#### Aus der dem Institut für Molekulare Onkologie (Prof. Dr. med. M. Dobbelstein) der Medizinischen Fakult ät der Universit ät Göttingen

# The role of chromosomal instability in therapy response of colorectal cancer

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Abbreviations

#### **Abbreviations**

C Degree celsius

5-FU 5-Fluoruracil

A-MTs Astral microtubules

APC/C Anaphase promotions complex or cyclosome

ATCC American type culture collection

ATM Ataxia-telangiectasia mutated

CFSs Common fragile sites

ch-TOG/CAKP5 Cytoskeleton-associated protein 5

Chk2 Checkpoint kinase 2

CIN Chromosome instability

CRC Colorectal cancer
DME Dimethylenastron

DMSO Dimethysulphoxide

DNA Deoxyribonucleic acid

DSB Double-strand DNA break

EDTA Ethylenediaminetetraacetic acid

EGFR Epidermal growth factor receptor

ER Estrogen receptor

et al. Et alii

FACS Fluorescence activated cell sorting

FCS Fetal calf serum

 $G_0$  Gap-phase 0 Gap-phase 1

G<sub>2</sub> Gap-phase 2

H<sub>2</sub>O Water

IP-MTs Inter-polar microtubules

min Minute

MIN/MSI Microsatellite instability

Mps1 Monopolar spindle 1

Abbreviations

MTs Microtubules

nM Nanomolar

ns Not significant

NSLCL Non-small-cell lung cancer

PI Propidium iodide

RNA Ribonucleic acid

RNase Ribonuc lease

RT Room temperature

S Synthesis

S-CIN Segmental chromosome instability

SAC Spindle assembly checkpoint

sem. Standard error of the mean

TS Thymidylate synthase

VEGF Endothelial growth factor

W-CIN Whole chromosome instability

μl Microliter

μM Micromolar

Abstract

#### **Abstract**

Chromosomal instability (CIN) represents a major hallmark of cancer and is defined as the perpetual gain or loss of whole chromosomes during mitotic cell division. It is thought that CIN can drive tumor cell evolution by contributing to the generation of genetic heterogeneity in cancer. Importantly, tumor evolution might also fuel therapy resistance, a major problem for cancer patients in the clinic. However, whether CIN contributes directly to the generation of therapy resistance is unclear. So far it was not possible to systematically investigate the role of CIN and perpetual mitotic chromosome missegregation for the development of therapy resistance due to the fact that CIN could not be suppressed in chromosomally instable cancer cells. However, most recently, our lab has established means to correct an important molecular trigger for CIN in colorectal cancer (CRC) cells, namely increased microtubule dynamics during mitosis. In this way, it became possible to suppress chromosome missegregation and the evolvement of an euploidy in otherwise chromosomally instable CRC cells. This now opens the possibility to investigate the role of CIN in therapy response, which was the aim of this study.

I used various cell systems to compare the therapy response towards commonly used chemotherapeutic drugs in isogenic CIN and non-CIN cells. These include chromosomally instable CRC cells, in which CIN was suppressed by treatment with low doses of Taxol or by partial suppression of the microtubule polymerase chTOG/CKAP5. In addition, CIN was induced in chromosomally stable CRC cells by Aphidicolin treatment mediated replication stress or by inhibition of the mitotic spindle assembly checkpoint kinase Mps1. CIN and non-CIN cells were treated with Oxaliplatin, Cisplatin, 5-FU, Adriamycin, and Irinotecan. I found an increased resistance towards Oxaliplatin only in CIN cells with *CHK2* deficiency. Other CIN cells (e.g. SW620, chromosomally stable HCT116 cells treated by Aphidicolin or MPS1-IN-3) did not show any response differences compared with non-CIN cells. These results might indicate the CIN phenotype *per se* does not confer drug resistance, but loss of *CHK2* function itself might contribute to the drug resistance.

#### 1. Introduction

#### 1.1. The eukaryotic cell cycle

The cell cycle is an accurate and ordered process, during which a parental cell replicates its genome and distributes the copies evenly onto two daughter cells. This process is divided into two stages: interphase and mitosis. Interphase comprises three distinct phases: gap-phase 1 ( $G_1$ ) phase, synthesis (S) phase, and  $G_2$  phase. Mitosis consists of five distinct phases: prophase, prometaphase, metaphase, anaphase and telophase (Vermeulen et al. 2003) (Figure 1-1).

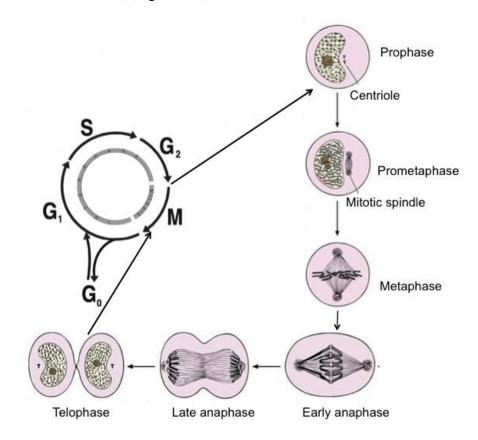


Figure 1-1 The eukaryotic cell cycle.

The eukaryotic cell cycle is divided into  $G_1$ -, S-,  $G_2$ , and M phase. M phase is further subdivided into prophase, prometaphase, metaphase, anaphase and telophase. Cells can exit the cell cycle and enter a resting state called  $G_0$ . (Figure is modified from Vermeulen et al., 2003, p. 132)

The  $G_1$  and  $G_2$  phases of the cell cycle are "gap phases" that occur between the two main events of the cell cycle, DNA synthesis and mitosis. In G<sub>1</sub> phase the cells prepare for DNA replication. When the extracellular environment lack of nutrient supply or during differentiation, the cells can exit the cell cycle to enter the resting  $G_0$ phase. Upon certain proliferative stimuli, the cells enter G<sub>1</sub> and proceed into S phase, during which the DNA as well as the centrosomes are duplicated. Once the DNA replication is achieved, cells enter mitosis. During prophase, chromatin is condensed and chromosomes become visible. At this stage, each chromosome consists of two sister chromatids that are attached to each other at the centromere. The nuclear envelope breaks down, and the mitotic spindle is assembled during prometaphase. In addition, the kinetochores assemble at the centromeric region of the sister chromatids, thereby providing binding sites for the microtubules. Firstly, the chromosomes are randomly attached to microtubules in a process called "search and capture" (Heald et al. 1996). Then they are aligned on the metaphase plate during mitosis (Caspersson et al. 1968). During early anaphase, cohesion protein complexes that link the sister chromatid are cleaved by separase (Abrieu et al. 2001; Nakajima et al. 2007). Due to microtubule shortening, the sister chromatids are separated and move towards the spindle poles. The two spindle poles move apart during late anaphase (Saxton and McIntosh 1987). During telophase, two new daughter nuclei are formed, and during cytokinesis, the separation of the daughter cells is completed by cleavage of the cytoplasm (Terada et al. 1998).

## 1.2. Mitotic spindle assembly and the mitotic spindle assembly checkpoint

The mitotic spindle is a self-organized and dynamic macromolecular structure, which is composed of microtubules (MTs), MT-associated proteins and motor proteins. Mitotic spindle assembly is dependent on the highly regulated nucleation of MTs (Prosser and Pelletier 2017). Three broad categories of MTs exist within a mitotic spindle: kinetochore MTs (K-MTs), astral MTs (A-MTs) and inter-polar MTs (IP-MTs) (Dumont and Mitchison 2009). K-MTs attach the chromosome to spindle poles via the kinetochores. A-MTs radiate from the spindle poles and interact with the

cell cortex, which is crucial for spindle positioning (Khodjakov et al. 2000; McNally 2013). IP-MTs originate from opposite poles, which helps to separate the poles and stabilizes the spindle (Prosser and Pelletier 2017).

During chromosome alignment MTs act in a highly dynamic manner and constantly change from a growing to a shrinking state. This characteristic of MTs is known as "dynamic instability" (Mitchison and Kirschner 1984). A major regulator of MT growth is the MT polymerase ch-TOG/CKAP5, which resides at the growing plus tips of the MTs and act as a MT stabilizer (Al-Bassam and Chang 2011; Tournebize et al. 2000).

Before cells initiate sister chromatid segregation during anaphase, each chromosome has to be aligned at the metaphase plate. This is ensured by a signaling pathway known as the spindle assembly checkpoint (SAC) (Musacchio and Salmon 2007; Sacristan and Kops 2015). The SAC comprises several kinetochore-based proteins including Mad1, Mad2, Bub1, BubR1 and the Mps1 kinase (Foley and Kapoor 2013). The SAC is activated in response to unattached kinetochores that are present when chromosomes are not properly aligned at the metaphase plate. In turn, the SAC inhibits the ubiquitin ligase activity of the anaphase promotions complex or cyclosome (APC/C) and thereby prevents the degradation of its key substrates including cyclin B and securin (Foley and Kapoor 2013; Musacchio and Salmon 2007). Thus, activation of the SAC in the early phases of mitosis prevents premature sister chromatic separation and exit from mitosis.

#### 1.3. Genome instability and tumor evolution

A major hallmark of human cancer is the presence of profound alterations of genome. Different forms of genome instability can be distinguished:

- Accumulations of point mutations, which are due to defects in mismatch or nucleotide excision repair (Wood 1997). A particular form of this phenotype in colorectal cancer (CRC) is known as microsatellite instability (MIN/MSI), where defects in mismatch repair genes account for instabilities of microsatellite sequences (Lengauer et al. 1997).
- 2. Accumulation of segmental or structural chromosome aberrations, which can be due to DNA repair or replication defects (Feuk et al. 2006). This form of

instability is termed as segmental or structural chromosome instability (S-CIN) (Geigl et al. 2008).

3. Accumulation of numerical aneuploidy, which arises upon whole chromosome missegregation during mitosis. This form of instability is called whole chromosome instability (W-CIN) (Geigl et al. 2008). In fact, chromosomally stable cells show less than 1% of cell division missegregation events, whereas in W-CIN cells this rate is increased to 20%-50% (Lengauer et al. 1997; Thompson and Compton 2008).

#### 1.3.1. Causes of W-CIN

Different causes responsible for the induction of W-CIN have been discussed (Bastians 2015; Thompson et al. 2010). For instance, malfunction of the spindle assembly checkpoint (Musacchio and Salmon 2007), the presence of supernumerary centrosomes (Pihan et al. 1998) or defects in the chromatid cohesion (Barber et al. 2008) can account for the mitotic chromosome missegregation and W-CIN. A recent study revealed that DNA replication stress can also cause W-CIN (Burrell et al. 2013). In fact, while induction of replication stress induced an euploidy, alleviating replication stress in cancer cells reduced the frequency of chromosome missegregation (Burrell et al. 2013).

A major source for W-CIN appears to be the generation of erroneous microtubule-kinetochore interactions (Foley and Kapoor 2013). Three types of erroneous attachments can occur (1) Monotelic attachments, where only one of the sister kinetochores attaches to microtubules. (2) Syntelic attachments, where both sister kinetochores attach to the microtubules from the same spindle pole. (3) Merotelic attachments, where one kinetochore attaches to microtubules from both spindle poles (Figure 1-2) (Tanaka and Hirota 2009, 2016). Monotelic and syntelic attachments can directly or indirectly be sensed by the SAC, which detects the lack of microtubule attachment to the kinetochores or the lack of proper tension generated between the two kinetochores (Tanaka and Hirota 2009). The SAC delays anaphase onset until the errors are corrected. However, merotelic attachments, cannot be sensed by the SAC and thus, can lead to missegregation of chromosomes (Gregan et al. 2011). It is thought that merotelic attachments are a leading cause for W-CIN and are

associated with the generation of lagging chromosomes during anaphase (Figure 1-2b) (Gregan et al. 2011; Nicholson and Cimini 2013).

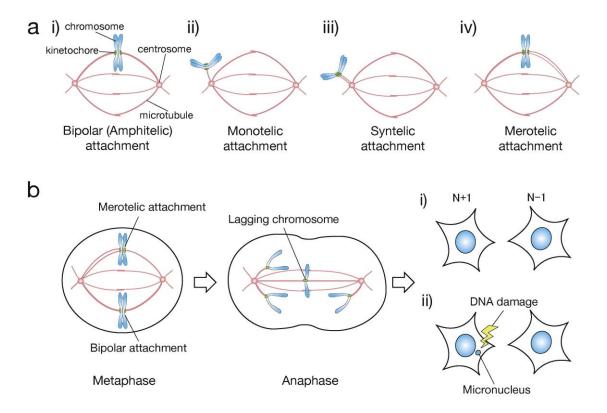


Figure 1-2 Classification of kinetochore-microtubule attachments

(a) Four types of kinetochore-microtubule attachments are described. (i) Bipolar (amphitelic) attachments describe kinetochores attached to microtubules emanating from opposite spindle poles. (ii) Monotelic attachments involve kinetochores attached to the microtubules emanating from the same pole. (iii) Syntelic attachments are defined as kinetochores attached to the microtubules emanating from the same spindle pole. (iv) Merotelic attachments are conditions where a single kinetochore is attached to microtubules from both spindle poles. (b) Merotelic attachments can lead to lagging chromosomes during anaphase. (i) The lagging chromosomes can segregate to the wrong side resulting in whole chromosome aneuploidy. (ii) Lagging chromosomes can be entrapped in micronuclei and maybe subsequently damaged by the recapture of micronuclei, which can lead to structural aneuploidy. (Figure is modified from Tanaka and Hirota, 2016, p. 67)

Interestingly, the presence of supernumerary centrosomes can lead to the formation of transient multipolar spindle intermediates that support the formation of merotelic kinetochore attachments and thereby, causes chromosome missegregations and W-CIN.

Recently, our lab established that increased microtubule plus-end assembly rates within mitotic spindles can contribute to CIN. By analyzing the plus-end assembly rates during mitosis in MIN/MSI and CIN colorectal cancer (CRC) cell lines, it was revealed that elevated MT growth rates are present only in CIN cells. Moreover, restoration of proper microtubule assembly rates in CIN cells by chemical suppression of microtubule dynamics (by treatment with low-doses of Taxol) or by partial repression of the microtubule polymerase *ch-TOG/CKAP5* was sufficient to suppress W-CIN. *Vice versa*, by genetic means (e.g. by overexpression of *Aurora-A* or by the loss of *CHK2*) or by treatment with low-doses of nocodazole, microtubule plus-end assembly rates were increased, thereby inducing the generation of lagging chromosomes, chromosome missegregation and CIN. These findings revealed that abnormally increased microtubule growth rates during mitosis can act as a trigger for the induction of CIN. Importantly, by the use of Taxol treatment or by repression of *ch-TOG/CKAP5* CIN can be efficiently suppressed in otherwise chromosomally instable cancer cells (Ertych et al. 2014).

#### 1.3.2. Consequences of CIN

CIN is a key characteristic of almost all solid cancers (Ohyashiki et al. 2017). It is thought that CIN can drive tumor cell evolution by altering gene expression that may facilitate rapid cell adaptation (McGranahan et al. 2012). In this way, CIN can contribute to genetic heterogeneity in cancer and thereby might drive therapy resistance, a major problem in the clinic (Chen et al. 2012; Gerlinger et al. 2014; Turner and Reis-Filho 2012). The relationship between cancer prognosis and CIN has been explored across multiple types of cancers.

In non-small-cell lung cancer (NSLCL), several independent studies found that CIN was a poor prognosis factor. It was independent of conventional risk factors such as sex, age, and tumor stage in variate analysis (Choi et al. 2009; Nakamura et al. 2003; Yoo et al. 2010). In breast cancers, however, CIN is a prognostic factor that is

dependent on the estrogen receptor (ER) state. In ER-positive breast cancers, CIN is associated with tumor progression and unfavorable prognosis (Smid et al. 2011). While in ER-negative breast cancer, CIN is associated with an improved prognosis (Birkbak et al. 2011; Roylance et al. 2011). In colorectal cancer (CRC) CIN correlated with a worse prognosis regarding overall survival or progress-free survival compared to the non-CIN CRC (Walther et al. 2008). Studies in other cancers such as oral, ovarian, synovial, and endometrial cancers, together with diffuse large B-cell lymphomas have also demonstrated that CIN is associated with poor prognosis (Bakhoum et al. 2011; Murayama-Hosokawa et al. 2010; Nakagawa et al. 2006; Sato et al. 2010). Hence, these studies have established that CIN is an important prognosis factor in a wide range of cancer types.

#### **1.3.3.** Cancer genome evolution

The basic evolution principles of Darwin evolution that the differential fitness variation is heritable can be applied in the context of cancer evolution (Nowell 1976). When a tumor is detected, it has undergone many generations of cell division, and cells have stochastically acquired somatic mutations in each generation (Gerlinger et al. 2014; Rosenthal et al. 2017). Among these mutations, a small subset of mutations called driver events may show evolutionary advantage that allows the cells to outcompete others (Rosenthal et al. 2017). Also, the clonal selection and evolution of the cells may lead to outgrowth of subclones that lead to branched evolutionary phylogenies (Gerlinger et al. 2012; Gundem et al. 2015).

The majority of established driver events are clonal, which indicates that the clonal driver events may occur in the early stage of tumor evolution (McGranahan et al. 2015; McGranahan and Swanton 2015). Whereas subclonal driver events that have been identified across numerous cancers are believed to play a role in tumor maintenance and progression (Yates et al. 2015). Subclonal populations of cancer cells induce a heterogeneous environment within the tumor. However, each subclone is not an isolated entity (Rosenthal et al. 2017). Studies have also revealed that genetically distinct subclones interact with each other to some extent during tumor evolution and this interaction may be competitive or cooperative (Marusyk et al. 2014). For vital resources such as nutrients, oxygen, or space, one subclone may

outcompete another (Marusyk and Polyak 2010). To many aspects, clonal cooperation contributes to tumor growth and progression (Neelakantan et al. 2015; Polyak and Marusyk 2014). For example, through endocrine signaling networks, low-frequency clones may promote resistance to treatment or support the growth of dominant clones (Acharyya et al. 2012; Chung et al. 2013; Hobor et al. 2014). Clonal interference can also result in tumor collapse. When a subclone that outcompetes the subclone that drives tumor growth is dependent on the current microenvironment, a change in the tumor environment may lead to tumor collapse (Marusyk et al. 2014).

In sum, tumors represent a complex dynamic ecological system, in which heterogeneity can promote tumor development and progression but not only a substrate of evolution.

#### 1.3.4. CIN and responses to anti-cancer treatment

Assuming that all cancer cells are sensitive to a given treatment to the same extent, any therapy that kills the cancer cells faster than they divide would eventually result in a cure of the disease. Unfortunately, the tumor heterogeneity prevents this from happening in most cases. Drug resistance is a severe problem for cancer treatment. Numerous examples reveal that tumor heterogeneity can drive drug resistance. Epidermal growth factor receptor (EGFR) gene heterogeneity within non-small-cell lung cancers results in a reduced gefitinib response (Taniguchi et al. 2008). In CRCs, the clonal evolution drives anti-EGFR treatment resistance (Siravegna et al. 2015). To assess the association between CIN and drug response in CRC, Lee and colleagues treated CIN and non-CIN cell lines of CRC individually with a library of kinase inhibitors. They found that CIN cell lines showed significantly increased multidrug resistance compared to non-CIN cells, which was independent of somatic mutation status. Tetraploid isogenic cells showed generally higher resistance compared to their diploid counterparts (Lee et al. 2011).

Taken together, these studies indicate that tumor heterogeneity is related with drug resistance and poor clinical outcome in diversity cancers.

#### 1.4. Colorectal cancer

Colorectal cancer (CRC) is a premier model for studying CIN. It is the third most diagnosed cancer in worldwide (Rao et al. 2016). MIN/MSI and CIN are two main distinct patterns of genomic instability in CRC (Lengauer et al. 1998). 80%-90% of CRC cases are characterized by CIN and this is thought to contribute to progression and recurrence of the disease (Rao et al. 2016). Due to its high incidence, the investigation of CIN in CRCs has a high clinical relevance. CRCs often show nonmucinous histology, moderate differentiation and less tumor-infiltrating lymphocytes (Silver et al. 2012; Sinicrope et al. 2006). Most CRCs exhibit *APC*, *KRAS*, and *TP53* mutation and these genetic alterations are associated with CIN (Rowan et al. 2005). Moreover, CIN is clearly associated with bad prognosis and reduced the patient survival in CRC (Watanabe et al. 2012).

The treatment of CRCs is based on number, size, localization and progression of the tumor, presence or absence of biochemical markers and the health condition of the patients. The treatment strategies for CRCs include surgical resection, chemotherapy, and monoclonal antibodies against EGFR and vascular endothelial growth factor (VEGF) in KRAS wild-type tumors combined with traditional chemotherapy. Most patients with metastatic CRC disease are treated with chemotherapy. The first line of chemotherapy with fluoropyrimidines (5-FU or Capecitabine) combined with Leucovorin, and other cytotoxic agents, such as Irinotecan (5-FU/LV/Irinotecan (FOFIRI)), (5-FU/Leucovorin/oxaliplatin Oxaliplatin (FOLFOX)) (Capecitabine/Leucovorin/Oxaliplatin (CAPOX)). Leucovorin can increase the reaction rate of fluoropyrimidines. When tumors relapse, and the patients have good tolerance a second line chemotherapy is frequently used. When patients are refractory to Irinotecan, the Oxaliplatin-containing regimens FOLFOX or CAPOX can be used. When refractory to Oxaliplatin, Irinotecan monotherapy or FOLFIRI can be utilized (Benson et al. 2017).

#### 1.5. Scope of the study

This thesis project aimed to address whether ongoing chromosome missegregation constituting a W-CIN phenotype affects therapy response in CRC cells *in vitro*. For this, I used chromosomally instable CRC cells, in which the W-CIN phenotype and

chromosome missegregation could be specifically suppressed. On the other hand, I also induced the W-CIN phenotype in chromosomally stable CRC cells. CRC cells with or without W-CIN were treated with clinical relevant chemotherapeutic drugs including 5-FU, Oxaliplatin, Irinotecan, Cisplatin, and Adriamycin. The drug responses were assessed by colony formation assays and FACS analysis. The goal of the project was to investigate whether W-CIN, perpetual chromosome missegregation or aneuploidy affects therapy responses.

#### 2. Materials and Methods

#### 2.1. Materials

All the working materials including cell culture dishes, pipette tips and reaction tubes were purchased from Sarstedt (Nümbrecht, Germany), Eppendorf (Hamburg, Germany).

#### 2.1.1. Equipment

Equipment used to assist this study is listed in Table 2-1.

**Table 2-1 Equipment** 

Equipment	Model	Company	
CO <sub>2</sub> Incubator	HERAcell 240 CO <sub>2</sub>	Thermo Fisher Scientific,	
	Incubator	Karlsruhe, Germany	
Cooling Centrifuge	Multifuge X3R	Thermo Fisher Scientific,	
		Karlsruhe, Germany	
Electrophoresis Power	Power supply EV231	Peqlab, Erlangen, Germany	
Supply			
Flow Cytometer	BD FACSCanto <sup>©</sup> II	Becton Dickinson, San Jose,	
		CA, USA	
Electroporation Device	GenePulser Xcell <sup>©</sup>	BioRad Laboratories,	
		M ünchen, Germany	
Magnetic Mixer	IKAMAG <sup>©</sup> RCT	IKA Laboratories, München,	
		Germany	
Microscope	Zeiss Axio Imager Z1	Zeiss, Göttingen, Germany	
Microscope Camera	A3474-07	Hamamatsu Photonics,	
Adaptor		Hamamatsu, Japan	
Pipettes	Pipetman <sup>©</sup>	Gilson International,	
		LimburgOffheim, Germany	
Pipettor	Pipetboy acu	Intergra Biosciences,	
		Fernwald, Germany	

Equipment	Model	Company	
Sterile Workbench	HERAsafeM	Thermo Fisher Scientific,	
		Karlsruhe, Germany	
Tabletop Centrifuge	Biofuge pico	Thermo Fisher Scientific,	
		Karlsruhe	
Tabletop Centrifuge	Biofuge fresco	Thermo Fisher Scientific,	
cooling		Karlsruhe	
Vortex Mixer	VORTEX-GENIE <sup>©</sup> 2	Scientific Industries Inc.,	
		Bohemia, NY, USA	
Quato IntelliScan	Quato IntelliScan 1600	Quatographic Technology,	
		Schleswig - Holstein,	
		Germany	

#### 2.1.2. Software

The software used in the study is listed in Table 2-2

**Table 2-2 Software** 

Software	Company
Hokawo Laucher	Hamamatsu Photonics, Hamamatsu,
	Japan
ImageJ	NIH Image, Bethesda, MD, USA
BD FACSDivaTM	Becton Dickinson, San Jose, CA, USA
Prism 6	Graphpad, La Jolla, CA, USA

#### 2.1.3. Chemotherapeutic drugs and inhibitors

All chemotherapeutic drugs and inhibitors used in this study were purchased from Sigma-Aldrich (Taufkirchen, Germany), VWR international (West Chester, PA, USA), Th. Geyer (Höxter, Germany), Santa Cruz (Dallas, TX, USA), Calbiochem (La Jolla, CA, USA).

Chemotherapeutic drugs and inhibitors used in this study and their respective working concentrations and effects are listed in Table 2-3.

**Table 2-3 Chemicals** 

	Used			Stock	
Chemical	concentration	Effect	Dissolvent	concentration	Company
Adriamycin (Myers et	5, 10, 15, 20,	Intercalates	H <sub>2</sub> O	500 μΜ	Th. Geyer,
al. 1977)	30, 50, 400,	into DNA and			Höxter,
	600 nM	stabilizes			Germany
		topoisomerase			
		II			
Oxaliplatin (Arango	0.1, 0.2, 0.4,	Forms DNA	DMSO	50 mM	VW R
et al. 2004)	0.8, 1, 4, 8 μΜ	adducts,			International,
		disrupts DNA			West Chester,
		replication			PA, USA
		and			
		transcription			
Cisplatin (Siddik	0.2, 04, 0.8,	Forms DNA	PBS	5 mM	Santa Cruz,
2003)	1.6, 2 μΜ	adducts,			Dallas, TX,
		disrupts DNA			USA
		replication			
		and			
		transcription			
5-FU (Longley et al.	0.2, 0.5, 1, 2,	Inhibition	DMSO	50 mM	Sig ma-Aldrich
2003)	4, 5, 10 μΜ	thymidylate			Taufkirchen,
		synthase (TS)			Germany
		and			
		incorporation			
		its metabolites			
		into RNA and			
		DNA			

	Used			Stock	
Chemical	concentration	Effect	Dissolvent	concentration	Company
Irinotecan (Hurwitzet	0.05, 0.1, 0.2,	Inhibition	DMSO	30 mM	VW R
al. 2004)	0.4, 0.6 μΜ	topoisomerase			International,
		I			West Chester,
					PA, USA
Dimethylenastron	2 μΜ	Inhibition	DMSO	10 mM	Calbiochem,
(DME) (Gartner et al.		EG5-kinesin			La Jolla, CA,
2005)					USA
Puromycin (Nathans	1μg/ml	Inhibition of	DMSO	1 mg/ml	Sig ma-Aldrich
1964)		translation			Taufkirchen,
					Germany
Taxol (Schiff et al.	0.5 nM	Stabilization	DMSO	5 μΜ	Sig ma-Aldrich
1979)		of			Taufkirchen,
		microtubules			Germany
Aphidicolin (Ikegami	1, 2 μg/ml	Inhibition	DMSO	10 mg/ml	Santa Cruz,
et al. 1978)		DNA			Dallas, TX,
		polymerase δ			USA
MPS1-IN-3 (Tannous	0.5 μΜ	Inhibition	DMSO	10 mM	Sig ma-Aldrich
et al. 2013)		MPS1			Taufkirchen,
					Germany

#### 2.1.4. Human cell lines

Human cell lines used for this study are listed in Table 2-4. The table also provides information about the culture medium, the selection antibiotics, origin and their reference.

Table 2-4 Human cell lines

Cell Line	Medium	Selection	Origin	Reference
HCT116	RPMI	None	Colon	(Brattain et al.
	1640		carcinoma	1981)
SW620	RPMI	None	Colon	(Leibovitz et
	1640		carcinoma	al. 1976)
HCT116- <i>CHK2</i> -/-	RPMI	G418	Colon	(Jallepalli et
	1640		carcinoma	al. 2003)
HCT116- <i>CHK2</i> -/sh <i>ch-TOG</i>	RPMI	Puromycin	Colon	(Ertych et al.
	1640		carcinoma	2014)
SW620-shch-TOG	RPMI	Puromycin	Colon	(Ertych et al.
	1640		carcinoma	2014)

Colorectal cancer HCT116 and SW620 cell lines were purchased from the American Type Culture Collection (ATCC; Manassas, VA, USA). HCT116-*CHK2*-/- cells were kindly provided by Prof. Bert Vogelstein (John Hopkins University, Baltimore, Maryland, USA).

#### 2.2. Methods

#### 2.2.1. Cultivation of human cell lines

Human cell lines were cultured in RPMI 1640 medium (Sigma-Aldrich, Taufkirchen, Germany) supplemented with 10% (v/v) Fetal Calf Serum (FCS) (GE Healthcare, Chalfont St. Giles, Great Britain), 100 μg/ml streptomycin and 100 U/ml penicillin (Sigma-Aldrich, Taufkirchen, Germany) at 37 °C with 5% CO<sub>2</sub> in a humidified incubator. Cells were splitted every 2-3 days to enable enough space and sufficient nutrient supply for proliferation. To do this, cells were washed with 10 ml PBS once and detached by 1 ml trypsin-EDTA (Sigma-Aldrich, Taufkirchen, Germany) treatment. A defined dilution of cell suspension was transferred in to a new cell culture dish containing RPMI 1640 medium. Stable cell lines expressing shRNA that

targeting *ch-TOG/CKAP5* and the control scrambled shRNAs were growing in the presence of 1  $\mu$ g/ml puromycin. HCT116-*CHK2*<sup>-/-</sup> cells were growing in the presence of 300  $\mu$ g/ml G418.

Cells were stored in liquid nitrogen for long time storage. For this, cells were harvested and centrifuged at 1,000 rpm, then resuspended in 400 µl freezing medium, which containing 70%(v/v) RPMI 1640, 20%(v/v) FCS and 10% (v/v) DMSO. The cell suspensions were slowly cooling down to -80 °C by using a cryo freezing box filled with 2-propanol (VWR international, West Chester, PA, USA) and transferred to the vapor phase of liquid nitrogen after 24 h.

### 2.2.2. Generation of single cell clones in the presence of Aphidicolin or MPS1-IN-3.

1,000 HCT116 cells were seeded into 10 cm cell culture dish 24 h before the treatment. The cells were treated with RPMI 1640 medium containing  $1\,\text{ng/ml}$  or 2 ng/ml Aphidicolin or 0.5  $\mu$ M MPS1-IN-3 or DMSO. RPMI 1640 medium containing drug was changed every 2-3 days. After 7 days small colonies were transferred into a 24-well plate, and further cultivated in the presence of the drug. After growing for 30 generations, single cell clones were analyzed.

#### 2.2.3. Karyotype analysis by metaphase chromosome counting

Cells were treated with 2 uM DME for 4h to arrest in mitosis. Afterwards the cells were harvested in 15 ml Falcon tube and centrifuged at 1,000 rpm. To swell the cells, the cell pellets were resuspended in 2 ml hypotonic solution (40%(v/v) RPMI 1640 medium in aqua dest) and incubated at room temperature (RT) for 20 min. Subsequently, the swelled cells were fixed with 1 ml ice-cold Carnoy's fixdative (75%(v/v) methanol, 25%(v/v) glacial acetic acid) and centrifuged at 2,000 rpm for 5 min. The fixation step was repeated 3 times. Then the cells were directly processed or stored at -20 °C until further usage. Cells were resuspended in 100 - 500  $\mu$ l 100% glacial acetic acid and dropped onto a pre-cooled, wet objective slide from a vertical height of about 30 cm. The objective slides with cell drops were incubated at 42 °C in a wet chamber for 5 min. Afterwards the slides were dried at RT. After the objective

slides had been thoroughly dried, they were stained with 8% (v/v) Giemsa staining solution (Merck, Darmstadt, Germany) for 25 min. Objective slides were then washed and dried at RT. After thoroughly dried, the objective slides were embedded into Euparal (Carl Roth, Karlsruhe, Germany). The stained objective slides were analyzed by a Zeiss Axioscope FS microscope (Zeiss, Oberkochen, Germany) equipped with a Hamamatsu C4742-95 camera and the Hokawo Launcher 2.1 software (Hamamatsu Photonics, Hamatsu, Japan).

#### 2.2.4. Flow cytometry

A BD FACS Canto II (Becton Dickinson, San Jose, CA, USA) was used to perform Fluorescence Activated Cell Sorting (FACS) analysis. BD FACS Diva<sup>TM</sup> (Becton Dickinson, San Jose, CA, USA) software was used to analyze the data. Cells were harvested in 15 ml Falcon tube and centrifuged 5 min at 1,000 rpm. Afterwards the cells were resuspended in 200 μl PBS. After fixing in 1 ml 70% (v/v) ice-cold ethanol, which was added dropwise while the suspension was continuously vortexing, the cells were subsequently stored at 4 °C overnight. DNA intercalating dye propidium iodide (PI) (Sigma-Aldrich, Taufkirchen, Germany) was used to determine the DNA content. Fixed cells were centrifuged at 2,000 rpm for 5 min, the cell pellet was washed with 1 ml PBS once, then resuspended in 100 ul 1μg/ml DNA free RNase A (Applichem, Darmstadt, Germany) and incubated at RT for 15 min. After adding 10 μl 50 μg/ml PI the cells were analyzed.

#### 2.2.5. Colony formation assay

3,000 cells were seeded in 6-well plate 24 h before the treatment. The cells were treated with different concentrations of Oxaliplatin (VWR International, West Chester, PA, USA), Adriamycin (Th. Geyer, Höxter, Germany), 5-FU (Sigma-Aldrich Taufkirchen, Germany), Irinotecan (VWR International, West Chester, PA, USA), Cisplatin (Santa Cruz, Dallas, TX, USA). Cells were incubated at 37 °C and 5% CO<sub>2</sub> for 10 days. The RPMI1640 medium containing the drugs was changed every 2-3 days. The growing colonies were fixed with 70% (v/v) ethanol and stained with crystal violet solution (0,1%(w/v) Crystal violet, 20% (v/v) ethanol in H<sub>2</sub>O). The growth area was scanned using a Quato IntelliScan 1600 (Quatographic Technology,

Schleswig - Holstein, Germany) and colony area was determined by using ColonyArea plugin of ImageJ (NIH Image, Bethesda, MD, USA) (Guzman et al. 2014).

#### 2.2.6. Statistical analysis

All data are shown as mean  $\pm$  standard error of the mean (sem.). One tailed Student's t-test was performed by Prism software package, version 6 (Graphpad, La Jolla, CA, USA).

#### 3. Results

3.1. Responses towards platinum drugs in cells exhibiting CIN and after suppression of CIN.

3.1.1. Suppression of CIN in HCT116-*CHK2*-/- but not in SW620 by treatment with low-dose of Taxol results in increased sensitivity towards Oxaliplatin treatment.

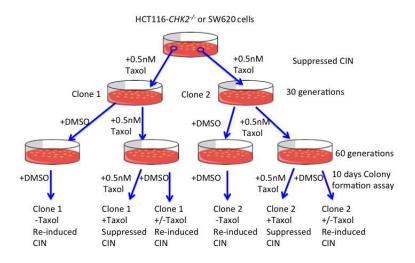


Figure 3-1 Schematic overview of single cell clones in the presence or absence of low-dose of Taxol.

Two independent single cell clones derived from HCT116-*CHK2*-/- or SW620 were treated with 0.5 nM Taxol for 30 generations. These cell clones were cultured either in the presence of 0.5 nM Taxol (+Taxol) or absence of Taxol (-Taxol) for another 30 generations. After 60 generations, these cell clones were treated with different chemotherapeutic drugs for 10 days for colony formation assay. The cells continuously cultured with 0.5 nM Taxol were also treated with different drugs in the absence of 0.5 nM Taxol during the assay of 10 days (+/-Taxol).

Treatment with low-dose of Taxol restores proper mitotic microtubule assembly rates and suppresses CIN in chromosomally unstable colorectal cancer cells (Ertych et al. 2014). I investigated whether suppression of CIN impacted on drug response towards chemotherapeutic drugs. For this, I used two independent single cell clones of HCT116-*CHK2*<sup>-/-</sup> and SW620 cells, both of which exhibited increased microtubule plus-end assembly rates and CIN, which were treated with Taxol for 30 generations thereby suppressing CIN. Single cell clones generated in the presence of Taxol were used for the subsequent colony formation assays. Each cell clone was either treated with Taxol for another 30 generations (suppressed CIN) or left untreated for another 30 generations (re-induced CIN). I treated these cell clones with increasing concentrations of Oxaliplatin in the presence of Taxol (suppressed CIN) or in the absence of Taxol (CIN) (Figure 3-1).

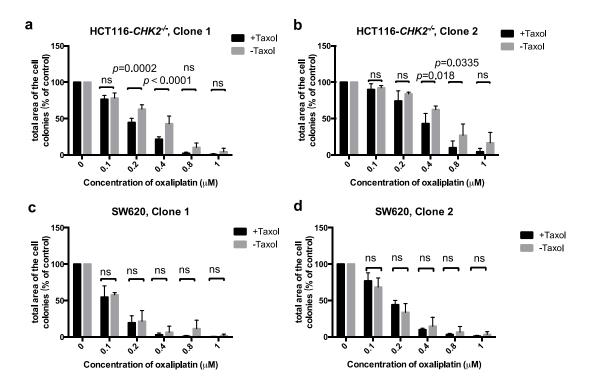


Figure 3-2 Quantification of the area of the cell colonies of HCT116-*CHK2*<sup>-/-</sup> and SW620 cells treated with different concentration of Oxaliplatin in the presence or absence of low-dose of Taxol.

(a) Cells of HCT116-*CHK2*-/- cell clone 1 were treated with increasing concentrations of Oxaliplatin in the presence or absence of 0.5 nM Taxol and the area of the cell

colonies was determined after ten days. (b) Cells of HCT116- $CHK2^{-/-}$  cell clone 2 were treated with increasing concentrations of Oxaliplatin in the presence or absence of 0.5 nM Taxol and the area of the cell colonies was determined after ten days. (c) Cells of SW620 cell clone 1 were treated with increasing concentrations of Oxaliplatin in the presence or absence of 0.5 nM Taxol and the area of the cell colonies was determined after ten days. (d) Cells of SW620 cell clone 2 were treated with increasing concentrations of Oxaliplatin in the presence or absence of 0.5 nM Taxol and the area of the cell colonies was determined after ten days. For the colony formation assays, 3,000 cells were seeded 24 h before treatment, and five different concentrations of oxaliplatin were used as indicated. After ten days of the area of the cell colonies covered by the cells was determined. The areas of the cell colonies were normalized to control treated cells and represented as bar graphs (mean  $\pm$  sem., t-test, n=3 independent experiments, ns = not significant).

Colony formation assays in the continuous presence of Oxaliplatin revealed that HCT116- $CHK2^{-/-}$  cells that grown in the absence of Taxol were more resistant towards Oxaliplatin compared to the same clone grew in the presence of low-does Taxol (Figure 3-2a and 3-2b). In HCT116- $CHK2^{-/-}$  single clone 1 cells, the area of the cell colonies in the absence of Taxol was 1.41-fold greater than the cells in the presence of Taxol when treated with 0.2  $\mu$ M Oxaliplatin, and was 1.97-fold greater when treated with 0.4  $\mu$ M Oxaliplatin (Figure 3-2a). In the second single cell clone of HCT116- $CHK2^{-/-}$  cells, the area of the cell colonies in the absence of Taxol was 1.44-fold greater than the cells in the presence of Taxol when treated with 0.4  $\mu$ M Oxaliplatin, and was 1.71-fold greater when treated with 0.8  $\mu$ M Oxaliplatin (Figure 3-2b). However, no significant differences in drug sensitivity were detectable in two independent cell clones of SW620 cells that grown in the presence or absence of Taxol (Figure 3-2c and 3-2d).

# 3.1.2. Short-term re-induction of chromosome missegregation mediated by short-term removal of Taxol results in decreased sensitivity towards Oxaliplatin in HCT116-CHK2<sup>-/-</sup> cells, but not in SW620 cells.

Long-time (30 days) removal Taxol can re-induce CIN and aneuploidy in the same clone generated in the presence of low-dose of Taxol (Ertych et al. 2014). To investigate whether short-term removal of Taxol and thus, acute chromosome missegregation without significant alterations of the karyotype impacted on the drug response, I used two cell clones for HCT116-*CHK2*-/- and two cell clones for SW620 cells that were continuously grown in the presence of Taxol to suppress CIN. These cells were then treated with increasing concentrations of Oxaliplatin in the presence or absence of Taxol during the colony formation assay for ten days only (Figure 3-1).

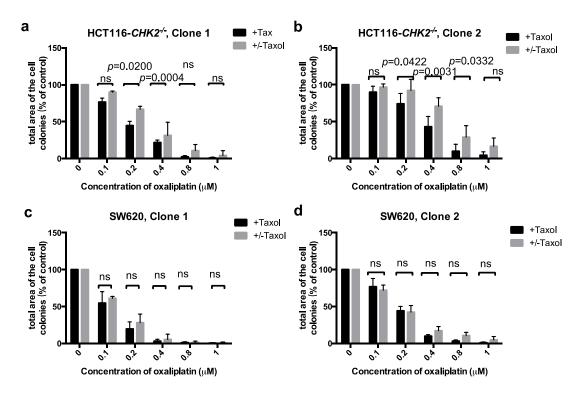


Figure 3-3 Quantification of the area of the cell colonies of HCT116-*CHK2*<sup>-/-</sup> and SW620 cells treated with different concentration of Oxaliplatin in the presence or short time absence of low-dose of Taxol.

(a) HCT116-*CHK2*-/- cells of Taxol-treated clone 1 were treated with increasing concentrations of Oxaliplatin in the presence or absence of 0.5 nM Taxol during the assay, and the area of the cell colonies was determined after ten days. (b) HCT116-*CHK2*-/- cells of Taxol treated clone 2 were treated with increasing

concentrations of Oxaliplatin in the presence or absence of 0.5 nM Taxol during the assay, and the area of the cell colonies was determined after ten days. (c) SW620 cells of Taxol treated clone 1 were treated with increasing concentrations of Oxaliplatin in the presence or absence of 0.5 nM Taxol during the assay, and the area of the cell colonies was determined after ten days. (d) SW620 cells of Taxol treated clone 2 were treated with increasing concentrations of Oxaliplatin in the presence or absence of 0.5 nM Taxol, and the area of the cell colonies was determined after ten days. The areas of the cell colonies were normalized to control treated cells and represented as bar graphs (mean  $\pm$ sem., t-test, n=3 independent experiments, ns = not significant).

These analyses revealed that HCT116-*CHK*2<sup>-/-</sup> cells that grew in the absence of Taxol during the assay were more resistant towards Oxaliplatin compared to the same cells cultured in the presence of Taxol (Figure 3-3a and 3-3b). In clone 1 of HCT116-*CHK*2<sup>-/-</sup> cells, the area of the cell colonies in the absence of Taxol during the assay was 1.18-fold greater than the cells in the presence of the Taxol when treated with 0.2 μM Oxaliplatin, and was 1.49-fold greater when treated with 0.4 μM Oxaliplatin (Figure 3-3a). Whereas the area of the cell colonies in the absence of Taxol was 1.24-fold greater than the cells in the presence of Taxol when treated with 0.2 μM Oxaliplatin, 1.65-fold greater when treated with 0.4 μM Oxaliplatin, and 2.91-fold greater when treated with 0.8 μM Oxaliplatin in clone 2 of HCT116-*CHK*2<sup>-/-</sup> cells (Figure 3-3b). However, no significant response differences were found in two independent clones of SW620 cells that were growing in the presence or short-term absence of Taxol (Figure 3-3 c and 3-3d).

# 3.1.3. Suppression of CIN by stable knockdown of *ch-TOG/CKAP5* in HCT116-*CHK2*-/- and SW620 results in increased sensitivity towards Oxaliplatin treatment.

Partial stable knockdown of *ch-TOG/CKAP5* restores proper mitotic plus-end microtubule assembly rates and suppresses CIN in chromosomally unstable colorectal cancer cells (Ertych et al. 2014). I used two independent stable *ch-TOG/CKAP5* knockdown single cell clones of HCT116-*CHK2*-/- and SW620 cells to investigate

whether suppression CIN affects drug response towards Oxaliplatin independently of Taxol treatment. Compared with the control cell clones, *ch-TOG/CKAP5* knockdown cells were more sensitive towards Oxaliplatin treatment in HCT-*CHK2*-/- cells (Figure 3-4a). In HCT116-*CHK2*-/- cells, the mean value of the area of the control cell colonies was 1.25-fold greater than *ch-TOG/CKAP5* knockdown cells when treated with 0.1 μM Oxaliplatin, 1.85-fold greater when treated with 0.2 μM Oxaliplatin, and 5.38-fold greater when treated with treated with 0.4 μM Oxaliplatin (Figure 3-4a). SW620-sh*ch-TOG* clones showed increased sensitivity towards Oxaliplatin (0.1 and 0.2 μM) as well, albeit at a lesser extent (Figure 3-4b).

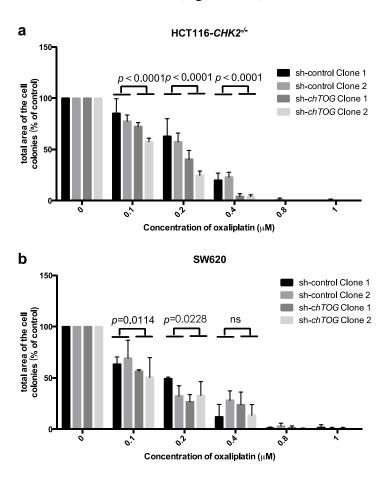


Figure 3-4 Quantification of area of the cell colonies treated with different concentration of Oxaliplatin in HCT116-CHK2<sup>-/-</sup>-shch-TOG and SW620-shch-TOG cells.

(a) Two independent shRNA control single cell clones and two different sh*ch-TOG* single cell clones derived from HCT116-*CHK*2<sup>-/-</sup> were treated with increasing concentrations of Oxaliplatin, and the area of the cell colonies was determined after

ten days. (b) Two independent shRNA control single cell clones and two different shch-TOG single cell clones derived from SW620 were treated with increasing concentrations of Oxaliplatin, and the area of the cell colonies was determined after ten days. The areas of the cell colonies were normalized to control scrambled cells and represented as bar graphs (mean  $\pm$  sem., t-test, n=3 independent experiments, ns = not significant).

### 3.1.4. Suppression of CIN in HCT116-CHK2<sup>-/-</sup> cells by low-dose of Taxol does not result in acute response differences towards Oxaliplatin.

To further investigate the acute cellular response towards higher concentrations of Oxaliplatin in HCT116-*CHK2*-/- cells after CIN suppression, I used FACS analyses to analyze the acute cell response in the presence or absence of low-dose of Taxol treated with increasing concentrations (1 μM, 4 μm and 8 μM) of Oxaliplatin in cells of HCT116-*CHK2*-/- clone 1. These cells were cultured in the presence of low-dose Taxol (+Taxol), only in the absence of Taxol for 30 days (-Taxol), or absence of Taxol only during the Oxaliplatin treatment (+/-Taxol). After 48 h of treatment, the proportion of cells with a Sub-G<sub>1</sub> DNA content, which represents apoptotic cells (Kajstura et al. 2007), was determined by FACS.

These analyses overall revealed no drug response differences torwards Oxaliplatin between CIN and after suppression CIN by Taxol. Only after treatment with 8  $\mu$ M Oxaliplatin, cells that were grown in the absence of Taxol showed more apoptotic cells in response of the drug treatment (Figure 3-5).

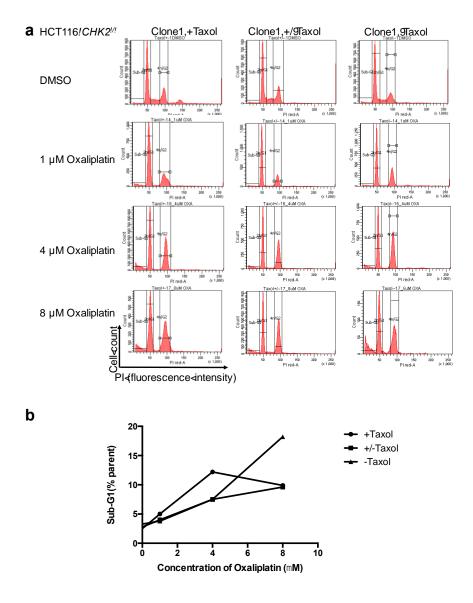


Figure 3-5 Analyses of the acute cellular response towards different concentrations of Oxaliplatin treatment in cells of HCT116-*CHK2*-/- Clone 1 in the presence or absence of Taxol.

(a) DNA content profiles of HCT116- $CHK2^{-/-}$  in the presence or absence of low-dose Taxol after 48 h of Oxaliplatin treatment. (b) The proportion of cells with a Sub-G<sub>1</sub> DNA content after 48 h different concentrations of Oxaliplatin treatment was determined. (n=1 experiment)

## 3.1.5. Suppression of CIN treated by low-dose of Taxol does not result in response differences towards Cisplatin neither in HCT116-CHK2<sup>-/-</sup> nor in SW620 cells.

Cisplatin is the first generation of platinum compounds. Its cytotoxic mode of action is mediated by its interaction with DNA to form DNA adducts, which is similar to Oxaliplatin (Siddik 2003). I used Cisplatin to test whether it had a similar effect as Oxaliplatin on cell growth after CIN suppression. On a cell growth after CIN suppression, however, unlike Oxaliplatin, colony formation assays revealed that no differences in drug sensitivity in the presence or absence of Taxol in HCT116-CHK2<sup>-/-</sup> cells (Figure 3-6a and 3-6b). Similar results were observed in two independent cell clones of SW620 cells (Figure 3-6c and 3-6d).

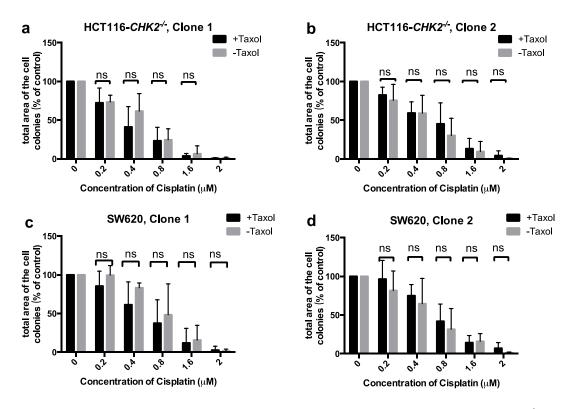


Figure 3-6 Quantification of the area of the cell colonies of HCT116-*CHK2*<sup>-/-</sup> and SW620 cells after treatment with different concentration of Cisplatin in the presence or absence of low-dose of Taxol.

(a) Cells of HCT116-*CHK2*-/- cell clone 1 were treated with increasing concentrations of Cisplatin in the presence or absence of 0.5 nM Taxol and the area of the cell colonies was determined after ten days. (b) Cells of HCT116-*CHK2*-/- cell clone 2

were treated with increasing concentrations of Cisplatin in the presence or absence of 0.5 nM Taxol and the area of the cell colonies was determined after ten days. (c) Cells of SW620 cell clone 1 were treated with increasing concentrations of Cisplatin in the presence or absence of 0.5 nM Taxol and the area of the cell colonies was determined after ten days. (d) Cells of SW620 cell clone 2 were treated with increasing concentrations of Cisplatin in the presence or absence of 0.5 nM Taxol and the area of the cell colonies was determined after ten days. The areas of the cell colonies were normalized to control treated cells and represented as bar graphs (mean  $\pm$  sem., t-test, n=3 independent experiments, ns = not significant).

# 3.1.6. Short-term re-induction of chromosome missegregation does not result in response differences towards Cisplatin in HCT116-CHK2<sup>-/-</sup> and SW620 cells.

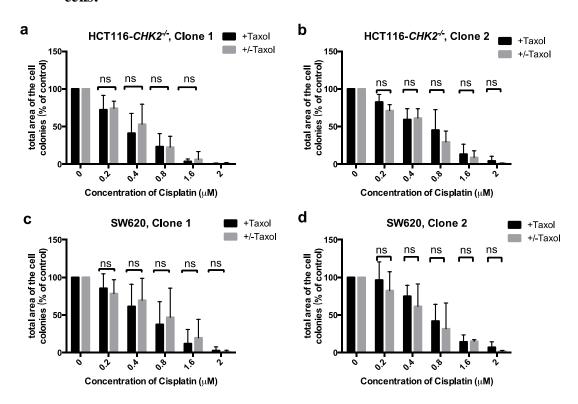


Figure 3-7 Quantification of the area of cell colonies of HCT116-*CHK2*<sup>-/-</sup> and SW620 cells treated with different concentration of Cisplatin in the presence or short-term absence of low-dose of Taxol.

(a) Cells of HCT116-CHK2<sup>-/-</sup> single cell clone 1 were treated with increasing concentrations of Cisplatin in the presence or absence of 0.5 nM Taxol during the

assay, and the area of the cell colonies was determined after ten days. (**b**) Cells of HCT116- $CHK2^{-/-}$  single cell clone 2 were treated with increasing concentrations of Cisplatin in the presence or absence of 0.5 nM Taxol during the assay, and the area of the cell colonies was determined after ten days. (**c**) Cells of SW620 single cell clone 1 were treated with increasing concentrations of Cisplatin in the presence or absence of 0.5 nM Taxol during the assay, and the area of the cell colonies was determined after ten days. (**d**) Cells of SW620 cell single cell clone 2 were treated with increasing concentrations of Cisplatin in the presence or absence of 0.5 nM Taxol during the assay, and the area of the cell colonies was determined after ten days. The areas of the cell colonies were normalized to control treated cells and represented as bar graphs (mean  $\pm$  sem., t-test, n=3 independent experiments, ns = not significant).

Removal of Taxol during the colony formation assay was also used during Cisplatin treatment. However, no drug sensitivity differences towards Cisplatin were found in two independent cell clones of HCT116-*CHK2*-/- cells that grown in the absence of Taxol during the colony formation assay (Figure 3-7a and 3-7b). Similar results were obtained for two independent clones of SW620 cells that were grown in the presence or short-term absence of Taxol (Figure 3-7c and 3-7d).

#### 3.1.7. Taxol treatment does not affect drug response towards Oxaliplatin or Cisplatin *per se*.

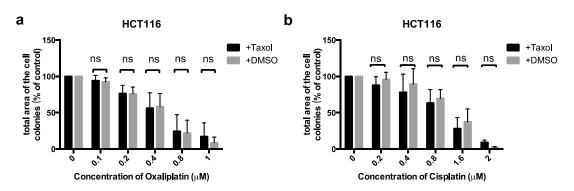


Figure 3-8 Quantification of the area of cell colonies of cell populations of HCT116 treated with different concentrations of Oxaliplatin or Cisplatin.

(a) HCT116 cells were treated with increasing concentrations of Oxaliplatin in the presence of 0.5 nM Taxol or DMSO, and the area of the cell colonies was determined

after ten days. (**b**) HCT116 cells were treated with increasing concentrations of Cisplatin in the presence of 0.5 nM Taxol or DMSO, and the area of the cell colonies was determined after ten days. The areas of the cell colonies were normalized to control treated cells and represented as bar graphs (mean  $\pm$  sem., t-test, n=4 independent experiments, ns = not significant).

To investigate whether low-dose treatment of Taxol itself affects drug response, I used chromosomally stable HCT116 cells and treated them with Oxaliplatin or Cisplatin in the presence or absence of Taxol. After ten days of treatment, no drug response differences were detectable (Figure 3-8). Thus, low-dose of Taxol does not affect drug response towards Oxaliplatin or Cisplatin *per se*.

# 3.1.8. Suppression of CIN by knockdown of *ch-TOG/CKAP5* results in decreased sensitivity in HCT116-*CHK2*-/-, but increased sensitivity in SW620 towards Cisplatin treatment.

The *ch-TOG/CKAP5* stable knockdown cells of HCT116-*CHK2*-/- and SW620 showed increased sensitivity towards Oxaliplatin treatment (Figure 3-4), to test whether these cells also exhibit increased sensitivity towards Cisplatin, the cells were treated with increasing concentrations of Cisplatin. Surprisingly, compared with the control cell clones, *ch-TOG/CKAP5* knockdown HCT116-*CHK2*-/- cells were more resistant towards Cisplatin treatment (Figure 3-9a). When treated with 0.2 μM Cisplatin, the mean area of the *ch-TOG/CKAP5* knockdown cell colonies was 1.23-fold greater than the control cells, 1.41-fold greater when treated with 0.4 μM Cisplatin, and 1.60-fold greater when treated with 0.8 μM Cisplatin (Figure 3-9a). In contrast, stable *ch-TOG/CKAP5* knockdown cells derived from SW620 cells showed increased sensitivity towards Cisplatin (Figure 3-9b). The area of *ch-TOG/CKAP5* knockdown cell colonies was 1.46-fold lower than the control cells when treated with 0.4 μM Cisplatin, and 1.33-fold lower when treated with 0.8 μM Cisplatin in SW620 cells (Figure 3.9b). Thus, knockdown of *ch-TOG/CKAP5* shows different effects towards Ciplatin treatment in HCT116-*CHK2*-/- and SW620 cells.

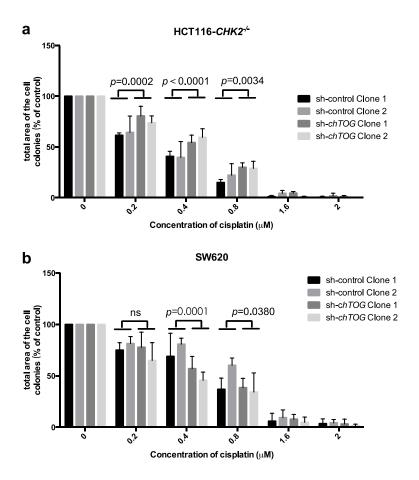


Figure 3-9 Quantification of the area of cell colonies of HCT116-CHK2<sup>-/-</sup>-shch-TOG and SW620-shch-TOG cell clones treated with different concentrations of Cisplatin

(a) Two independent shRNA control single cell clones and two independent sh-chTOG clones from HCT116- $CHK2^{-/-}$  were treated with increasing concentrations of Cisplatin, and the area of the cell colonies was determined after ten days. (b) Two independent shRNA control single cell clones and two independent sh-chTOG clones derived from SW620 were treated with increasing concentrations of Cisplatin, and the area of the cell colonies was determined after ten days. The areas of the cell colonies were normalized to control scrambled cells and represented as bar graphs (mean  $\pm$  sem., t-test, n=3 independent experiments, ns = not significant).

### 3.2. Drug responses towards other chemotherapeutic drugs in cells exhibiting CIN and after suppression of CIN

After evaluating the CIN-dependent drugs responses towards platinum compounds, the cellular response towards various other chemotherapeutic drugs that are used for the treatment of CRC were also investigated.

In fact, 5-FU is used as a single drug treatment or combined with other chemotherapeutic drugs in CRC treatment (Longley et al. 2003). Adriamycin has exhibited a broad spectrum of anti-tumor effect, particular against solid cancers including CRC (Myers et al. 1977). Irinotecan has anti-tumor activity against CRC and is used as the first-line treatment or after the failure of 5-FU or Oxaliplatin as a second-line treatment (Pitot et al. 1997; Rougier et al. 1997; Saltz et al. 2000). Two independent single cell clones of HCT116-CHK2<sup>-/-</sup> and SW620 described in Figure 3-1 were treated with increasing concentrations of 5-FU, Adriamycin, and Irinotecan and the cellular response were evaluated by colony formation assays.

The assays in the continuous presence of 5-FU, Adriamycin, and Irinotecan treatment revealed no differences in drug sensitivity in two independent cell clones of HCT116-*CHK2*-/- or SW620 cells in the presence or absence of Taxol (Figure 3-10, 3-11, and 3-12).

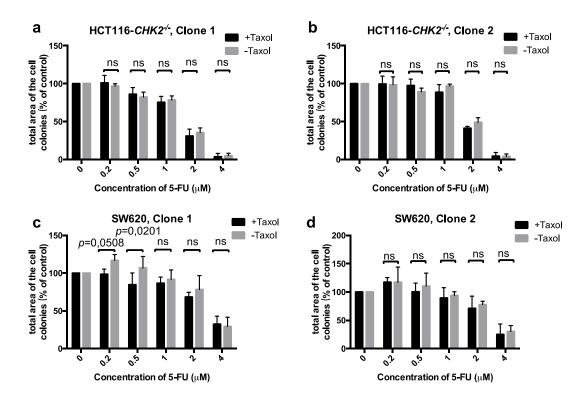


Figure 3-10 Quantification of the area of cell colonies of HCT116-CHK2<sup>-/-</sup> and SW620 cells treated with different concentrations of 5-FU in the presence or absence of low-dose of Taxol.

(a) Cells of HCT116-*CHK2*<sup>-/-</sup> single cell clone 1 were treated with increasing concentrations of 5-FU in the presence or absence of 0.5 nM Taxol and the area of the cell colonies was determined after ten days. (b) Cells of HCT116-*CHK2*<sup>-/-</sup> single cell clone 2 were treated with increasing concentrations of 5-FU in the presence or absence of 0.5 nM Taxol and the area of the cell colonies was determined after ten days. (c) Cells of SW620 single cell clone 1 were treated with increasing concentrations of 5-FU in the presence or absence of 0.5 nM Taxol and the area of the cell colonies was determined after ten days. (d) Cells of SW620 single cell clone 2 were treated with increasing concentrations of 5-FU in the presence or absence of 0.5 nM Taxol and the area of the cell colonies was determined after ten days. The areas of the cell colonies were normalized to control treated cells and represented as bar graphs (mean ±sem., *t*-test, n=3 independent experiments, ns = not significant).

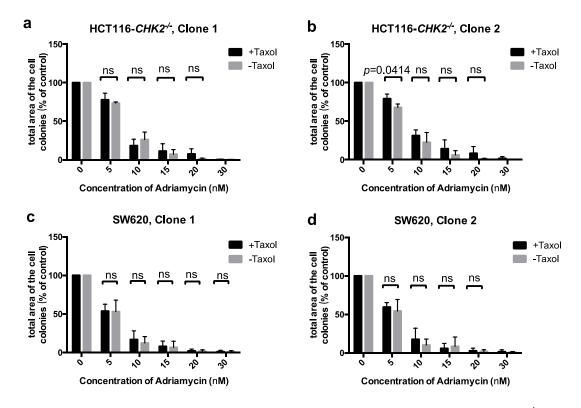


Figure 3-11 Quantification of the area cell colonies of HCT116-*CHK2*-/- and SW620 cells treated with different concentrations of Adriamycin in the presence or absence of low-dose of Taxol.

(a) Cells of HCT116- $CHK2^{-/-}$  single cell clone 1 were treated with increasing concentrations of Adriamycin in the presence or absence of 0.5 nM Taxol and the area of the cell colonies was determined after ten days. (b) Cells of HCT116- $CHK2^{-/-}$  single cell clone 2 were treated with increasing concentrations of Adriamycin in the presence or absence of 0.5 nM Taxol and the area of the cell colonies was determined after ten days. (c) Cells of SW620 single cell clone 1 were treated with increasing concentrations of Adriamycin in the presence or absence of 0.5 nM Taxol and the area of the cell colonies was determined after ten days. (d) Cells of SW620 single cell clone 2 were treated with increasing concentrations of Adriamycin in the presence or absence of 0.5 nM Taxol and the area of the cell colonies was determined after ten days. The areas of the cell colonies were normalized to control treated cells and represented as bar graphs (mean  $\pm$  sem, t-test, n=3 independent experiments, ns = not significant).

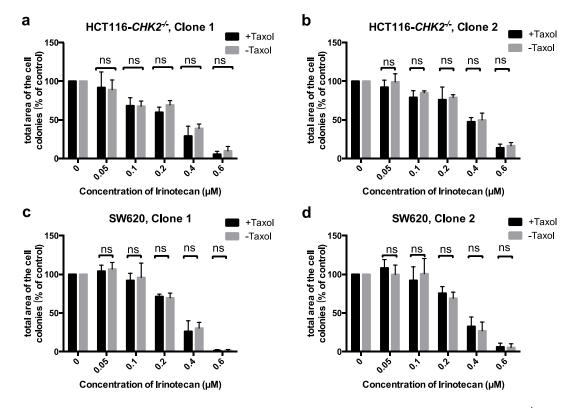


Figure 3-12 Quantification of the area of cell colonies for HCT116-*CHK2*<sup>-/-</sup> and SW620 cells treated with different concentration of Irinotecan in the presence or absence of low-dose of Taxol.

(a) Cells of HCT116- $CHK2^{-/-}$  single cell clone 1 were treated with increasing concentrations of Irinotecan in the presence or absence of 0.5 nM Taxol and the area of the cell colonies was determined after ten days. (b) Cells of HCT116- $CHK2^{-/-}$  single cell clone 2 were treated with increasing concentrations of Irinotecan in the presence or absence of 0.5 nM Taxol and the area of the cell colonies was determined after ten days. (c) Cells of SW620 single cell clone 1 were treated with increasing concentrations of Irinotecan in the presence or absence of 0.5 nM Taxol and the area of the cell colonies was determined after ten days. (d) Cells of SW620 single cell clone 2 were treated with increasing concentrations of Irinotecan in the presence or absence of 0.5 nM Taxol and the area of the cell colonies was determined after ten days. The areas of the cell colonies were normalized to control treated cells and represented as bar graphs (mean  $\pm$  sem., t-test, n=3 independent experiments, ns = not significant).

I also investigated the effect of short-time removal of Taxol (Figure 3-1) for 5-FU, Adriamycin, and Irinotecan treatment in HCT116-*CHK*2<sup>-/-</sup> and SW620 cell clones. Again, no differences were observed (Figure 3-13, 3-14, and 3-15).

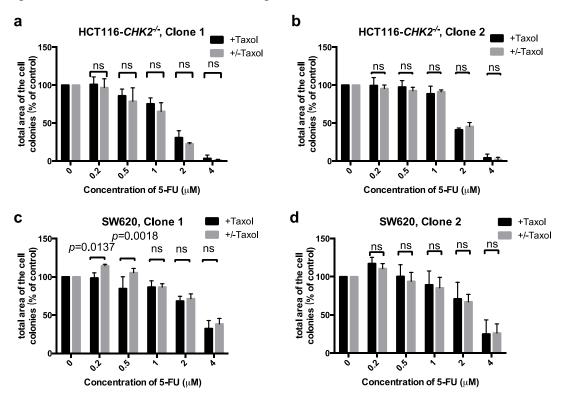


Figure 3-13 Quantification of the area of cell colonies of HCT116-*CHK2*-/- and SW620 cells treated with different concentration of 5-FU in the presence or short-term absence of low-dose of Taxol.

(a) Cells of HCT116-*CHK*2<sup>-/-</sup> single cell clone 1 were treated with increasing concentrations of 5-FU in the presence or absence of 0.5 nM Taxol during the assay, and the area of the cell colonies was determined after ten days. (b) Cells of HCT116-*CHK*2<sup>-/-</sup> single cell clone 2 were treated with increasing concentrations of 5-FU in the presence or absence of 0.5 nM Taxol during the assay and the area of the cell colonies was determined after ten days. (c) Cells of SW620 single cell clone 1 were treated with increasing concentrations of 5-FU in the presence or absence of 0.5 nM Taxol during the assay, and the area of the cell colonies was determined after 10 days. (d) Cells of SW620 single cell clone 2 was treated with increasing concentrations of 5-FU in the presence or absence of 0.5 nM Taxol during the assay, and the area of the cell colonies was determined after ten days. The areas of the cell

colonies were normalized to control treated cells and represented as bar graphs (mean  $\pm$  sem., t-test, n=3 independent experiments, ns = not significant).

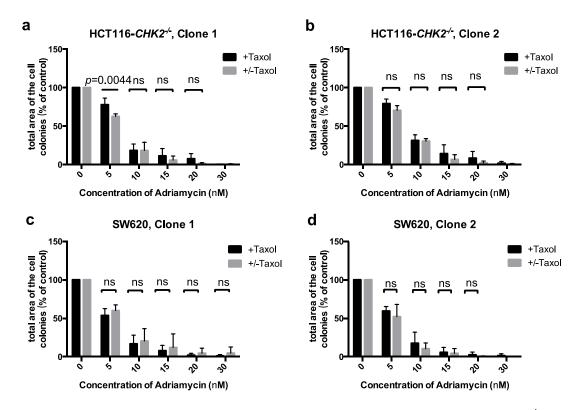


Figure 3-14 Quantification of the area of cell colonies of HCT116-*CHK2*<sup>-/-</sup> and SW620 cells treated with different concentrations of Adriamycin in the presence or short-time absence of low-dose of Taxol.

(a) Cells of HCT116-*CHK*2<sup>-/-</sup> single cell clone 1 were treated with increasing concentrations of Adriamycin in the presence or absence of 0.5 nM Taxol during the assay, and the area of the cell colonies was determined after ten days. (b) Cells of HCT116-*CHK*2<sup>-/-</sup> single cell clone 2 were treated with increasing concentrations of Adriamycin in the presence or absence of 0.5 nM Taxol during the assay, and the area of the cell colonies was determined after ten days. (c) Cells of SW620 single cell clone 1 were treated with increasing concentrations of Adriamycin in the presence or absence of 0.5 nM Taxol during the assay, and the area of the cell colonies was determined after ten days. (d) Cells of SW620 single cell clone 2 were treated with increasing concentrations of Adriamycin in the presence or absence of 0.5 nM Taxol during the assay, and the area of the cell colonies was determined after ten days. The

areas of the cell colonies were normalized to control treated cells and represented as bar graphs (mean  $\pm$  sem., t-test, n=3 independent experiments, ns = not significant).

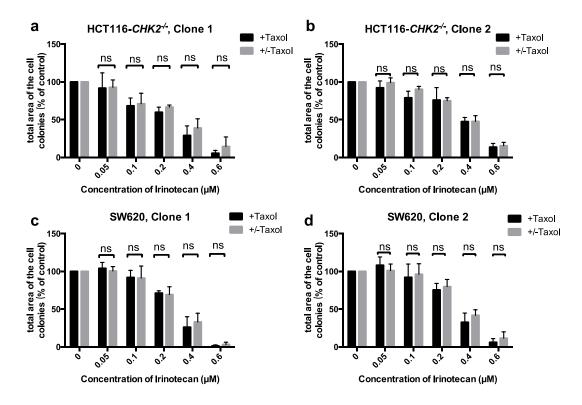


Figure 3-15 Quantification of area of cell colonies of HCT116-*CHK2*-/- and SW620 cells treated with different concentration of Irinotecan in the presence or short-term absence of low-dose of Taxol.

(a) Cells of HCT116-*CHK2*--- single cell clone 1 were treated with different concentrations of Irinotecan in the presence or absence of 0.5 nM Taxol during the assay and the area of the cell colonies was determined after ten days. (b) Cells of HCT116-*CHK2*--- single cell clone 2 were treated with increasing concentrations of Irinotecan in the presence or absence of 0.5 nM Taxol during the assay and the area of the cell colonies was determined after ten days. (c) Cells of SW620 single cell clone 1 were treated with increasing concentrations of Irinotecan in the presence or absence of 0.5 nM Taxol during the assay and the area of the cell colonies was determined after ten days. (d) Cells of SW620 cell clone 2 were treated with increasing concentrations of Irinotecan in the presence or absence of 0.5 nM Taxol, and the area of the cell colonies was determined after ten days. The areas of the cell colonies were

normalized to control treated cells and represented as bar graphs (mean  $\pm$  sem., t-test, n=3 independent experiments, ns = not significant).

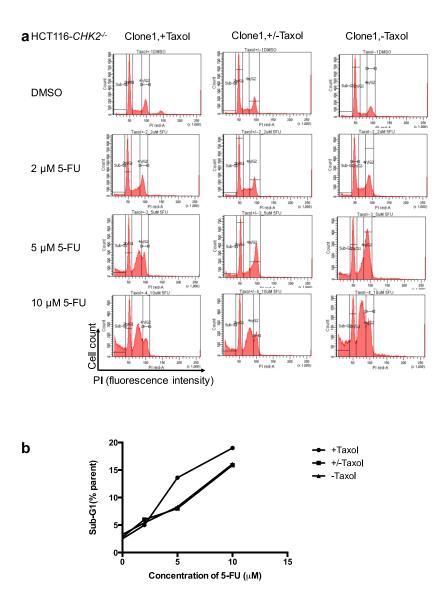
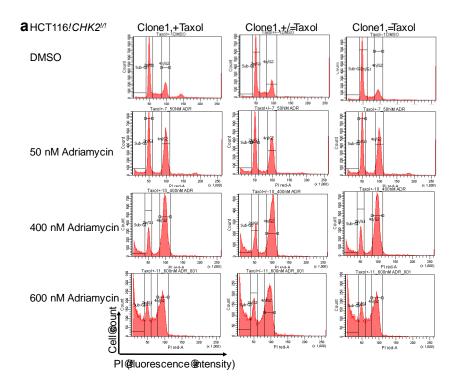


Figure 3-16 Analyses of the acute response towards different high concentrations of 5-FU treatment in cells of HCT116-*CHK2*-/- Clone 1 in the presence or absence of Taxol.

(a) DNA content profiles of HCT116-*CHK2*-/- in the presence or absence of low-does Taxol after 48 h of 5-FU treatment. (b) The proportion of cells with a Sub-G<sub>1</sub> DNA content after 48 h different concentrations of 5-FU treatment was determined. (n=1 experiment)



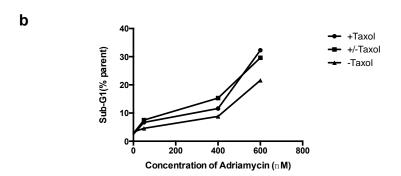


Figure 3-17 Analyses of the acute response towards different high concentrations of Adriamycin in cells of HCT116-*CHK2*<sup>-/-</sup> clone 1 in the presence or absence of Taxol.

(a) DNA content profiles of HCT116-*CHK2*-/- cells in the presence or absence of low-does Taxol after 48 h of Adriamycin treatment. (b) The proportion of cells with a Sub-G<sub>1</sub> DNA content after 48 h different concentrations of Adriamycin treatment was determined. (n=1 experiment)

Finally I investigated the acute response towards 5-FU and Adriamycin in HCT116-CHK2<sup>-/-</sup> cells by FACS analyses. Also, these experiments showed no

significant differences in the cellular response towards higher concentrations of 5-FU or Adriamycin treatment (Figure 3-16 and 3-17).

In sum, suppression of CIN does not cause drug response differences towards other chemotherapeutic drugs such as 5-FU, Adriamycin, or Irinotecan.

### 3.3. Drug responses in chromosomally stable CRC cells and after induction of CIN by DNA replication stress.

#### 3.3.1. Induction of CIN by Aphidicolin treatment in HCT116 cells.

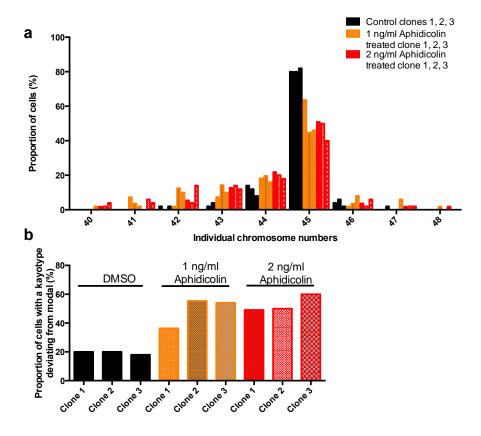


Figure 3-18 Aphidicolin induces CIN in chromosomally stable HCT116 cells.

(a) Karyotype analysis by chromosome counting of metaphase spreads of single cell clones derived from HCT116 cells treated with DMSO, 1 or 2 ng/ml Aphidicolin for 30 generations (n=50 cells). (b) The percentage of cells with chromosome numbers deviating from the modal were calculated.

Aphidicolin is a reversible inhibitor of the DNA polymerase  $\alpha$  and thus, inhibits proper DNA replication during S phase, thereby inducing replication stress (Ikegami et al. 1978). Since replication stress was associated with numerical aneuploidy (Burrell et al. 2013), I tested whether low-dose Aphidicolin treatment is sufficient to induce CIN. For this, HCT116 cells were treated with DMSO (control) or with two concentrations of Aphidicolin (1 and 2 ng/ml). Single cell clones were grown for 30 generations. Subsequently, the number of chromosomes per cell were determined by chromosome counting in metaphase spreads. The proportion of cells with chromosome numbers deviating from the modal (45 chromosomes) was analyzed.

### 3.3.2. Inducing CIN by Aphidicolin does not cause response differences towards Oxaliplatin or Cisplatin treatment in HCT116 cells.

To investigate whether induction of CIN upon replication stress would affect drug response in CRC cells, I used two HCT116 single cell clones that were either treated with DMSO or 2 ng/ml Aphidicolin. Colony formation assays in the continuous presence of Oxaliplatin or Cisplatin showed no significant response differences between Aphidicolin and DMSO treated HCT116 cells (Figure 3-19). These results indicate that acute induction of CIN in chromosomally stable CRC cell by replication stress is not sufficient to alter drug sensitivities towards Oxaliplatin or Cisplatin.

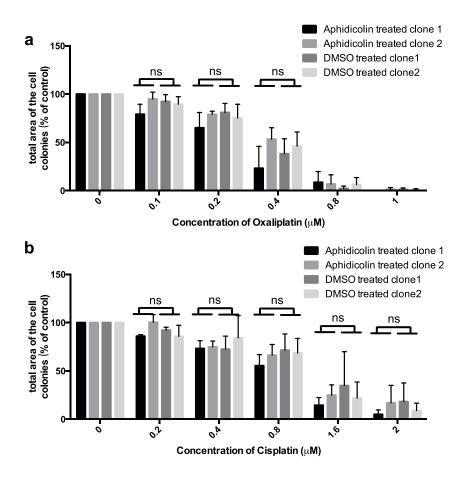


Figure 3-19 Quantification of the area of cell colonies after treatment with different concentration of Oxaliplatin or Cisplatin in Aphidicolin- and DMSO-treated single cell clones.

(a) Two independent DMSO-treated control single cell clones and two independent 2 ng/ml Aphidicolin-treated single cell clones of HCT116 cells were treated with increasing concentrations of Oxaliplatin, and the area of the cell colonies was determined after ten days. (b) Two independent DMSO-treated control single cell clones and two independent 2 ng/ml Aphidicolin-treated single cell clones of HCT116 cells were treated with increasing concentrations of Cisplatin, and the area of the cell colonies was determined after ten days. The areas of the cell colonies were normalized to control treated cells and represented as bar graphs (mean  $\pm$  sem., t-test, n=3 independent experiments, ns = not significant).

3.3.3. Short-term removal of Aphidicolin does not affect the drug response towards Oxaliplatin treatment, but increases resistance towards Cisplatin treatment in one single cell clone.

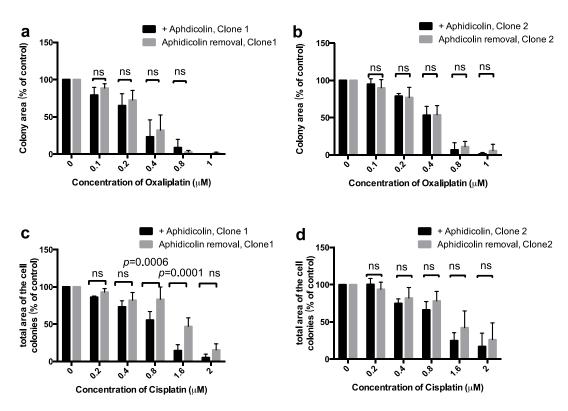


Figure 3-20 Quantification of the area of cell colonies of Aphidicolin treated cells treated with different concentration of Oxaliplatin or Cisplatin in the presence or absence of Aphidicolin.

(a) Cells of single cell clone 1 derived from 2 ng/ml Aphidicolin treated HCT116 cells were treated with increasing concentrations of Oxaliplatin in the presence or absence of Aphidicolin during the assay, and the area of the cell colonies was determined after ten days. (b) Cells of single cell clone 2 derived from 2 ng/ml Aphidicolin treated HCT116 cells were treated with increasing concentrations of Oxaliplatin in the presence or absence of Aphidicolin during the assay, and the area of the cell colonies was determined after ten days. (c) Cells of single cell clone 1 derived from 2 ng/ml Aphidicolin treated HCT116 cells were treated with increasing concentrations of Cisplatin in the presence or absence of Aphidicolin during the assay, and the area of the cell colonies was determined after ten days. (d) Cells of single cell clone 2 derived from 2 ng/ml Aphidicolin treated HCT116 cells were treated with

increasing concentrations of Cisplatin in the presence or absence of aphidicolin during the assay, and the area of the cell colonies was determined after ten days. The areas of the cell colonies were normalized to control treated cells and represented as bar graphs (mean  $\pm$ sem., t-test, n=3 independent experiments, ns = not significant).

Removal of Aphidicolin during the colony formation assay is expected to reveal whether ongoing chromosome missegregation or an euploidy itself would affect drug response. On the other hand, it could also show whether Aphidicolin itself impacts on the drug response. Hence, I used two aneuploid single cell clones of 2 ng/ml Aphidicolin treated HCT116 cells and treated them with increasing concentrations of Oxaliplatin or Cisplatin in the presence or absence of Aphidicolin during the assay. These colony formation assays showed that upon Oxaliplatin treatment, no response differences were observed in the presence or absence Aphidicolin during the assay (Figure 3-20a and 3-20b). Upon Cisplatin treatment, single cell clone 1 derived from Aphidicolin treated cells showed a slightly higher resistant towards two concentrations of Cisplatin (0.8 and 1.6 µM) in the absence of Aphidicolin during the assay when compared to in the presence of Aphidicolin (Figure 3-20c). However, using a second single clone derived from Aphidicolin treated HCT116 cells, no significant differences were detectable towards Cisplatin treatment in the presence or absence of Aphidicolin during the assay (Figure 3-20d), indicating that the observed slight effect is not representative.

Together, induction of CIN by Aphidicolin-triggered replication stress does not affect the cellular response towards Oxaliplatin or Cisplatin.

### 3.4. Drug response in chromosomally stable CRC cells and after induction of CIN by treatment with a Mps1 inhibitor.

### 3.4.1. Pharmacological inhibition of the mitotic spindle assembly checkpoint as a strategy to induce CIN.

The Mps1 kinase plays a critical role in SAC signaling (Abrieu et al. 2001). Inhibition of the Mps1 kinase with the small molecular inhibitor MPS1-IN-3 causes chromosomal misalignment, and inhibition of the spindle checkpoint and thus, leads

to chromosome missegregation and aneuploidy (Tannous et al. 2013). To induce CIN in chromosomally stable HCT116 cells, cells were treated with 0.5  $\mu$ M MPS1-IN-3 or treated with DMSO as a control. Single cell clones were grown for 30 generations of treatment and the chromosome numbers were analyzed by chromosome counting. Subsequently, the proportion of cells with chromosome numbers deviating from the modal was determined. These analyses showed, as expected, that 0.5  $\mu$ M MPS1-IN-3 treated cells had a higher karyotype variability than the control treated cells, with a proportion of deviating from the modal from ~20% to 45-52% (Figure 3-21). Thus, treatment of HCT116 cells with the MPS1-IN-3 causes transient induction of CIN during inhibitor treatment.

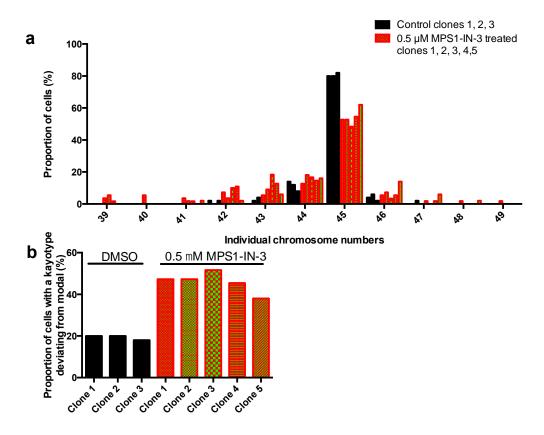
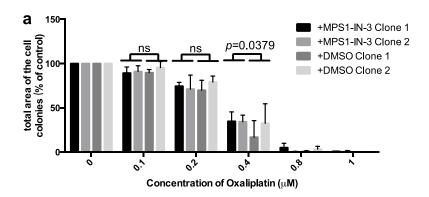


Figure 3-21 Treatment with the MPS1 inhibitor MPS1-IN-3 exhibits CIN.

(a) Karyotype analysis by chromosome counting in metaphase spreads of the indicated single cell clones derived from HCT116 cells treated with DMSO or 0.5  $\mu$ M MPS1-IN-3 for 30 generations (n=50 cells). (b) The percentage of cells with chromosome numbers deviating from the modal were calculated.

# 3.4.2. Induction of CIN mediated by Mps1 inhibitor does not result in drug response differences towards Oxaliplatin or Cisplatin treatment in HCT116 cells.



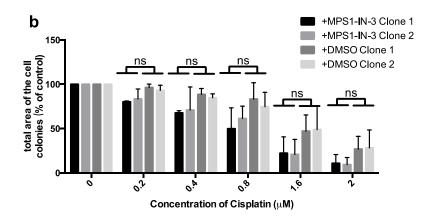


Figure 3-22 Quantification of the area of cell colonies of MPS1-IN-3 and DMSO-treated HCT116 cells treated with different concentration of Oxaliplatin or Cisplatin.

(a) Two independent DMSO-treated control single cell clones and two separate 0.5  $\mu$ M MPS1-IN-3-treated single cell clones derived from HCT116 cells were treated with increasing concentrations of Oxaliplatin, and the area of the cell colonies was determined after ten days. (b) Two independent DMSO-treated control single cell clones and two independent 0.5  $\mu$ M MPS1-IN-3-treated single cell clones from HCT116 cells were treated with increasing concentrations of Cisplatin, and the area of the cell colonies was determined after ten days. The areas of the cell colonies were normalized to control treated cells and represented as bar graphs (mean  $\pm$  sem., t-test, n=3 independent experiments, ns = not significant).

To investigate whether induction of CIN by inhibition of the Mps1 kinase would affect drug responses in CRC cells, I used two independent single cell clones derived from  $0.5~\mu M$  MPS1-IN-3 or DMSO treated HCT116 cells. These cell clones were treated with various concentrations of Oxaliplatin or Cisplatin and colony formation assays were performed. These analyses showed no significant differences in drug response towards Oxaliplatin (Figure 3-22a) or Cisplatin (Figure 3-22b)

Thus, induction of CIN by inhibition of the spindle assembly checkpoints in chromosomally stable CRC cells does not affect the drug responses towards Oxaliplatin or Cisplatin.

# 3.4.3. Short-term removal of MPS1-IN-3 does not result in drug response differences towards Oxaliplatin, but increases the resistance towards Cisplatin in one cell clone.

As treatment with Mps1 inhibitor induces CIN transiently, removal of MPS1-IN-3 is expected to reduce ongoing chromosome missegregation in cells. Hence, the two single cell clones of MPS1-IN-3 treated HCT116 cells were treated with different concentrations Oxaliplatin or Cisplatin in the presence or absence of MPS1-IN-3 and colony formation assays were performed.

These analyses showed that upon Oxaliplatin treatment, no significant response differences were detectable in the presence or absence MPS1-IN-3 during the assay (Figure 3-23a and 3-23b). Upon Cisplatin treatment, two concentrations of Cisplatin (0.8 and 1.6  $\mu$ M) were slightly more resistant in the absence of MPS1-IN-3 during the assay in the first MPS1-IN-3 treated single cell clone (Figure 3.23c). However, using the second MPS1-IN-3 treated single cell clone of HCT116, no significant differences were found (Figure 3-23d).

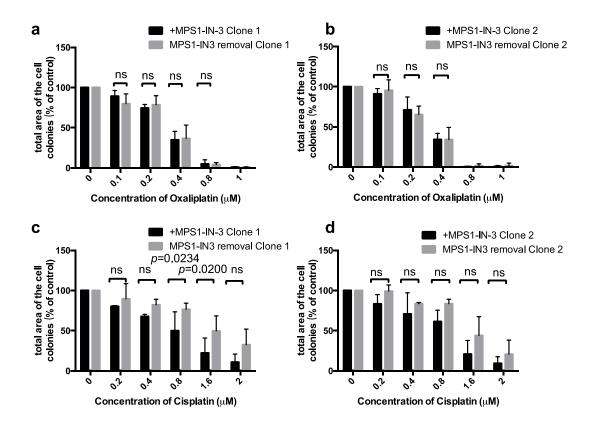


Figure 3-23 Quantification of the area of cell colonies of MPS1-IN-3 treated cells treated with different concentration of Oxaliplatin or Cisplatin in the presence or absence of MPS1-IN-3.

(a) Cells of MPS1-IN-3 treated clone 1 from HCT116 cells were treated with increasing concentrations of Oxaliplatin in the presence or absence of MPS1-IN-3, and the area of the cell colonies was determined after ten days. (b) Cells of MPS1-IN-3 treated clone 2 from HCT116 cells was treated with increasing concentrations of Oxaliplatin in the presence or absence of MPS1-IN-3, and the area of the cell colonies was determined after ten days. (c) Cells of MPS1-IN-3 treated clone 1 from HCT116 cells were treated with increasing concentrations of Cisplatin in the presence or absence of MPS1-IN-3, and the area of the cell colonies was determined after ten days. (d) Cells of MPS1-IN-3 treated clone 1 from HCT116 cells were treated with increasing concentrations of Cisplatin in the presence or absence of MPS1-IN-3, and the area of the cell colonies was determined after ten days. The areas of the cell colonies were normalized to control treated cells and represented as bar graphs (mean ±sem., t-test, n=3 independent experiments, ns = not significant).

Hence, induction of replication stress by Aphidicolin and inhibition of Mps1 are sufficient to cause CIN in chromosomally stable CRC cells. However, inducing of CIN by these two means does not result in drug response differences towards Oxaliplatin or Cisplatin compared to chromosomally stable cells.

#### 4. Discussion

# 4.1. Drug responses towards commonly used chemotherapeutic drugs in CRC cells exhibiting CIN and after suppression of CIN.

The aim of my study was to investigate whether chromosomal instability (CIN) is causally related to differential drug responses in colorectal cancer cells. For this, I used two different cell systems based on *CHK2* deficient HCT116 cells and on SW620 cells that are both chromosomally unstable. In both cases, previous work from our lab has established that the CIN phenotype and thus, perpetual chromosome missegregations during mitosis are triggered by an increase in microtubule dynamics. Intriguingly, this defect can be corrected, e.g. by treatment of the cells with low doses of Taxol or by partial repression of the microtubule polymerase *ch-TOG/CKAP5* (Ertych et al. 2014). Therefore, I was able to directly compare the drug responses in individual single cell clones that were grown either in the absence or in the presence of Taxol or upon repression *ch-TOG/CKAP5*.

During the course of my work, I found that HCT116-*CHK2*-/- cells that grew in the absence of Taxol were more resistant toward Oxaliplatin compared to cells growing in the presence of Taxol (Figure 3-2a and 3-2b). Even short-term removal of Taxol had a similar effect (Figure 3-3a, and 3-3b). This might indicate that ongoing chromosome missegregations during mitosis may cause drug resistance, which is not dependent on karyotype evolvement over longer periods of time. Similarly, partially repression of *ch-TOG/CKAP5* caused a higher sensitivity towards Oxaliplatin in HCT116-*CHK2*-/- cells (Figure 3-4a), which might further confirm that ongoing chromosome missegregation during mitosis causes drug resistance.

Regarding the immediate response towards higher concentrations of Oxaliplatin, no response differences were observed in the presence or absence of Taxol (Figure 3-5). Since chromosome missegregation occurs only in 20%-50% CIN cells per cell cycle (Lengauer et al. 1997; Thompson and Compton 2008), this might not be sufficient to result in drug response differences between CIN cells and cells where CIN was suppressed.

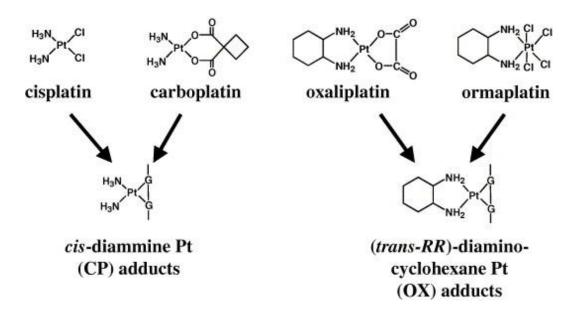
In contrast to *CHK2* knockout HCT116 cells, no drug response differences towards Oxaliplatin were observed in two independent clones of SW620 cells that were grown in the presence or absence of Taxol (Figure 3-2c, 3-2d, 3-3c and 3.3d), although also in these cells a suppression of CIN in response to Taxol treatment have been established (Ertych et al. 2014). The SW620 cells with partial repression of *ch-TOG/CKAP5*, however, seemed to be more sensitive towards Oxaliplatin (Figure 3-4b). If we looked carefully into the drug response of the two independent clones of sh*ch-TOG* and sh*control*, the drug response of the two control clones was different. In this case, it is not possible to draw a clear conclusion that partially repression *ch-TOG/CKAP5* in SW620 causes more sensitivity towards Oxaliplatin.

Thus, while HCT116-CHK2<sup>-/-</sup> cells showed a decreased sensitivity towards Oxaliplatin that appears to be dependent on microtubule dynamics and/or CIN, this was not reproducible in SW620 cells. This might indicate that the suppression of chromosome missegregation in CHK2 deficient cells by low-dose of Taxol is more efficient than in SW620 cells. Since also the short-term removal of Taxol affects drug response, it might be that the acute chromosome missegregation determines the response towards Oxaliplatin. Another possibility is that the observed difference in the response towards Oxaliplatin might be specifically due to the loss of CHK2 rather than due to the presence of a CIN phenotype. Chk2 is a multifunctional kinase with known functions central to the induction of cell cycle arrest and apoptosis after DNA damage (Ahn et al. 2004; Antoni et al. 2007). Therefore, loss of CHK2 in the HCT116-CHK2<sup>-/-</sup> cells might directly affect the response towards various DNA damaging drugs including Oxaliplatin. However, previous work showed that the loss of CHK2 does neither affect p53 activation nor the DNA damage response after 5-FU-induced DNA damage (Jallepalli et al. 2003). It remains also unclear why Taxol treatment and partial repression of ch-TOG/CKAP5 would affect the drug response in CHK2 deficient cells. Nevertheless, my studies revealed that cancer cells with a loss of CHK2 expression can be sensitized towards Oxaliplatin treatment by co-treatment with subnanomolar concentrations of Taxol, which might represent an interesting addition to the current chemotherapeutic treatment scheme for the colorectal cancer.

In contrast to Oxaliplatin, other chemotherapeutic drugs, including 5-FU, Adriamycin, and Irinotecan showed no drug response differences in two independent clones of HCT116-*CHK2*-/- or SW620 before or after CIN-suppression (Figure 3-10 - 3-16). This might indicate that chromosome missegregation caused drug resistance is specific to platinum compounds but the molecular reason for this remains unclear.

To clarify whether the observed resistance is specific to Oxaliplatin, I investigated also the response towards a second platinum compound namely Cisplatin, which is also widely used in the clinic for cancer therapy. Surprisingly, no drug response differences for Cisplatin were detectable in HCT116-*CHK2*-/- or in SW620 in the presence or absence of Taxol (Figure 3-6 and 3-7). On the other hand, partially repression of *ch-TOG/CKAP5*, which suppressed CIN, caused an increasing resistance towards Cisplatin in HCT116-*CHK2*-/- (Figure 3-9a). For SW620 cells, the two independent control clones showed opposite response as exhibited in Oxaliplatin treatment (Figure 3-9b), which represent inconsistent results overall.

Why is there such a difference in response towards two related platinum compounds? Both, Cisplatin and Oxaliplatin form DNA adducts. However, the structure of DNA adducts in response to Cisplatin and Oxaliplatin treatment are different (Figure 4-1) (Chaney et al. 2005).



**Figure 4-1 Selected platinum compounds and their DNA adducts.** (from Chaney et al., 2005, p. 4)

Because of the structural differences of the Platinum-DNA adducts, these two platinum compounds have different affinity to cellular proteins. Binding of the cellular proteins to the Platinum-DNA adducts increases the cytotoxicity of the DNA adducts. Several studies showed that Cisplatin-DNA adducts has higher affinity to mismatch repair proteins and some damage-recognition proteins (McLaughlin et al. 1993; Wei et al. 2001). In contrast, Oxaliplatin-DNA adducts bypass translesion DNA polymerases, which determines whether the translesion synthesis is error-free or error-prone (Chaney et al. 2005). These differential outcomes of Cisplatin- and Oxaliplatin-DNA adducts are thought to contribute to the differences in cytotoxicity of Cisplatin and Oxaliplatin (Chaney et al. 2005), which might also explain why Cisplatin and Oxaliplatin showed entirely different responses regarding *ch-TOG/CKAP5* suppression of HCT116-*CHK2*-/- cells. But it is still unclear why no response difference towards Cisplatin was observed in HCT116-*CHK2*-/- in the presence or absence of Taxol.

# 4.2. Drug responses in chromosomally stable HCT116 cells and upon induction of CIN by replication stress or inhibition of the mitotic spindle assembly checkpoint.

Aphidicolin is a specific inhibitor of DNA polymerase α, which is primarily involved in DNA replication (Ikegami et al. 1978). Thus, Aphidicolin triggers replication fork instability and leads to instability of particular genomic regions called common fragile sites (CFSs), which are susceptible to replication-stress-induced double-strand breaks (Durkin and Glover 2007; Mazouzi et al. 2016). A recent study revealed that Aphidicolin triggers universal changes in both gene expression and protein phosphorylation patterns (Mazouzi et al. 2016). My work showed that treatment with low-doses of Aphidicolin treatment caused mitotic chromosome missegregation and CIN in chromosomally stable HCT116 cells (Figure 3-18). I used this condition to investigate whether induction of CIN affects drugs responses in CRC cells.

The second condition I used to induce CIN in chromosomally stable CRC cells was pharmacological inhibition of Mps1. Mps1 functions as an essential kinase that activates the spindle assembly checkpoint (SAC) to ensure proper segregation of

sister chromatids onto the daughter cells. It was demonstrated that small molecule inhibitors for the Mps1 kinase cause chromosome missegregation due to disruption of the SAC, thereby inducing CIN (Janssen et al. 2011). By karyotype analysis, I found that the prolonged treatment of HCT116 cells with the MPS1-IN-3 inhibitor indeed caused CIN and whole chromosome aneuploidy (Figure 3-21).

The mechanism of suppression of CIN by low-dose of Taxol or suppression of *ch-TOG/CKAP5* is by restoring proper microtubule assembly rates (Ertych et al. 2014). To compare the drug response between chromosomally stable and instable cells, other mechanisms leading to CIN were desired. Therefore, Aphidicolin and MPS1-IN-3 treated cells, both of which exhibiting CIN were used. However, after treatment with Oxaliplatin and Cisplatin, no drug response differences were observed between Aphidicolin or MPS1-IN-3-treated cells and control cells (Figure 3-19 and 3-22). Removal of Aphidicolin or MPS1-IN-3 resulted in slight resistance towards Cisplatin in one cell clone (Figure 3-20c and 3-23c), but no response differences in the other cell clone (Figure 3-20d and 3-23d), which indicates that the observed effect is not representative. Thus, inducing CIN by replication stress triggered by Aphidicolin or disturbing the spindle assembly checkpoint by treatment with a Mps1 inhibitor did not affect the drug response in HCT116 cells. While it cannot be excluded that the lack of response differences is specific for HCT116 cells, it might be desirable to investigate the induction of CIN in other cancer cell lines.

In summary, my results revealed microtubule dynamics-dependent resistance towards Oxaliplatin only in CIN cells with *CHK2* deficiency. Other CIN cells (e.g. SW620, chromosomally stable HCT116 cells treated by Aphidicolin or Mps1 inhibitor) did not show any response differences compared to non-CIN cells. These results are in contrast to a recent study by Lee et al. who showed that CIN is associated with multidrug resistance (Lee et al. 2011). The main difference between my study and Lee's study is that I used single cell clones with only little cell-to-cell heterogeneity. Several studies have suggested that tumor heterogeneity is associated with drug resistance in patients (Marusyk and Polyak 2010; Turner and Reis-Filho 2012). Clonal analysis of CIN and non-CIN cells are likely responsible for reduced genetic heterogeneity within the cell populations. Therefore, my results might indicate that

the CIN phenotype *per se* does not confer drug resistance, but that a high genetic heterogeneity within the cell population might contribute to altered drug responses.

### 4.3. CHK2 deficiency: a key for resistance towards Oxaliplatin treatment?

Since only chromosomally instable *CHK*2 deficient HCT116 cells showed a clear tendency of drug resistance towards Oxaliplatin, it seems plausible that the loss of *CHK*2 function itself that might contribute to drug resistance.

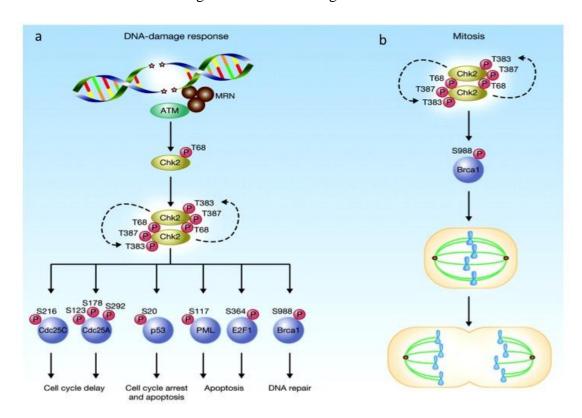


Figure 4-2 The role of Chk2 in DNA damage response and mitosis regulation.

(a) Upon DNA double strand breaks, the Chk2 kinase is activated by phosphorylation on threonine-68 by the ATM kinase. After homodimerization and *trans*-phosphorylation of threonine-383 and -387 located within the activation loop, the Chk2 kinase achieves its full activation. Subsequently, Chk2 can phosphorylate critical substrates such as Cdc25C, Cdc25A, p53, PML, E2F1 and Brca1, which is required to mediate cell cycle delay, cell cycle arrest, apoptosis and in response to DNA repair. (b) In the absence of DNA damage, the active Chk2 kinase can also

phosphorylate Brca1 on serine-988 during mitosis, which promotes the proper assembly of the normal mitotic spindle. (from Stolz et al., 2011, p. 402)

An important function of the Chk2 kinase is to operate downstream of ATM in response to DNA damage. Chk2 is phosphorylated at threonine-68 by the ATM kinase upon DNA double strand breaks (Ahn et al. 2004). After dimerization and full activation, the Chk2 kinase can mediate cell cycle arrest, apoptosis, and DNA repair through phosphorylating key substrates such as Cdc25C, Cdc25A, p53, PML, E2F1, and Brca1 (Figure 4-2a) (Stolz et al. 2011). In addition to DNA damage response, previous work from our lab also established Chk2 to be required for the maintenance of chromosomal stability during mitosis (Figure 4-2b). In fact, *CHK2* deficiency induces CIN in chromosomally stable cells by increasing microtubule assembly rates (Ertych et al. 2014; Stolz et al. 2010)

Cdc25C is a dual-specificity protein phosphatase that dephosphorylates Cdc2 thereby controlling the entry into mitosis (Peng et al. 1997). Upon DNA damage, Chk2 phosphorylates Cdc25C on serine-216, which causes its inhibition. As a result, the cell cycle arrests at the G<sub>2</sub>/M transition (Matsuoka et al. 1998). Cdc25A can activate CDK2 that is needed for entry in S-phase and for DNA synthesis (Hoffmann et al. 1994). However, in response to DNA damage, Chk2 phosphorylates Cdc25A on serine-123, which mediates Cdc25A ubiquitylation and is subsequent degradation, preventing the CDK2 activation at the G<sub>1</sub>/S transition (Falck et al. 2001; Jinno et al. 1994).

Previous studies revealed that *CHK2* deficient mice exhibit radioresistance (Falck et al. 2001; Takai et al. 2002), and this resistance is mediated by the ATM-Chk2-Cdc25A checkpoint pathway (Falck et al. 2001). Oxaliplatin forms DNA adducts and thereby also causes DNA damage. Thus, radioresistance and resistance towards Oxaliplatin might be mechanistically related. However, it remains elusive why the differential drug response is alleviated upon restoration of normal microtubule dynamics. It is advised that the future studies will address this important question.

Previous work from our lab also revealed that Chk2 activates Brca1 and thereby ensuring proper microtubule plus-end assembly and chromosomal stability during

mitosis. Loss function of Chk2 results in Aurora-A to act as a negative regulator of Brca1 during mitosis (Ertych et al. 2016). Interestingly, a recent study found that Brca1 inactivation causes resistance towards Oxaliplatin in CRC (Moutinho et al. 2014). Hence, Chk2 might act through Brca1 to regulate Oxaliplatin sensitivity. However, future work needs to address the underlying molecular mechanism leading to resistance towards Oxaliplatin treatment in CRC.

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## Curriculum Vitae

My name is Xiyang Liu, I was born on the 28<sup>th</sup> of November 1985 in Shaodong, Hunan, China. I was enrolled in Shuangquanpu Primary school, Hunan, China in September 1992. After 12-semester studies I completed my elementary study in July 1998. In September of this year, I began my studies in Shuangquanpu Junior High School, Hunan, China. I finished my junior high school in July 2001. After then I started my high school education in Shaodong First High School, Hunan, China in September 2001, and finished it in June 2004.

After school education, I started to study Clinical Medicine in September 2005 in Zhengzhou University, Henan, China. After 10-semester of studies I got my bachelor degree in July 2010. I continued my master studies in the same university, and specialized on oncology studies in September 2010. During the master study period, I studied the topic "Exploring the relationship between CD5 expression and the clinical pathologic features and therapeutic effect of diffuse large B-cell lymphoma" and was awarded with a Master degree in Oncology in July 2013. In addition, I passed the National Medical Practitioner's Qualification Exam and got the certificate in 2011.

In 2013, I got the scholarship from the China Scholarship Council for four years to pursue the doctoral studies in medicine in Germany. I was enrolled in Heidelberg University and started the project in the group of Prof. Dr. Thorsten Zenz in the institute of German Cancer Research Center (DKFZ) and National Center For Tumor Disease (NCT) in September 2013. However, after two years of studies in Heidelberg, I found the project I was working would not work out and I decided to move. I was luckily to meet Prof. Dr. Holger Bastians who offered me a position as a candidate of Dr. med. in his group. I started my M.D. thesis in his lab in Göttingen, and was enrolled in the Medical Faculty of Göttingen University in June 2016, and I expect to finish my M.D. studies in summer 2017.