 °C, washed and trypsinized to remove uninternalized particles. (B) Detection of virus progeny by IF 2 days p.i. in UT7/Epo cells and EPCs cultured under normoxic and hypoxic conditions.

### 3.7. VP1u conformation in the virus progeny differs from that of wild-type virus

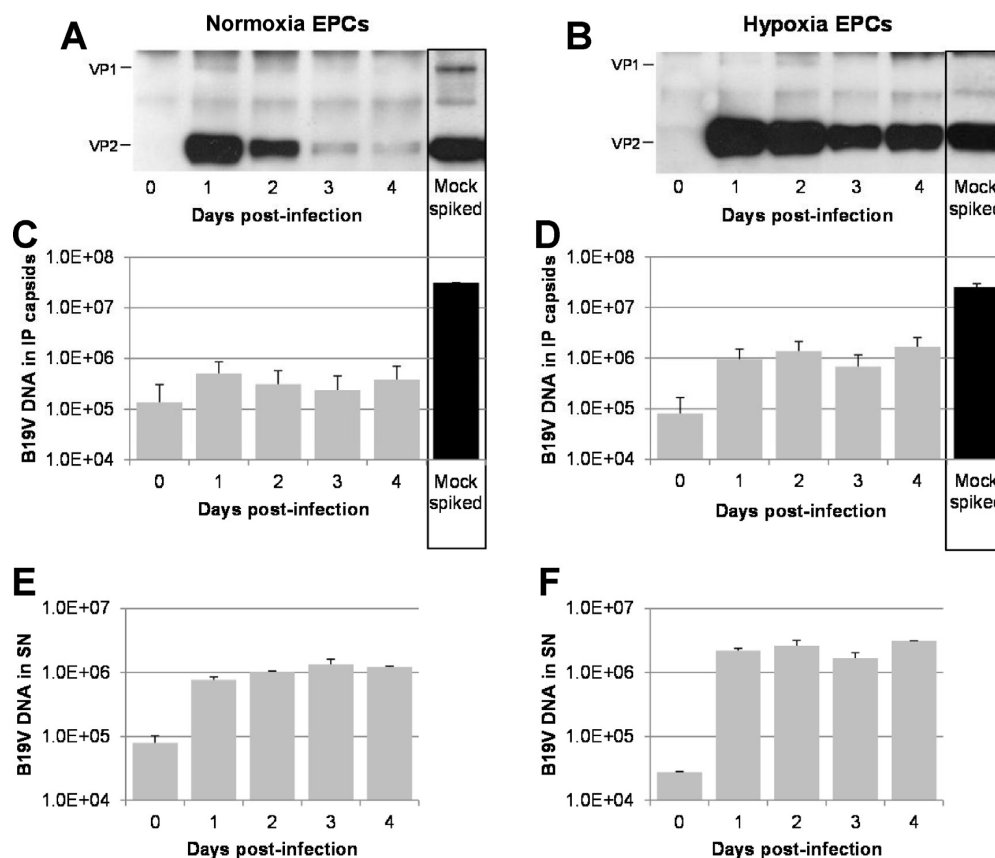
The pores at the fivefold symmetry axis are the portals for the encapsidation of the viral genome but also for the externalization of VP1u. The fivefold cylinder is narrow and constrictions of the channel impair the encapsidation of the viral genome and the externalization of VP1u (Farr and Tattersall, 2004; Bleker et al., 2005, 2006; Plevka et al., 2011). Examination of the VP1u conformation in the mostly empty virus progeny revealed, that differently to the wild-type virus, VP1u was partially exposed. The most N-terminal part was accessible to antibodies, while the C-terminal region remained internal and inaccessible (Fig. 8B and C). Similar to other parvoviruses (Cotmore et al., 1999; Vihinen-Ranta et al., 2002), exposure to mild temperature triggers the externalization of the N-terminal and C-terminal regions of VP1u from B19V without capsid disassembly (Ros et al., 2006). In clear contrast to the wild-type virus, heat treatment did not trigger the externalization of the C-terminal region of VP1u from the capsid progeny generated under normoxia and only discretely from capsids generated under hypoxia (Fig. 8D). Therefore, the failure to encapsidate the viral genome is possibly due to the constriction of the fivefold axis channel by a partially exposed and inflexible VP1u.

## 4. Discussion

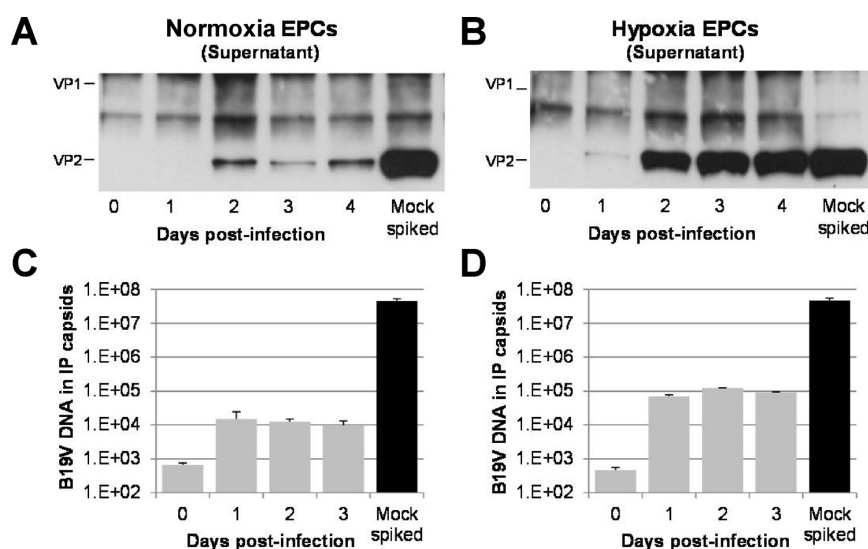
Discovered in 1975 (Cossart et al., 1975), today B19V is recognized as a major human pathogen involved in multiple syndromes.

However, the lack of a suitable cell culture system or an animal model restricts the availability of infectious virus and hampers seriously the studies with B19V. The virus has an extraordinary tropism for human erythroid progenitor cells (EPCs) in the bone marrow (Mortimer et al., 1983) where it can infect cells at the BFU-E and CFU-E stages of differentiation (Takahashi et al., 1990). During a natural infection B19V is able to replicate efficiently in the target cells, as judged by the typical high viremia observed in the infected individuals. However, the efficient B19V replication *in vivo* has not yet been mimicked *in vitro* with an established cell line, indicating the existence of highly restricted and still poorly understood cellular factors required for B19V replication. Some erythroleukemia cell lines, such as UT7/Epo (Shimomura et al., 1992) and KU812Ep6 (Miyagawa et al., 1999), have been shown to support B19V replication to a certain level, but none of them can produce significant quantities of infectious progeny. The human megakaryoblastic cell line UT7/Epo, has been shown to be the most permissive system for the *in vitro* replication of B19V (Wong and Brown, 2006) and it is used widely to study B19V infection.

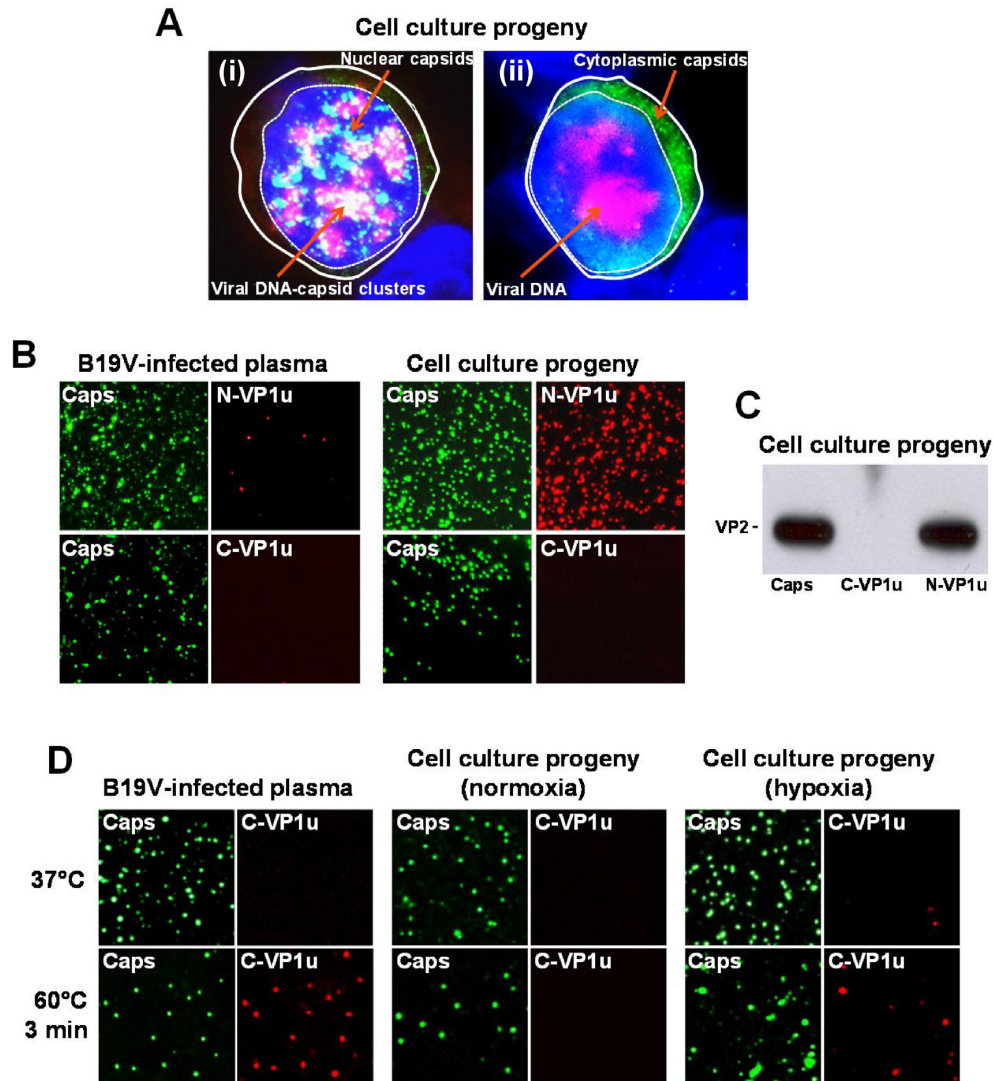
The reason for the defective replication of B19V in these cells has been shown to be multifactorial. Restrictions occur already at the cell surface, by the variable and limited expression of receptors and co-receptors required for binding and internalization of B19V (Brown et al., 1993; Munakata et al., 2005; Weigel-Kelley et al., 2003), but also by required intracellular factors restricted mainly to the erythroid lineage. Those intracellular factors can operate at the level of transcription, controlling the generation of sufficient full-length capsid-encoding transcripts (Guan et al., 2008; Liu et al.,



**Fig. 6.** Capsid progeny and quantitation of virions in EPCs. Cells ( $3 \times 10^5$ ) were infected with B19V under normoxia or hypoxia. At progressive times p.i., the supernatant was collected and the cells were lysed. (A and B) B19V capsids were immunoprecipitated from the cell extracts with mAb 860-55D, against intact capsids. As a reference control, B19V ( $4 \times 10^{10}$ ) was added to mock-infected cell extracts. (C and D) B19V DNA was quantified from the immunoprecipitated capsids. As a reference control, B19V ( $4 \times 10^{10}$  virions) was added to mock-infected cell extracts. (E and F) B19V DNA was quantified from the supernatant of the infected cells. Data are the mean  $\pm$  SD of two independent experiments.



**Fig. 7.** Virus egress in EPCs. Cells ( $3 \times 10^5$ ) were infected with B19V under normoxia or hypoxia. (A and B) At progressive times p.i., B19V capsids were immunoprecipitated from the cell supernatant with mAb 860-55D. As a reference control, B19V ( $4 \times 10^{10}$ ) was added to mock-infected cell supernatant. (C and D) B19V capsids were immunoprecipitated and B19V DNA was quantified. As a reference control, B19V ( $4 \times 10^{10}$  virions) was added to mock-infected cell supernatant. Data are the mean  $\pm$  SD of two independent experiments.



**Fig. 8.** Intracellular distribution of capsids and viral genomes and VP1u conformation in the capsid progeny. (A) Simultaneous detection of viral genomes and capsids in infected UT7Epo cells by FISH. Two representative cells are shown. (i) In some cells, B19V genomes and capsids were detectable in large clusters in the nucleus. (ii) In a larger proportion of cells, viral genomes were detected isolated in the nucleus while capsids were detected in the cytoplasm. (B) VP1u conformation in the plasma-derived virus differs from that of the cell culture progeny (UT7/Epo cells). Plasma-derived virus and cell culture progeny were concentrated by sucrose cushion centrifugation, spotted onto coverslips, fixed and detected by IF with mAb 860-55D or mAb 521-5D (Caps) and antibodies against the N-terminus and C-terminus of VP1u. (C) Immunoprecipitation of the cell culture progeny (UT7/Epo cells, 3 days p.i.) with mAb 860-55D (Capsids) and antibodies against the N-terminus and C-terminus of VP1u. (D) Flexibility of VP1u in the plasma-derived virus and cell culture progeny obtained under normoxia or hypoxia. Viruses were untreated (37°C) or heat-treated (60°C for 3 min) to trigger the exposure of VP1u and detected by IF with the indicated antibodies.

1992). In non-permissive cells the majority of viral mRNAs encode for NS1, with only limited production of the capsid-encoding transcripts. NS1 causes cell death by its cytotoxic or apoptotic characteristics (Moffatt et al., 1998). In contrast, more B19V RNAs are read through the multiple polyadenylation sites in permissive cells, which results in sufficient full-length capsid-encoding mRNAs (Liu et al., 1992). Studies have also shown that B19V replication and transcription were restricted to a small subset of cells but without production of capsid proteins, while in other cells, the single-stranded viral DNA was not converted to the double-stranded form (Gallinella et al., 2000). All the described restrictions at early (receptor/co-receptor) and late (replication/transcription) stages of the infection result in none or limited production of virus progeny.

Recently, two novel approaches based on hypoxic conditions (Caillaet-Fauquet et al., 2004b; Pillet et al., 2004) and the use of *ex vivo* expanded CD36+ primary human erythroid progenitor cells (CD36+ EPCs), previous CD34+ *in vitro* preselection (Pillet et al., 2008; Wong et al., 2008), or directly from unselected peripheral blood mononuclear cells (Filippone et al., 2010), have been shown to improve B19V infection. The obtained results are in agreement with previous observations, which showed that B19V replicates better in CD36+ EPCs, in particular under hypoxia (Chen et al., 2011). However, despite these improvements, the final genome encapsidation step was still insufficient, producing abundant but mostly non-infectious empty capsids. In the study by Chen et al. (2011), the use of EPCs under hypoxia was shown to improve B19V infection, however large quantities of infectious virus were not



recovered from the supernatant of the infected cells, as it should be expected for a lytic virus. Therefore, CD36+ EPCs cannot yet be considered as a highly permissive cell culture system to propagate B19V and a robust source of infectious virus. Moreover, compared to UT7/Epo cells, the generation of primary CD36+ EPCs remains time-consuming, requires large quantities of expensive growth factors and the permissivity to B19V is limited within a narrow and variable time-frame when B19V receptor and co-receptors are expressed in concert with a favorable intracellular microenvironment (Wong et al., 2008).

Parvoviruses pack their single-stranded, linear DNA genome into the pre-assembled capsids in the nucleus (Cotmore and Tattersall, 2005; King et al., 2001; Timpe et al., 2005). The helicase activity of the parvovirus nonstructural protein, which is present in the encapsidation complexes, functions as a molecular motor to translocate the viral genome into the empty capsid through the fivefold axes pore, a process that is also mediated by the terminal telomeric structures of the viral genome (Cotmore and Tattersall, 2005; King et al., 2001). Besides genome encapsidation, the channels at the fivefold symmetry axis are also used for the externalization of VP1u during the infection process (Bleker et al., 2005, 2006; Cotmore and Tattersall, 2012; Farr and Tattersall, 2004; Plevka et al., 2011). The channel is narrow and minor modifications of its diameter result in defective genome encapsidation and VP1u externalization (Bleker et al., 2005; Cotmore and Tattersall, 2012). Therefore, specific capsid and genome conformations play a critical role in the packaging step. VP1u from parvoviruses is not accessible, but can become exposed *in vitro* by mild heat or low pH treatments and *in vivo* during the intracellular trafficking of the virus (Cotmore et al., 1999; Kronenberg et al., 2005; Mani et al., 2006; Ros et al., 2006; Vihinen-Ranta et al., 2002) or upon receptor binding in the case of B19V (Bönsch et al., 2010a). In clear contrast to natural plasma-derived virus, VP1u was exposed partially in the capsid progeny. While the most N-terminal region was externalized and accessible to antibodies, the C-terminal region remained internal (Fig. 8). This particular conformation was irreversible and did not change upon heat treatment. The aberrant conformation and rigidity of VP1u might explain the encapsidation failure in semi-permissive cell systems. Further studies will elucidate whether the VP1u conformation in the virus progeny is due to an aberrant assembly or the lack of a final maturation step.

## 5. Conclusions

When compared to UT7/Epo cells and normoxia, hypoxic conditions or the use of CD36+ EPCs resulted in a significant acceleration of the infection/transfection, an increase in the number of infected cells and a modest increase in the yield of capsid progeny. However, despite these improvements, genome encapsidation was impaired seriously under all tested conditions and cells. The fivefold axes channel might be constricted in the virus progeny by the atypical partial exposure of VP1u hindering the packaging step, which arises as a major limiting factor for the *in vitro* propagation of B19V.

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## **Part III**

# **Discussion**





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