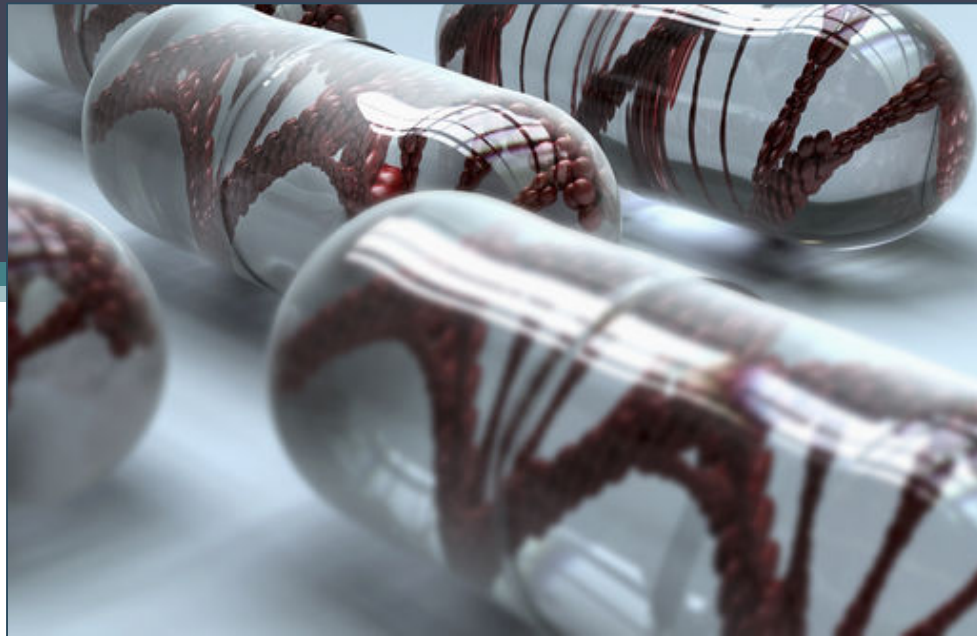


Whole-exome sequencing reveals defective *CYP3A4* variants predictive for paclitaxel dose-limiting neuropathy



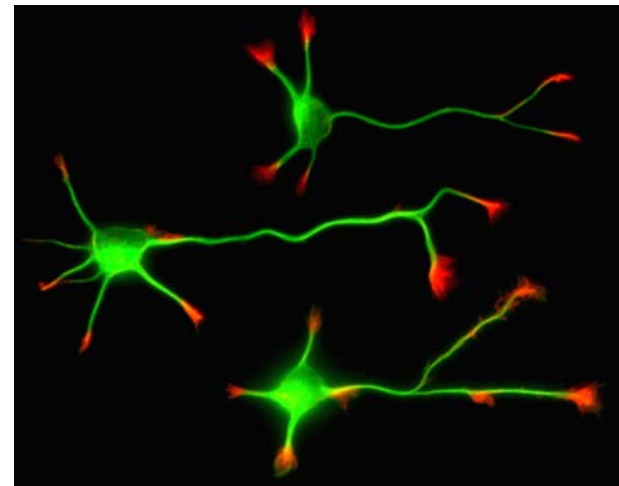
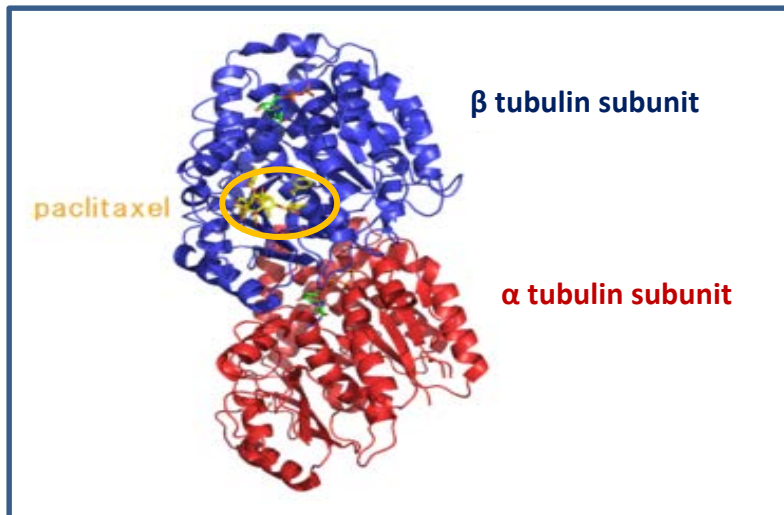
María Apellániz Ruiz

Spanish National Cancer Research Centre (CNIO)

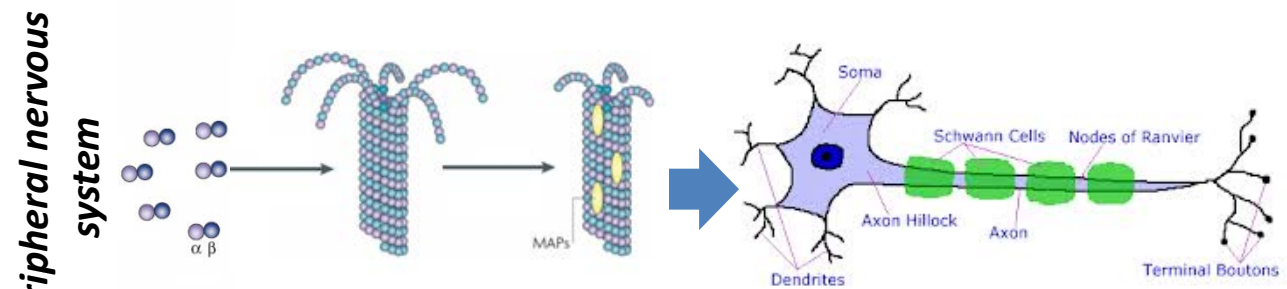
May 19th 2014

Paclitaxel

- **Microtubule binding drug**, effective for many solid tumors (breast, ovarian, lung)
- **Dose limiting toxicity: peripheral neuropathy** (30-50% of patients affected)
- Paclitaxel **dose reduction/ treatment suspension** in 10% patients
- **Large inter-individual variability**, some cases irreversible nerve damage
- No effective treatment to prevent or treat neuropathy



Genetic markers of paclitaxel neuropathy

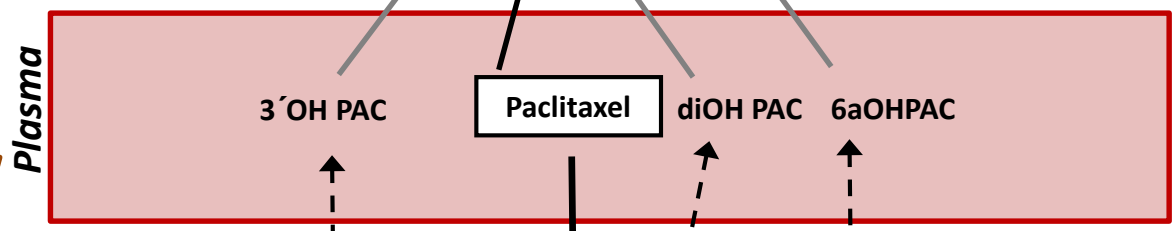
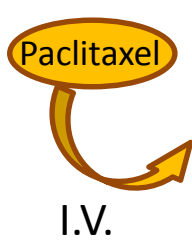


GWAS meta-analysis

- Balwin, *Clin Cancer Res* (2012)
- Leandro-Garcia, *J Med Genet* (2013)

EPHA5 → $P=1.4 \times 10^{-9}$

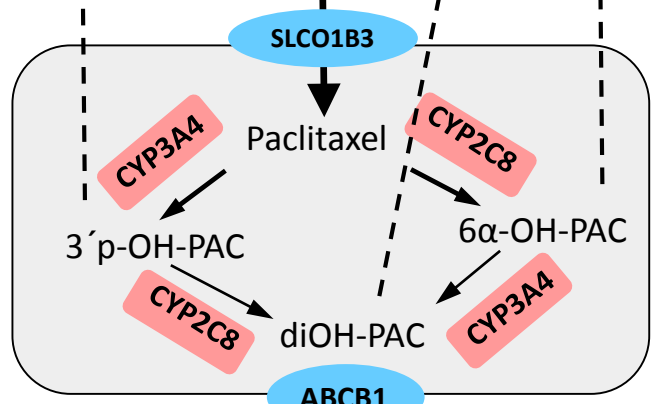
XKR4 → $P=3.1 \times 10^{-8}$



TUBB2A

-Leandro-Garcia, *Clin Cancer Res* (2012), $P=0.021$

Hepatocyte



CYP2C8

- Leskelä, *Pharmacogenomics J* (2011), $P=0.032$

- Hertz, *Ann Oncol* (2013), $P=0.006$

CYP3A4

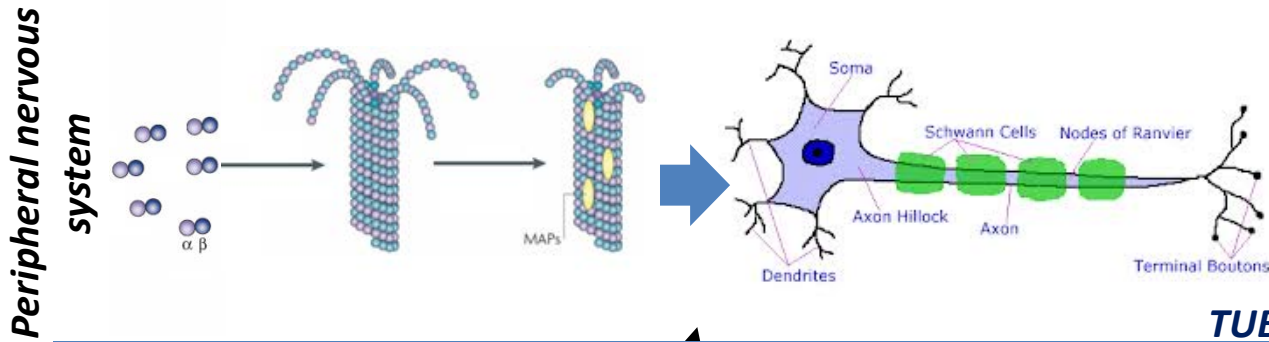
- de Graan, *Clin Cancer Res* (2013), $P=0.001$

ABCB1

- Sissung, *Eur J Cancer* (2006), $P=0.09$

Biliar canaliculi

Genetic markers of paclitaxel neuropathy



GWAS meta-analysis

- Balwin, *Clin Cancer Res* (2012)
- Leandro-Garcia, *J Med Genet* (2013)

EPHA5 → P=1.4 x 10⁻⁹

XKR4 → P=3.1 x 10⁻⁸

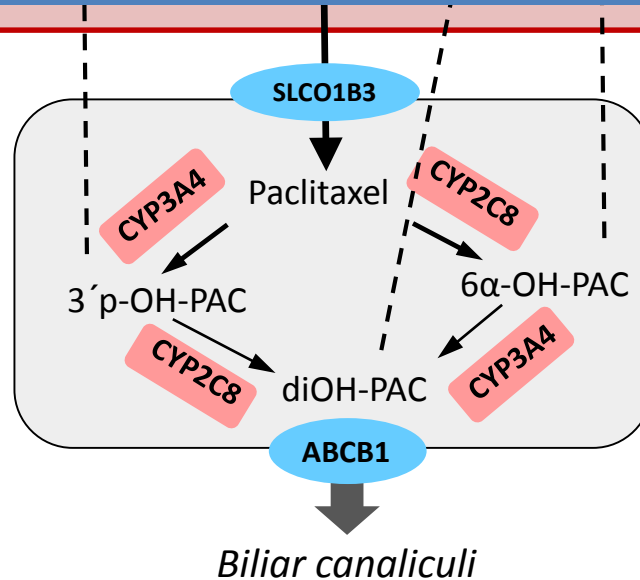
TUBB2A

21

Common variants (moderate effects)

I.V.

Hepatocyte



CYP2C8

- Leskelä, *Pharmacogenomics J* (2011), P=0.032
- Hertz, *Ann Oncol* (2013), P=0.006

CYP3A4

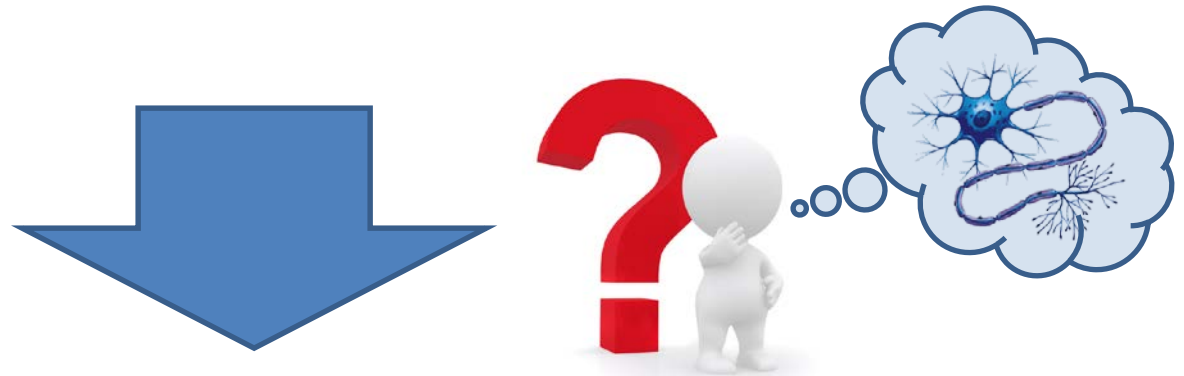
- de Graan, *Clin Cancer Res* (2013), P=0.001

ABCB1

- Sissung, *Eur J Cancer* (2006), P=0.09

Biliar canaliculi

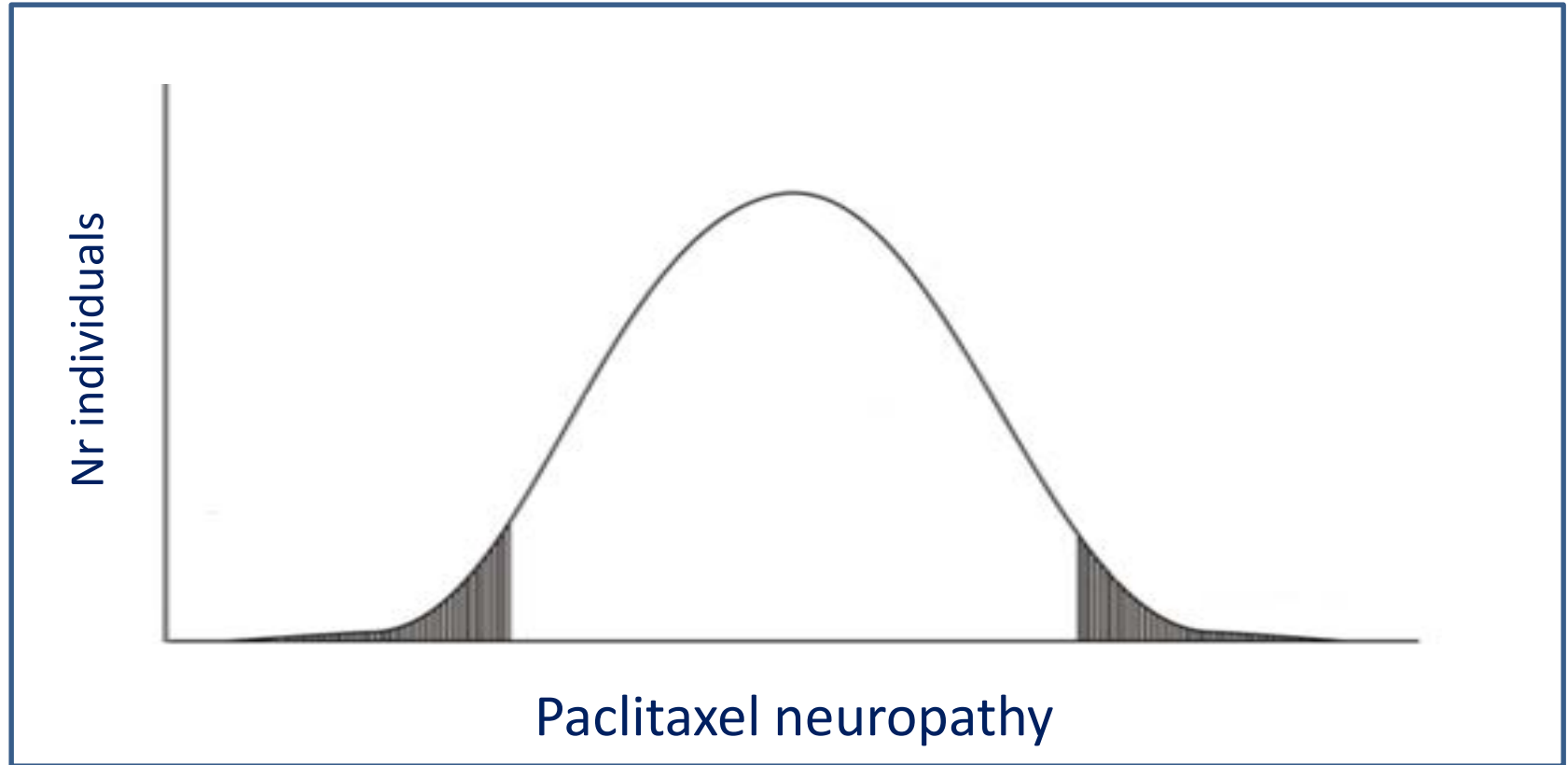
However, a large part of inter-individual differences in paclitaxel neuropathy susceptibility remain unexplained



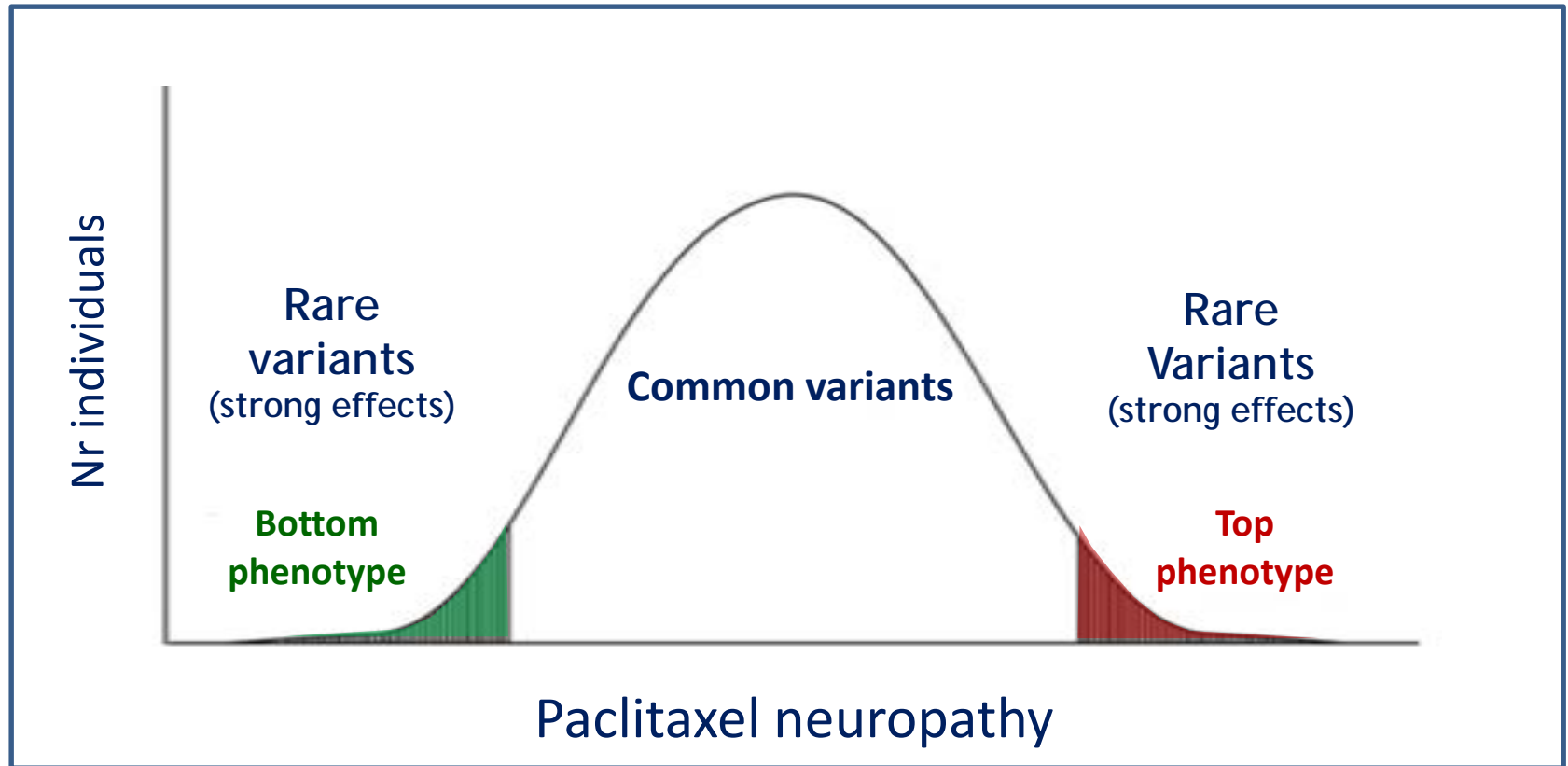
Objective:

Identify genetic markers predictive of paclitaxel neurotoxicity, taking into account low-frequency & rare variants

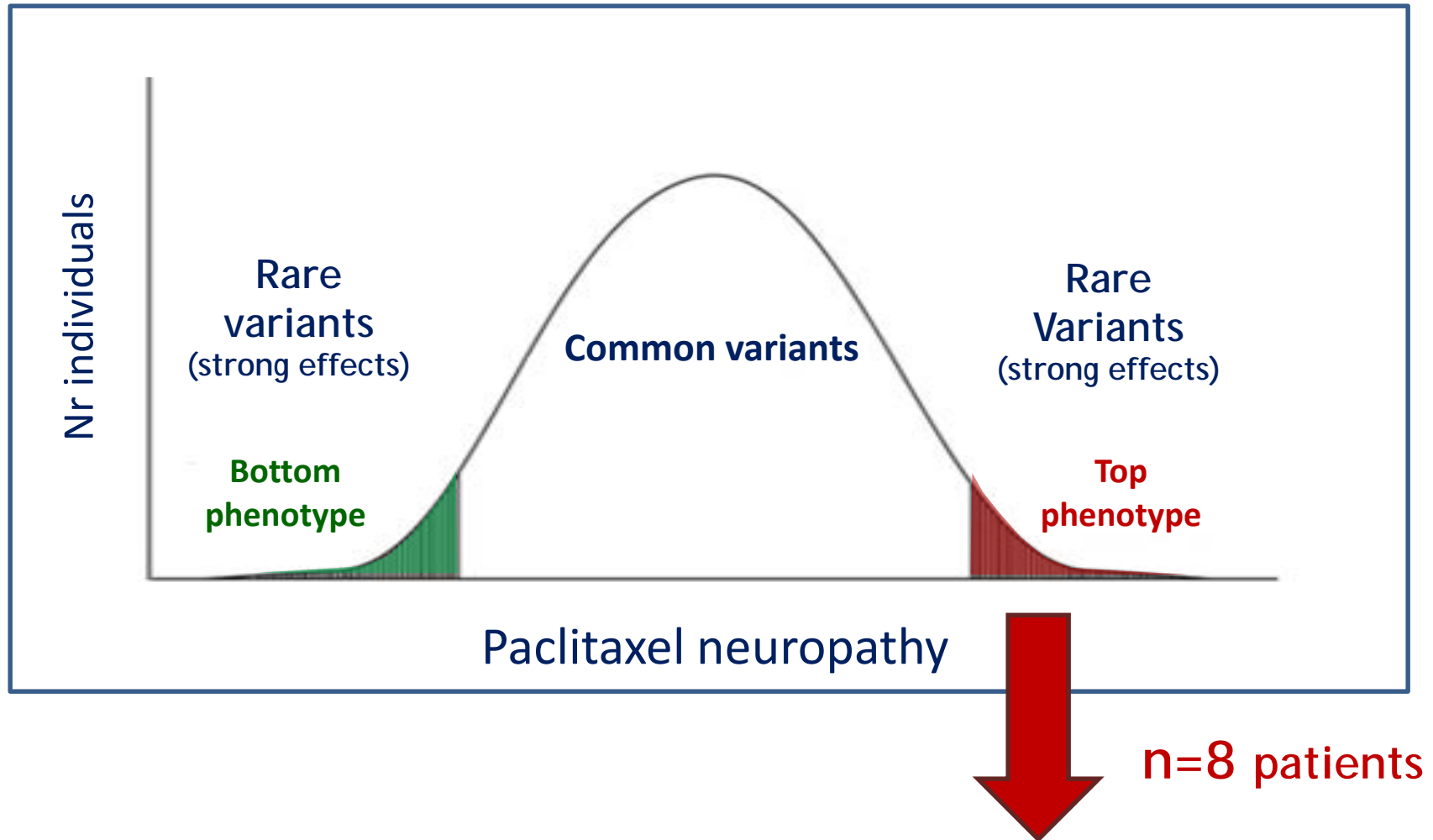
Extreme phenotype approach coupled with WES



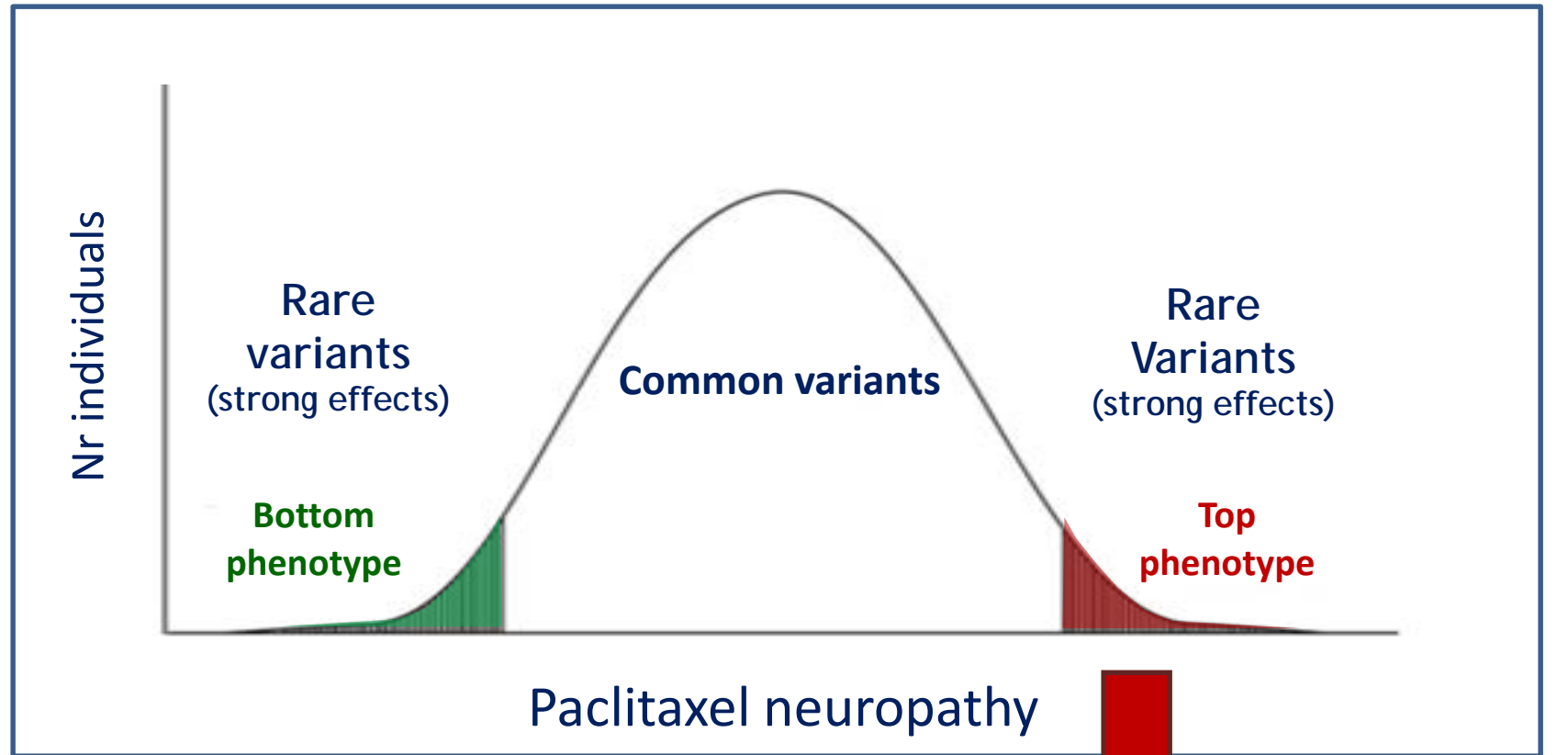
Extreme phenotype approach coupled with WES



Extreme phenotype approach coupled with WES



Extreme phenotype approach coupled with WES



n=8 patients

Whole exome sequencing (WES)

Characteristics of the patients with extreme neuropathy

Characteristics	Clinical data
Age (y)	57 (39-79)
Breast cancer	8
First line paclitaxel treatment	8
Nr. Chemotherapy cycles	5-8
Paclitaxel dose at grade 3 neuropathy (mg/m²)	750 (400-800)
Grade 3 neuropathy (CTC-NCI scale)	8
Treatment modifications due to neuropathy	8
Dose reduction	4
Treatment suspension	4
Duration of neuropathy grade 2-3 (years)	3.2 (1.6 – 5.5)

*Confounders ruled out (diabetes, alcohol intake, previous neuropathies..)

Characteristics of the patients with extreme neuropathy

Characteristics	Clinical data
Age (y)	57 (39-79)
Breast cancer	8
First line paclitaxel treatment	8
Nr. Chemotherapy cycles	5-8
Paclitaxel dose at grade 3 neuropathy (mg/m ²)	750 (400-800)
Grade 3 neuropathy (CTC-NCI scale)	8
Treatment modifications due to neuropathy	8
Dose reduction	4
Treatment suspension	4
Duration of neuropathy grade 2-3 (years)	<u>3.2 (1.6 – 5.5)</u>

*Confounders ruled out (diabetes, alcohol intake, previous neuropathies..)

Whole exome sequencing (WES)



- SureSelect XTHumanAllExon 50Mb
- HiSeq2000
- Median coverage 50x

DNA



Peripheral blood samples
(n=8)

SNVs and Indels

Variant Filtering

- Genome regions with low mappability
- With strand bias p-value < 0.001 in at least one sample
 - With low depth read (<15x)
- Alternative allele present in <20% of reads

Whole exome sequencing (WES)



- SureSelect XTHumanAllExon 50Mb
- HiSeq2000
- Median coverage 50x

DNA



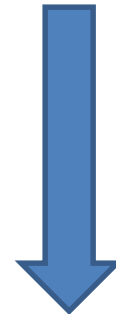
Peripheral blood samples
(n=8)



SNVs and Indels

Variant Filtering

- Genome regions with low mappability
- With strand bias p-value < 0.001 in at least one sample
 - With low depth read (<15x)
- Alternative allele present in <20% of reads



**Variants in genes
paclitaxel PD/ PK**

Coding variants in PD/PK genes

Gene	Variant / Name	Type of variant	Nr. variant carriers (het/hom)	MAF (%)		Effect prediction
				Obs	Eur	
TUBB2A	None	-	-	-	-	-
XKR4	None	-	-	-	-	-
EPHA5	N81T	Missense	2/0	12	7	Neutral
CYP3A4	P389S/ novel (*25)	Missense	1/0	6	ND	Defective
	P488Tfs*494/ *20	Frameshift	1/0	6	0.09	Defective
CYP2C8	R139K / *3	Missense	2/0	12	12	Neutral
	K399R / *3	Missense	2/0	12	12	Neutral
	I264M / *4	Missense	1/0	6	6	Neutral
	N21D	Missense	1/0	6	10	Neutral
ABCB1	N183S	Missense	1/0	6	0.2	Neutral
	A893S / 2677GT	Missense	5/1	43	43	Neutral
SLCO1B3	G653E	Missense	1/0	6	1	Neutral

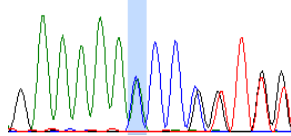
Coding variants in PD/PK genes

Gene	Variant / Name	Type of variant	Nr. variant carriers (het/hom)	MAF (%)		Effect prediction
				Obs	Eur	
<i>TUBB2A</i>	None	-	-	-	-	-
<i>XKR4</i>	None	-	-	-	-	-
<i>EPHA5</i>	N81T	Missense	2/0	12	7	Neutral
<i>CYP3A4</i>	P389S/ novel (*25)	Missense	1/0	6	ND	Defective
	P488Tfs*494/ *20	Frameshift	1/0	6	0.09	Defective
<i>CYP2C8</i>	R139K / *3	Missense	2/0	12	12	Neutral
	K399R / *3	Missense	2/0	12	12	Neutral
	I264M / *4	Missense	1/0	6	6	Neutral
	N21D	Missense	1/0	6	10	Neutral
<i>ABCB1</i>	N183S	Missense	1/0	6	0.2	Neutral
	A893S / 2677GT	Missense	5/1	43	43	Neutral
<i>SLCO1B3</i>	G653E	Missense	1/0	6	1	Neutral

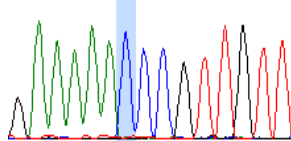
Rare *CYP3A4* high-impact variants in extreme neuropathy patients

Indel: Nonsense variant

P488Tfs*494 (*CYP3A420)**

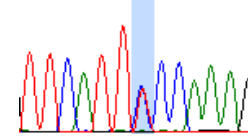


Wild type

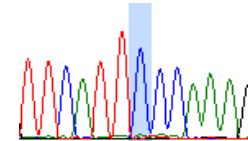


SNV: Missense variant

P389S



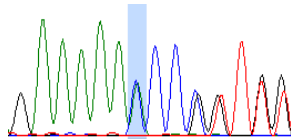
Wild type



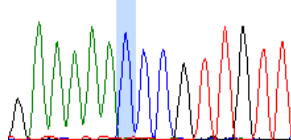
Rare *CYP3A4* high-impact variants in extreme neuropathy patients

Indel: Nonsense variant

P488Tfs*494 (*CYP3A4**20)

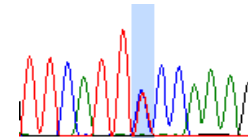


Wild type

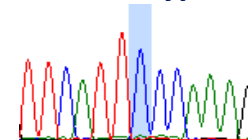


SNV: Missense variant

P389S



Wild type



CYP3A4 wt

```
~GGACTTCTTCAACCAGAAAAACCCGTTGTTCTAAAGGTTGAGTCAAGGGATGGCACCGTAAGTGGAGCCTGA  
G L L Q P E K P V V L K V E S R D G T V S G A *
```

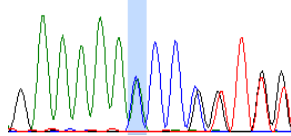
*CYP3A4**20

```
~GGACTTCTTCAACCAGAAAAACCCGTTGTTCTAAAGGTTGA  
G L L Q P E K T R C S K G *
```

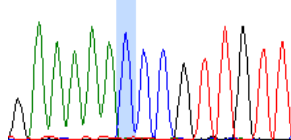
Rare *CYP3A4* high-impact variants in extreme neuropathy patients

Indel: Nonsense variant

P488Tfs*494 (*CYP3A4**20)

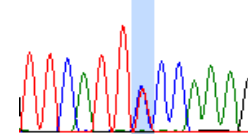


Wild type

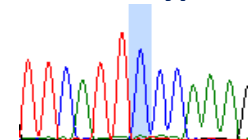


SNV: Missense variant

P389S



Wild type

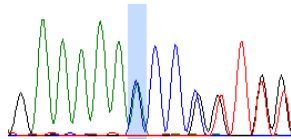


- Westlind-Johnsson *et al* 2006
 - Protein devoid of functional activity
 - 1 volunteer with a **6-fold higher exposure** of *CYP3A4* substrate
 - Not found in 428 Germans
- Rare variant (EVS:9 carriers in 6500 individuals)

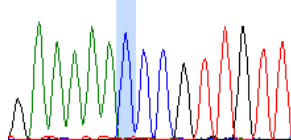
Rare *CYP3A4* high-impact variants in extreme neuropathy patients

Indel: Nonsense variant

P488Tfs*494 (*CYP3A4**20)

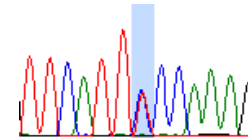


Wild type

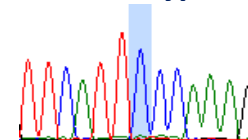


SNV: Missense variant

P389S



Wild type



- Westlind-Johnsson *et al* 2006

- Protein devoid of functional activity
- 1 volunteer with a **6-fold higher exposure** of *CYP3A4* substrate
- Not found in 428 Germans

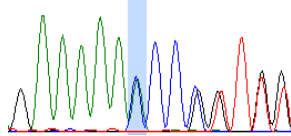
- Non-described

- Rare variant (EVS:9 carriers in 6500 individuals)

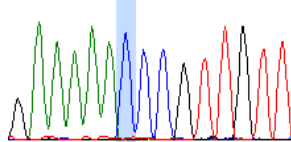
Rare *CYP3A4* high-impact variants in extreme neuropathy patients

Indel: Nonsense variant

P488Tfs*494 (*CYP3A4**20)

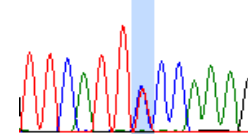


Wild type

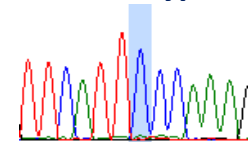


SNV: Missense variant

P389S



Wild type



- Westlind-Johnsson *et al* 2006

- Protein devoid of functional activity
- 1 volunteer with a **6-fold higher exposure** of *CYP3A4* substrate
- Not found in 428 Germans

- Rare variant (EVS:9 carriers in 6500 individuals)

- Non-described
- Conserved β -helix

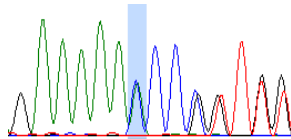
β4 helix

H. sapiens	"LRLFPVAMRLERVCCKDVEINGMFI	P	KGVVVMIPSYALHRDPKY
P. troglodites	LRLFPVAMRLERVCCKDVEINGMFI	P	KGVVVMIPSYALHRDPKY
X. tropicalis	LRLYPTAIRLERVSKKDVEINGVFI	P	KGIVVMIPYPLHRNPEY
M. musculus	LRLFPVAMRLERVSKQNVINGVSI	P	KGIVTLIPAYVLQRDPEY
D. rerio	MRLLPAPRLERSAKKTVVINGLTI	P	EGTLVGIPTVYVLSHDPDI
	:** * * **** .*: * ***: **:* :. ** * * :*:.		

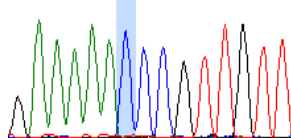
Rare *CYP3A4* high-impact variants in extreme neuropathy patients

Indel: Nonsense variant

P488Tfs*494 (*CYP3A4**20)

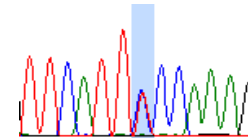


Wild type

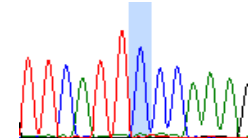


SNV: Missense variant

P389S



Wild type



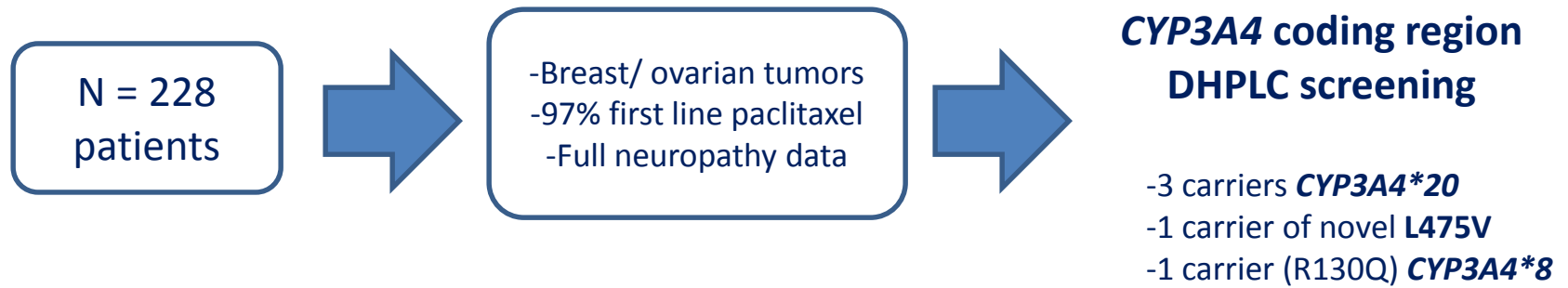
- Westlind-Johnsson *et al* 2006

- Protein devoid of functional activity
- 1 volunteer with a **6-fold higher exposure** of *CYP3A4* substrate
- Not found in 428 Germans

- Non-described
- Conserved β -helix
- Defective (4/4 software prediction)

- Rare variant (EVS:9 carriers in 6500 individuals)

Screening for *CYP3A4* coding variants



Screening for *CYP3A4* coding variants

Summary of *CYP3A4* variants

Patient	<i>CYP3A4</i> variant effect	<i>CYP3A4</i> variant allele	Detection technique	Max. Neuropathy grade	Total nr. cycles	Treatment modifications	Time with neuropathy (months)
1	Loss-of-function	*20	WES	3	8	Red (cycles 4 & 8)	(35)
2		*20	DHPLC	3	8	Red (cycle 4)	(9)
3		*20	DHPLC	3	12	Red (cycle 9)	(6)
4		*20	DHPLC	3	11	No	16
5	Decreased activity	P389S (*25)	WES	3	6	Susp (cycle 6)	19
6		R130Q (*8)	DHPLC	1	12	No	6
7	Pending	L475V (*26)	DHPLC	3	8	No	(19)

Screening for *CYP3A4* coding variants

Summary of *CYP3A4* variants

Patient	<i>CYP3A4</i> variant effect	<i>CYP3A4</i> variant allele	Detection technique	Max. Neuropathy grade	Total nr. cycles	Treatment modifications	Time with neuropathy (months)
1	Loss-of-function	*20	WES	3	8	Red (cycles 4 & 8)	(35)
2		*20	DHPLC	3	8	Red (cycle 4)	(9)
3		*20	DHPLC	3	12	Red (cycle 9)	(6)
4		*20	DHPLC	3	11	No	16
5	Decreased activity	P389S (*25)	WES	3	6	Susp (cycle 6)	19
6		R130Q (*8)	DHPLC	1	12	No	6
7	Pending	L475V (*26)	DHPLC	3	8	No	(19)

Screening for *CYP3A4* coding variants

Summary of *CYP3A4* variants

Patient	<i>CYP3A4</i> variant effect	<i>CYP3A4</i> variant allele	Detection technique	Max. Neuropathy grade	Total nr. cycles	Treatment modifications	Time with neuropathy (months)
1	Loss-of-function	*20	WES	3	8	Red (cycles 4 & 8)	(35)
2		*20	DHPLC	3	8	Red (cycle 4)	(9)
3		*20	DHPLC	3	12	Red (cycle 9)	(6)
4		*20	DHPLC	3	11	No	16
5	Decreased activity	P389S (*25)	WES	3	6	Susp (cycle 6)	19
6		R130Q (*8)	DHPLC	1	12	No	6
7	Pending	L475V (*26)	DHPLC	3	8	No	(19)

Screening for *CYP3A4* coding variants

Summary of *CYP3A4* variants

Patient	<i>CYP3A4</i> variant effect	<i>CYP3A4</i> variant allele	Detection technique	Max. Neuropathy grade	Total nr. cycles	Treatment modifications	Time with neuropathy (months)
1	Loss-of-function	*20	WES	3	8	Red (cycles 4 & 8)	(35)
2		*20	DHPLC	3	8	Red (cycle 4)	(9)
3		*20	DHPLC	3	12	Red (cycle 9)	(6)
4		*20	DHPLC	3	11	No	16
5	Decreased activity	P389S (*25)	WES	3	6	Susp (cycle 6)	19
6		R130Q (*8)	DHPLC	1	12	No	6
7	Pending	L475V (*26)	DHPLC	3	8	No	(19)

Screening for *CYP3A4* coding variants

Summary of *CYP3A4* variants

Patient	<i>CYP3A4</i> variant effect	<i>CYP3A4</i> variant allele	Detection technique	Max. Neuropathy grade	Total nr. cycles	Treatment modifications	Time with neuropathy (months)
1	Loss-of-function	*20	WES	3	8	Red (cycles 4 & 8)	(35)
2		*20	DHPLC	3	8	Red (cycle 4)	(9)
3		*20	DHPLC	3	12	Red (cycle 9)	(6)
4		*20	DHPLC	3	11	No	16
5	Decreased activity	P389S (*25)	WES	3	6	Susp (cycle 6)	19
6		R130Q (*8)	DHPLC	1	12	No	6
7	Pending	L475V (*26)	DHPLC	3	8	No	(19)

Eiselt *et al*, *Pharmacogenetics* (2001)

Screening for *CYP3A4* coding variants

Summary of *CYP3A4* variants

Patient	<i>CYP3A4</i> variant effect	<i>CYP3A4</i> variant allele	Detection technique	Max. Neuropathy grade	Total nr. cycles	Treatment modifications	Time with neuropathy (months)
1	Loss-of-function	*20	WES	3	8	Red (cycles 4 & 8)	(35)
2		*20	DHPLC	3	8	Red (cycle 4)	(9)
3		*20	DHPLC	3	12	Red (cycle 9)	(6)
4		*20	DHPLC	3	11	No	16
5	Decreased activity	P389S (*25)	WES	3	6	Susp (cycle 6)	19
6		R130Q (*8)	DHPLC	1	12	No	6
7	Pending	L475V (*26)	DHPLC	3	8	No	(19)

Functional characterization
(*25 & *26)

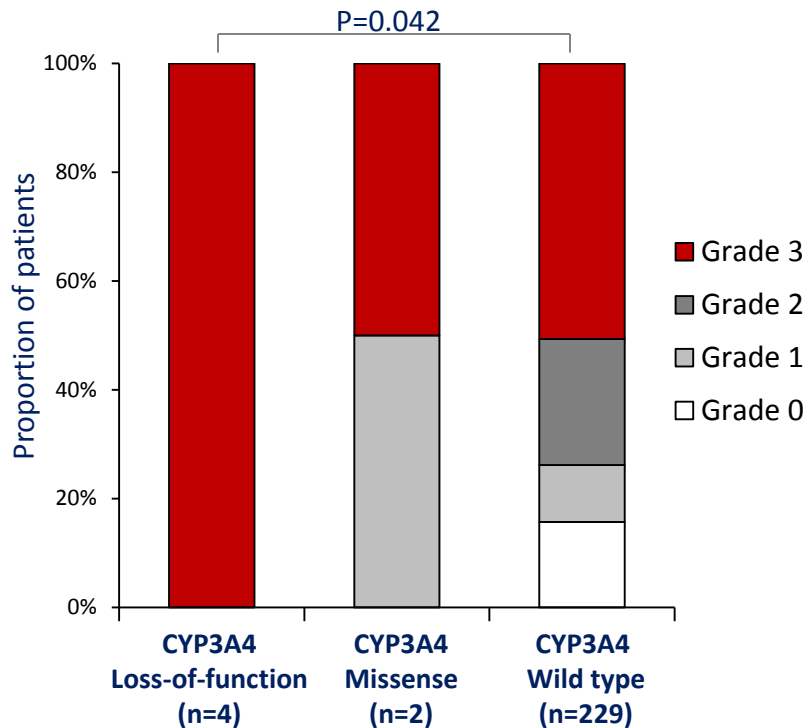
Mi-Young Lee
Magnus Ingelman-Sundberg
(Abstract P-187)



Karolinska
Institutet

Are *CYP3A4* defective variants clinically relevant?

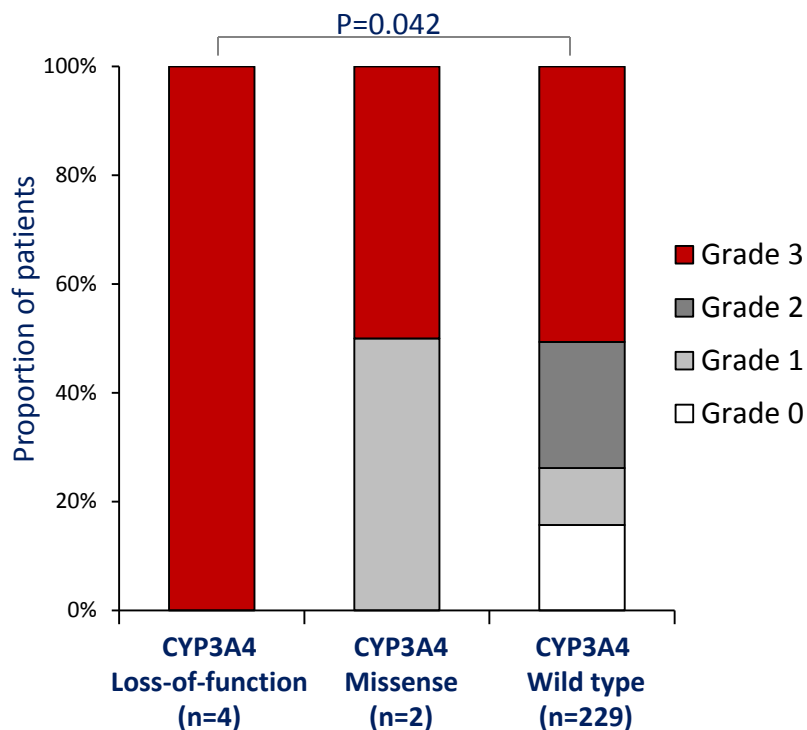
2-fold higher risk of Grade 3 neuropathy



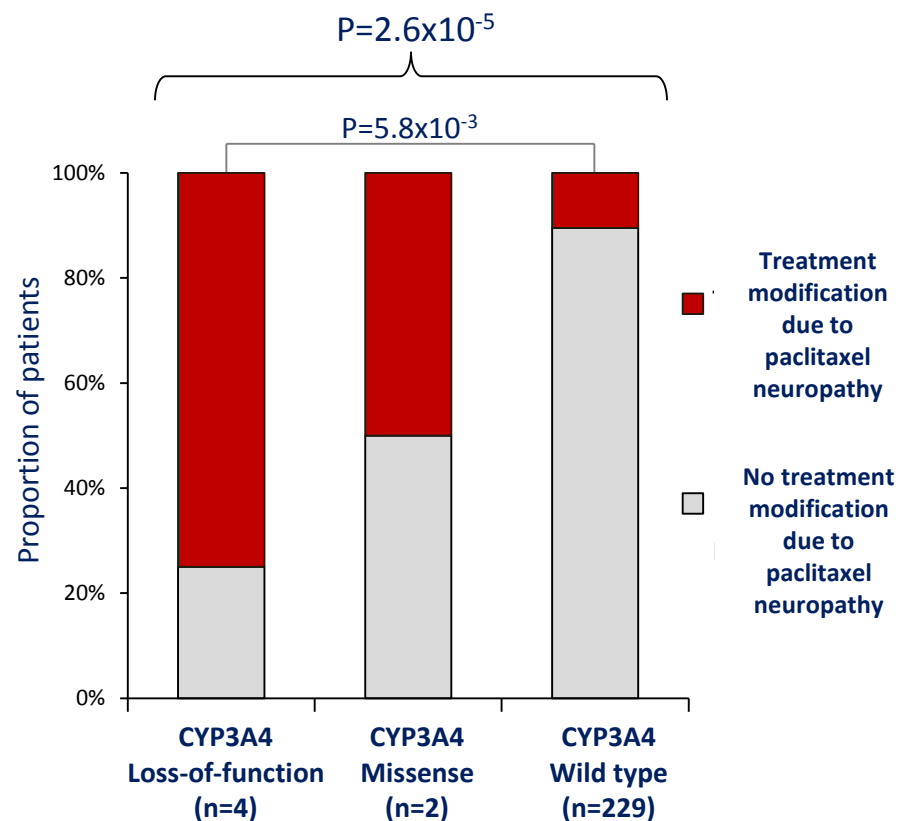
Correction for neuropathy risk factors or tumor type does not change association

Are *CYP3A4* defective variants clinically relevant?

2-fold higher risk of Grade 3 neuropathy



7-fold higher risk of treatment modifications



Correction for neuropathy risk factors or tumor type does not change association

Conclusions

- Patients carrying *CYP3A4* loss of function variants (*CYP3A4*20* allele) have increased risk of paclitaxel-induced neuropathy and higher risk of treatment modifications

Conclusions

- Patients carrying *CYP3A4* loss of function variants (*CYP3A4*20* allele) have increased risk of paclitaxel-induced neuropathy and higher risk of treatment modifications
- As expected, carriers of missense variants showed an intermediate phenotype concordant with a decreased but not abolished *CYP3A4* activity

Conclusions

- Patients carrying *CYP3A4* loss of function variants (*CYP3A4*20* allele) have increased risk of paclitaxel-induced neuropathy and higher risk of treatment modifications
- As expected, carriers of missense variants showed an intermediate phenotype concordant with a decreased but not abolished *CYP3A4* activity
- First description of a genetic marker predictive of paclitaxel dose-limiting toxicity

Conclusions

- Patients carrying *CYP3A4* loss of function variants (*CYP3A4*20* allele) have increased risk of paclitaxel-induced neuropathy and higher risk of treatment modifications
- As expected, carriers of missense variants showed an intermediate phenotype concordant with a decreased but not abolished *CYP3A4* activity
- First description of a genetic marker predictive of paclitaxel dose-limiting toxicity
- These variants may be potential markers for paclitaxel treatment individualization

Conclusions

- Patients carrying *CYP3A4* loss of function variants (*CYP3A4*20* allele) have increased risk of paclitaxel-induced neuropathy and higher risk of treatment modifications
- As expected, carriers of missense variants showed an intermediate phenotype concordant with a decreased but not abolished *CYP3A4* activity
- First description of a genetic marker predictive of paclitaxel dose-limiting toxicity
- These variants may be potential markers for paclitaxel treatment individualization
- Low-frequency/ rare variants may explain part of *CYP3A4* variability and could contribute to adverse drug reactions, specially for narrow therapeutic index drugs

Acknowledgements

Spanish National Cancer Research Centre (CNIO) Hereditary Endocrine Cancer Group



Mercedes Robledo ESP



Alberto Cascón ESP



Cristina Rodríguez ESP



Javier Leandro ESP



Iñaki Comino ESP



Aguirre Andrés de Cubas USA



Lucía Inglada ESP



Rocío Letón ESP



Lara Sánchez ESP



Veronika Mancikova SVK



Álvaro Gómez ESP



María Currás Freixes



**Karolinska
Institutet**

Magnus Ingelman-Sundberg
Mi-Young Lee
Souren Mkrtychian
Inger Johansson

Isabel Calvo
Laura G^a Estévez
Jesús García-Donás



Gerardo Gutiérrez
María Sereno



Eva Guerra
Óscar Pastor



Beatriz Castelo
Andrés Redondo

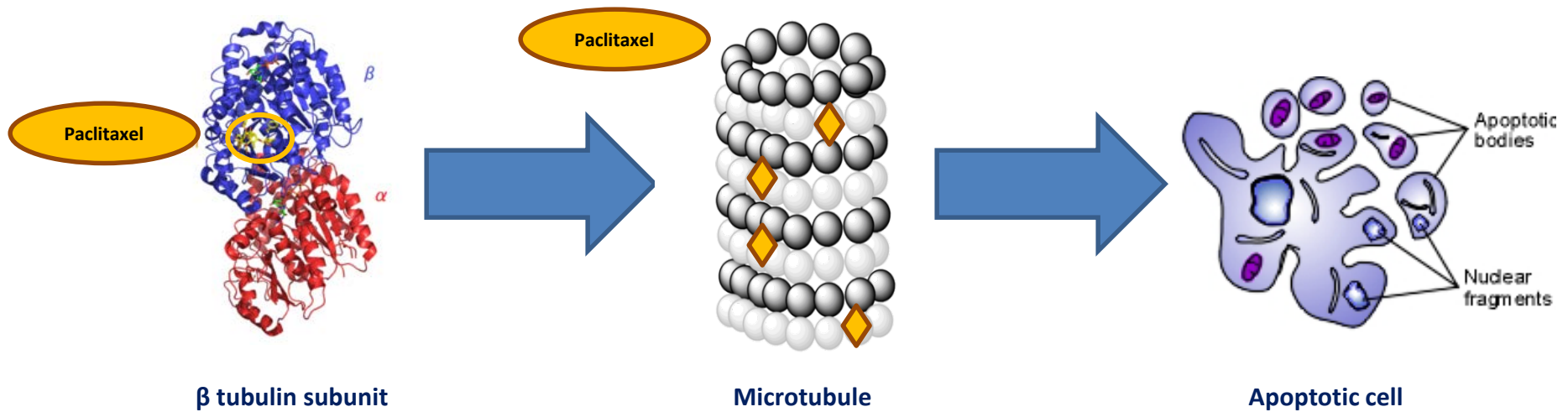


Founding



Obra Social
Fundación "la Caixa"

Paclitaxel



- **Effective therapy** for many solid tumors (breast, ovarian, lung, pancreas)
- Dose limiting toxicity: **peripheral neuropathy**



Genetic markers of paclitaxel neuropathy

TUBB2A

-Leandro-Garcia, *Clin Cancer Res* (2012), P=0.021

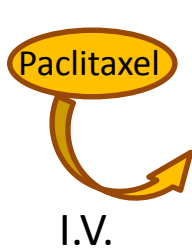
GWAS metanalysis

-Balwin, *Clin Cancer Res* (2012)

-Leandro-Garcia, *J Med Genet* (2013)

EPHA5 → P=1.4 x 10⁻⁹

XKR4 → P=3.1 x 10⁻⁸



CYP2C8

- Leskelä, *Pharmacogenomics J* (2011), P=0.032

- Hertz, *Ann Oncol* (2013), P=0.006

CYP3A4

- de Graan, *Clin Cancer Res* (2013), P=0.001

ABCB1

- Sissung, *Eur J Cancer* (2006), P=0.09

Genetic markers of paclitaxel neuropathy

TUBB2A

-Leandro-Garcia, *Clin Cancer Res* (2012), P=0.021

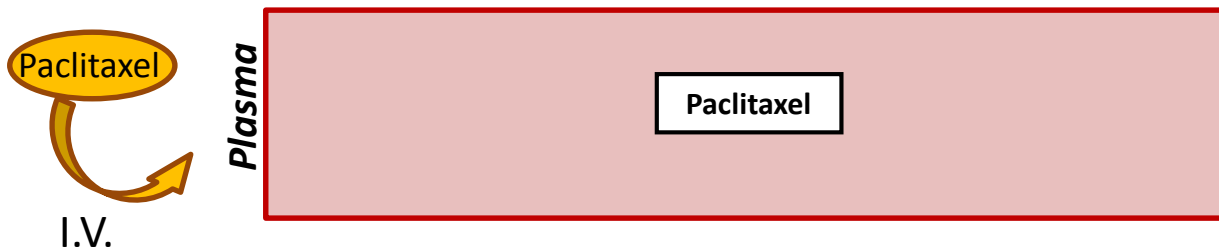
GWAS metanalysis

-Balwin, *Clin Cancer Res* (2012)

-Leandro-Garcia, *J Med Genet* (2013)

EPHA5 → P=1.4 x 10⁻⁹

XKR4 → P=3.1 x 10⁻⁸



CYP2C8

- Leskelä, *Pharmacogenomics J* (2011), P=0.032

- Hertz, *Ann Oncol* (2013), P=0.006

CYP3A4

- de Graan, *Clin Cancer Res* (2013), P=0.001

ABCB1

- Sissung, *Eur J Cancer* (2006), P=0.09

Genetic markers of paclitaxel neuropathy

TUBB2A

-Leandro-Garcia, *Clin Cancer Res* (2012), P=0.021

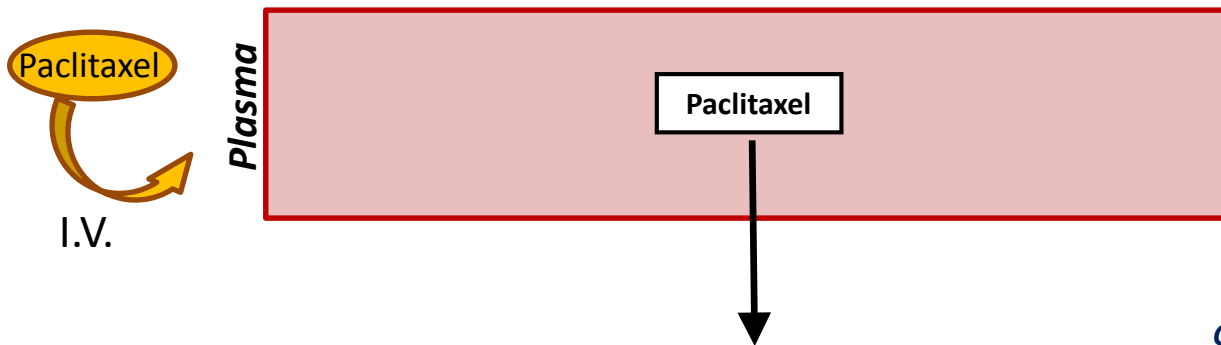
GWAS metanalysis

-Balwin, *Clin Cancer Res* (2012)

-Leandro-Garcia, *J Med Genet* (2013)

EPHA5 → P=1.4 x 10⁻⁹

XKR4 → P=3.1 x 10⁻⁸



CYP2C8

- Leskelä, *Pharmacogenomics J* (2011), P=0.032

- Hertz, *Ann Oncol* (2013), P=0.006

CYP3A4

- de Graan, *Clin Cancer Res* (2013), P=0.001

ABCB1

- Sissung, *Eur J Cancer* (2006), P=0.09

Genetic markers of paclitaxel neuropathy

TUBB2A

-Leandro-Garcia, *Clin Cancer Res* (2012), P=0.021

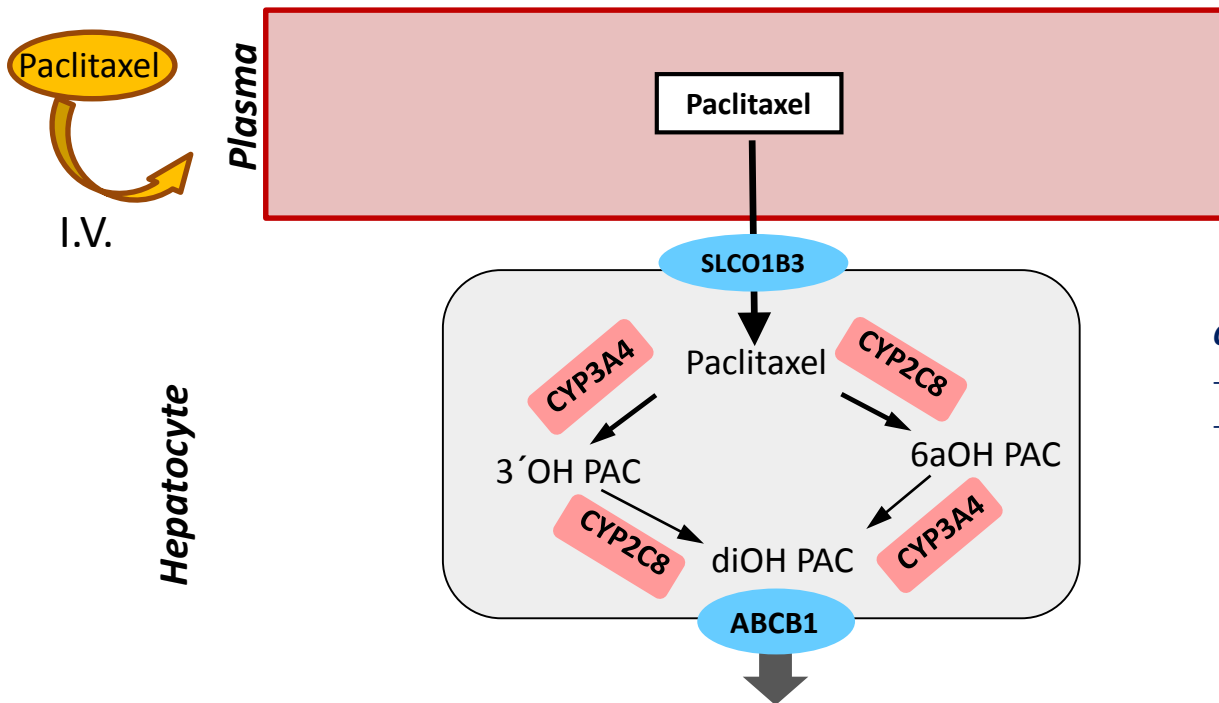
GWAS metanalysis

-Balwin, *Clin Cancer Res* (2012)

-Leandro-Garcia, *J Med Genet* (2013)

EPHA5 → P=1.4 x 10⁻⁹

XKRR4 → P=3.1 x 10⁻⁸



CYP2C8

- Leskelä, *Pharmacogenomics J* (2011), P=0.032

- Hertz, *Ann Oncol* (2013), P=0.006

CYP3A4

- de Graan, *Clin Cancer Res* (2013), P=0.001

ABCB1

- Sissung, *Eur J Cancer* (2006), P=0.09

Genetic markers of paclitaxel neuropathy

TUBB2A

-Leandro-Garcia, *Clin Cancer Res* (2012), P=0.021

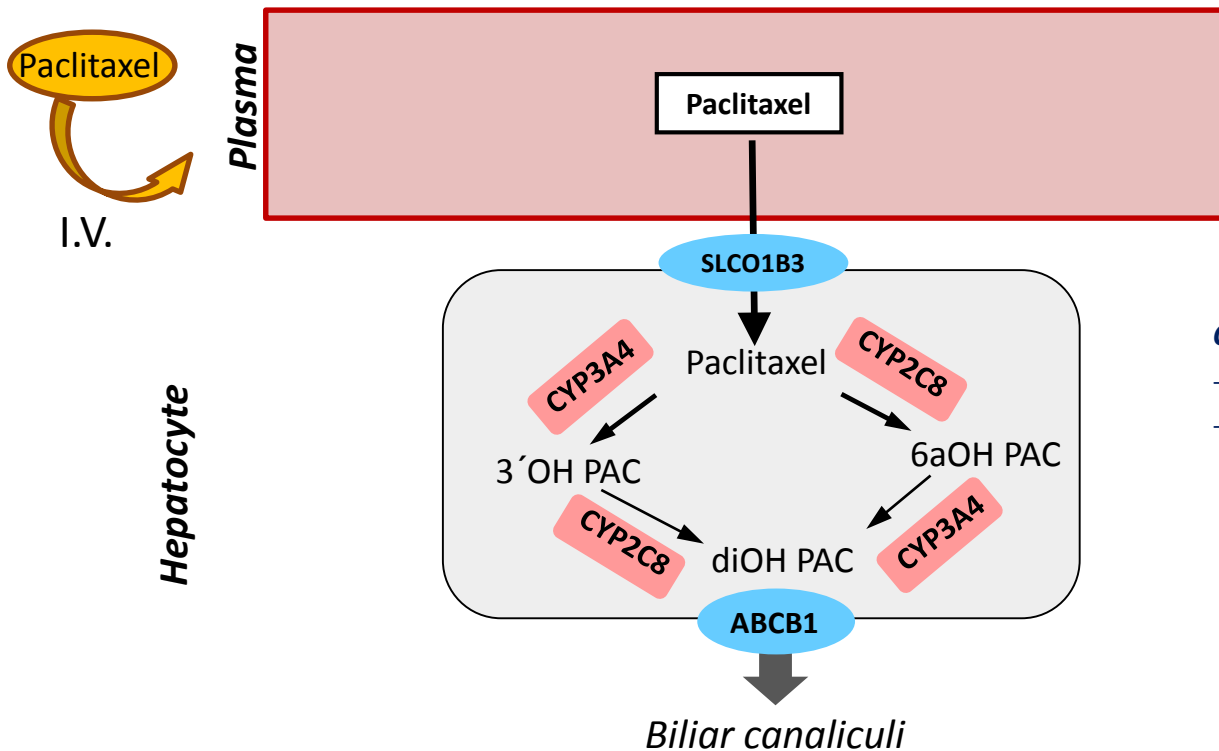
GWAS metanalysis

-Balwin, *Clin Cancer Res* (2012)

-Leandro-Garcia, *J Med Genet* (2013)

EPHA5 → P=1.4 x 10⁻⁹

XKRR4 → P=3.1 x 10⁻⁸



CYP2C8

- Leskelä, *Pharmacogenomics J* (2011), P=0.032

- Hertz, *Ann Oncol* (2013), P=0.006

CYP3A4

- de Graan, *Clin Cancer Res* (2013), P=0.001

ABCB1

- Sissung, *Eur J Cancer* (2006), P=0.09

Genetic markers of paclitaxel neuropathy

TUBB2A

-Leandro-Garcia, *Clin Cancer Res* (2012), P=0.021

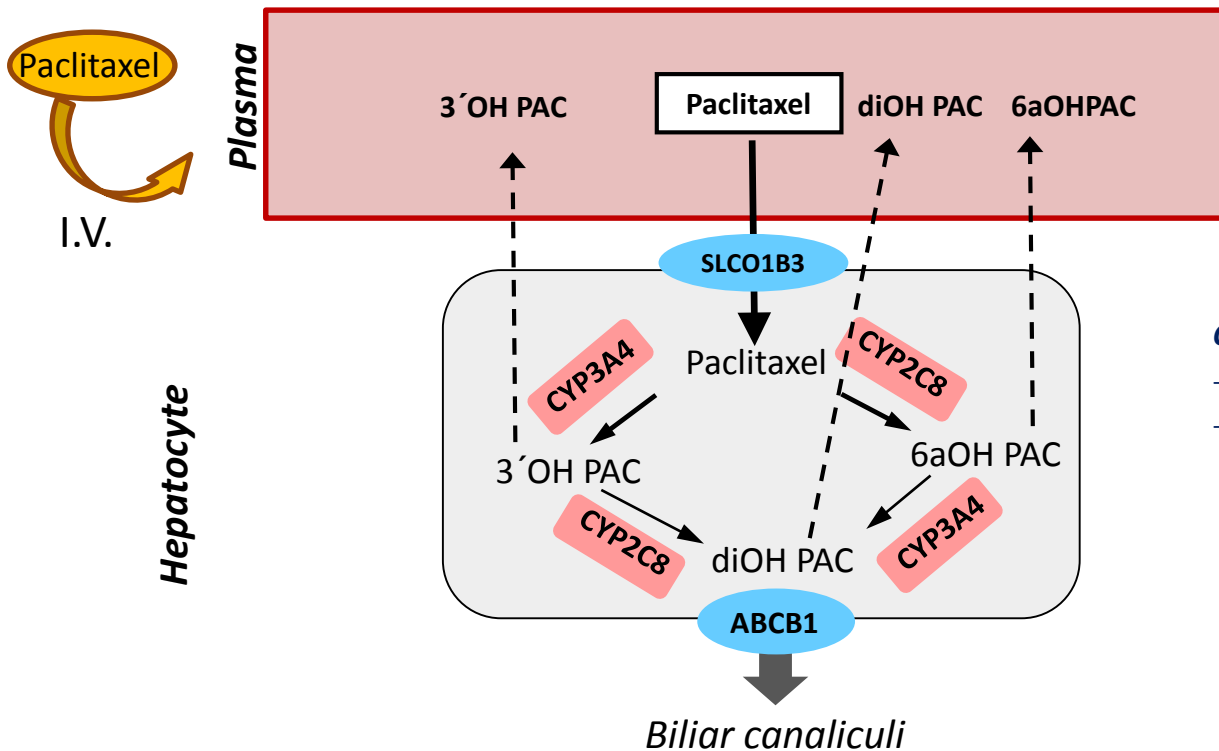
GWAS metanalysis

-Balwin, *Clin Cancer Res* (2012)

-Leandro-Garcia, *J Med Genet* (2013)

EPHA5 → P=1.4 x 10⁻⁹

XKR4 → P=3.1 x 10⁻⁸



CYP2C8

- Leskelä, *Pharmacogenomics J* (2011), P=0.032

- Hertz, *Ann Oncol* (2013), P=0.006

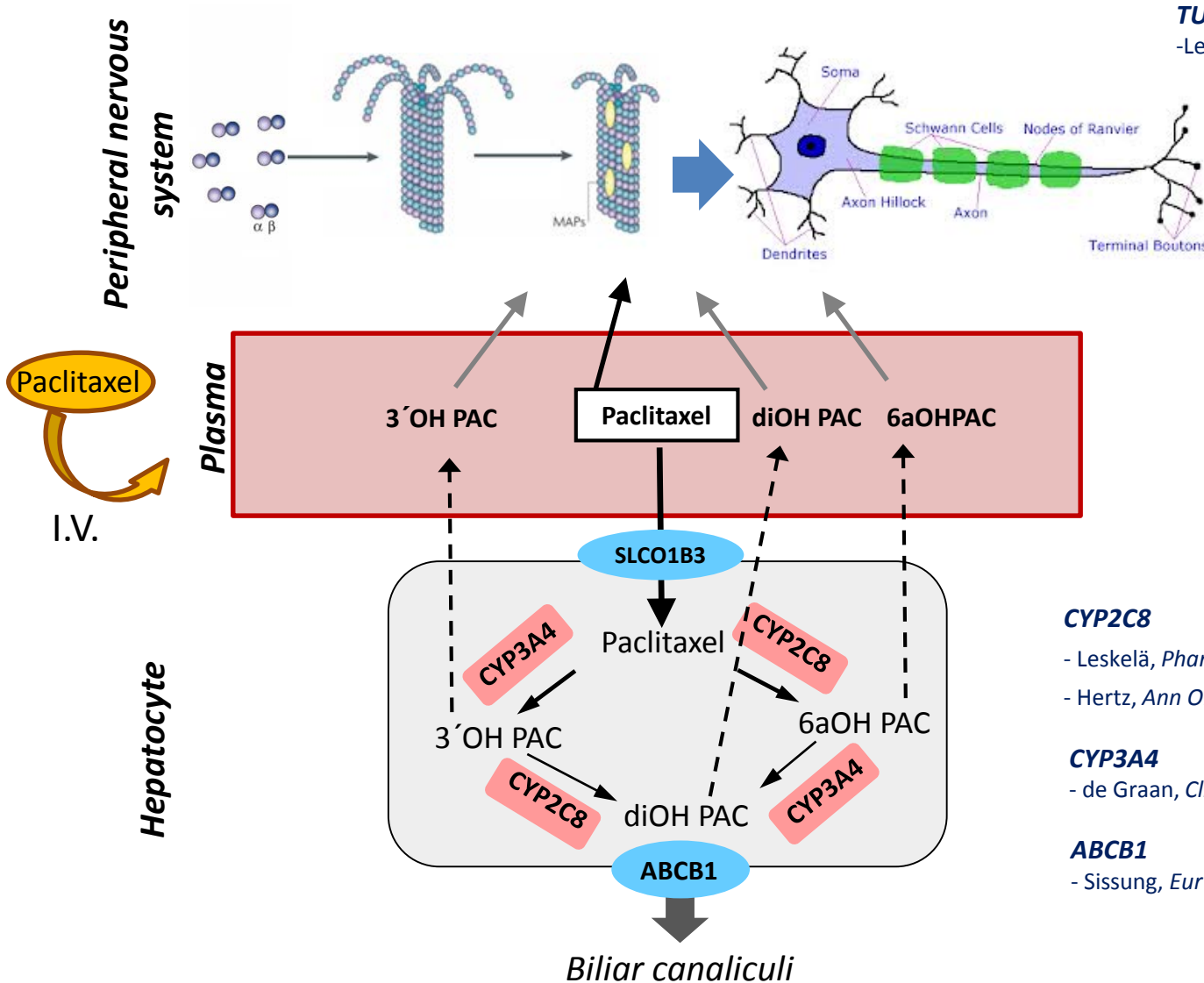
CYP3A4

- de Graan, *Clin Cancer Res* (2013), P=0.001

ABCB1

- Sissung, *Eur J Cancer* (2006), P=0.09

Genetic markers of paclitaxel neuropathy



TUBB2A

-Leandro-Garcia, *Clin Cancer Res* (2012), P=0.021

GWAS metanalysis

- Balwin, *Clin Cancer Res* (2012)
- Leandro-Garcia, *J Med Genet* (2013)

EPHA5 → P=1.4 x 10⁻⁹

XKR4 → P=3.1 x 10⁻⁸

CYP2C8

- Leskelä, *Pharmacogenomics J* (2011), P=0.032
- Hertz, *Ann Oncol* (2013), P=0.006

CYP3A4

- de Graan, *Clin Cancer Res* (2013), P=0.001

ABCB1

- Sissung, *Eur J Cancer* (2006), P=0.09

Genetic markers of paclitaxel neuropathy: genome wide approaches (GWAS)

- Balwin *Clin Cancer Res* (2012)

- Human 610k
- Paclitaxel 175mg/m², every 14 d
- Breast cancer, n=855
- Accumulated Pac dose to G2 neuropathy

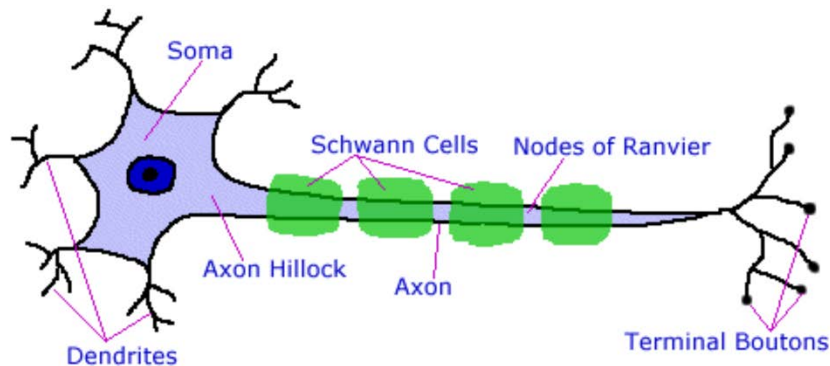
- Leandro-Garcia *J Med Genet* (2013)

- Human 660WQuad
- Paclitaxel 175mg/m² + Carboplatin 5-6 AUC, every 21 d
- Mainly ovarian cancer, n= 144
- Accumulated Pac dose to G2 neuropathy

Meta-analysis
top hits

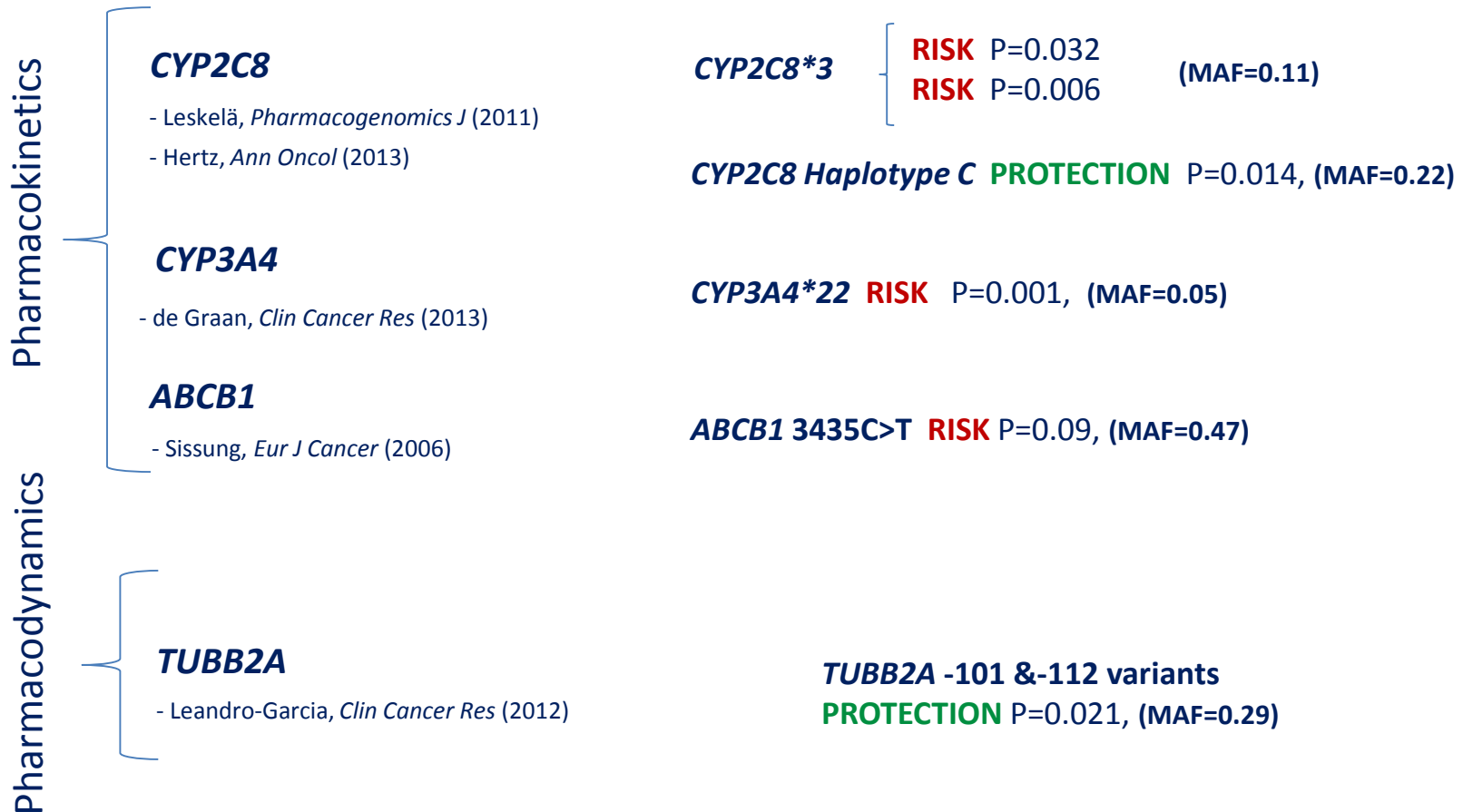
EPHA5 (rs7349683): HR=1.7, **P=1.4 x 10⁻⁹** (1x10⁻⁶; 3x10⁻⁴), MAF= 0.38

XKR4 (rs4737264): HR=1.7, **P=3.1 x 10⁻⁸** (2x10⁻⁶; 3x10⁻³), MAF=0.23



Genetic markers of paclitaxel neuropathy: candidate gene approaches

Genetic risk factors: common variants with moderate effects (HR=1.5-2.0)



Do patients with *CYP3A4* defective alleles have functional variants previously associated with neuropathy?

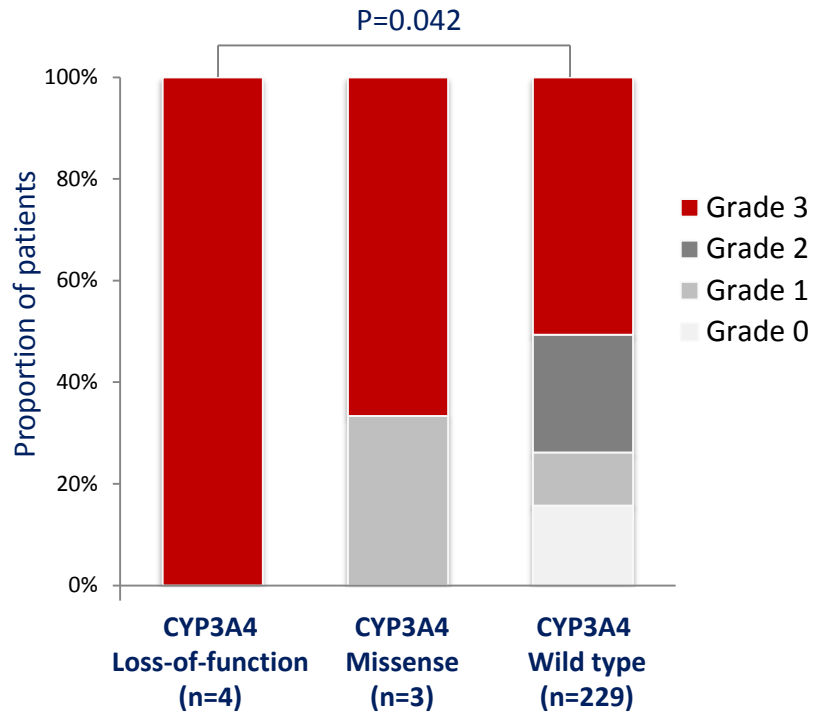
Gene	Variant name	Nr. of neuropathy risk alleles						
		Patient 1	Patient 2	Patient 3	Patient 4	Patient 5	Patient 6	Patient 7
CYP3A4	Frameshift (*20)	1	1	1	1	0	0	0
	Novel P389S (*25)	0	0	0	0	1	0	0
	Novel L475V (*27)	0	0	0	0	0	1	0
	R130Q (*8)	0	0	0	0	0	0	1
CYP3A4	<i>CYP3A4</i> *22	1	0	0	0	0	0	0
CYP2C8	<i>CYP2C8</i> *3	1	1	0	0	0	0	1
EPHA5	rs7349683	0	2	0	0	1	2	0
XKR4	rs4737264	1	1	0	0	1	0	1
<i>CYP3A4</i> coding variants		Loss-of-function (no activity)				Missense (decreased activity)		
Paclitaxel-induced neuropathy (grade/ dose modif.)^a		3/ Red (2)	3/ Red	3/ Red	3/ -	3/ Susp	3/ -	1/ -

Do patients with *CYP3A4* defective alleles have functional variants previously associated with neuropathy?

Gene	Variant name	Nr. of neuropathy risk alleles						
		Patient 1	Patient 2	Patient 3	Patient 4	Patient 5	Patient 6	Patient 7
CYP3A4	Frameshift (*20)	1	1	1	1	0	0	0
	Novel P389S (*25)	0	0	0	0	1	0	0
	Novel L475V (*27)	0	0	0	0	0	1	0
	R130Q (*8)	0	0	0	0	0	0	1
CYP3A4	<i>CYP3A4</i> *22	1	0	0	0	0	0	0
CYP2C8	<i>CYP2C8</i> *3	1	1	0	0	0	0	1
EPHA5	rs7349683	0	2	0	0	1	2	0
XKR4	rs4737264	1	1	0	0	1	0	1
<i>CYP3A4</i> coding variants		Loss-of-function (no activity)				Missense (decreased activity)		
Paclitaxel-induced neuropathy (grade/ dose modif.)^a		3/ Red (2)	3/ Red	3/ Red	3/ -	3/ Susp	3/ -	1/ -

Are *CYP3A4* defective variants clinically relevant?

2-fold higher risk of Grade 3 neuropathy



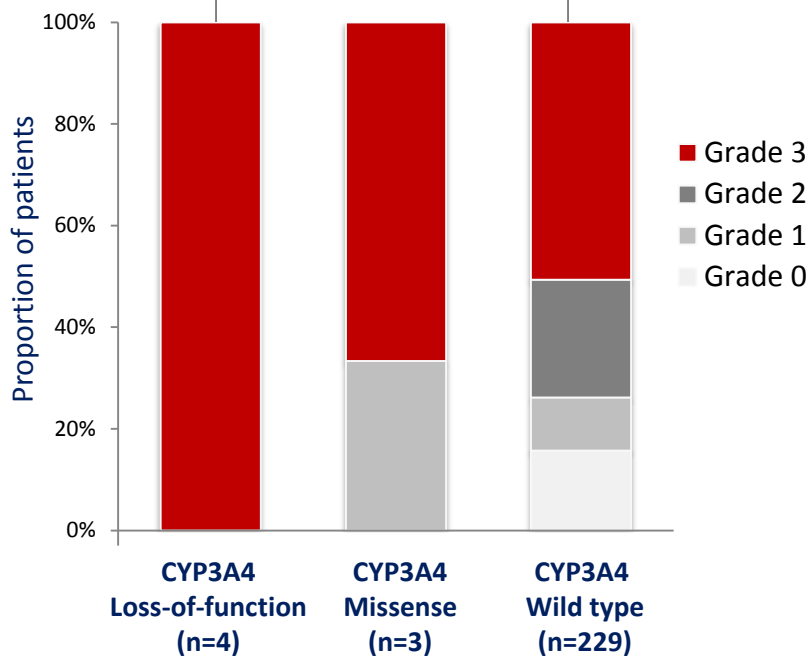
Correction for neuropathy risk factors or tumor type does not change association

Are *CYP3A4* defective variants clinically relevant?

2-fold higher risk of Grade 3 neuropathy

P=0.045

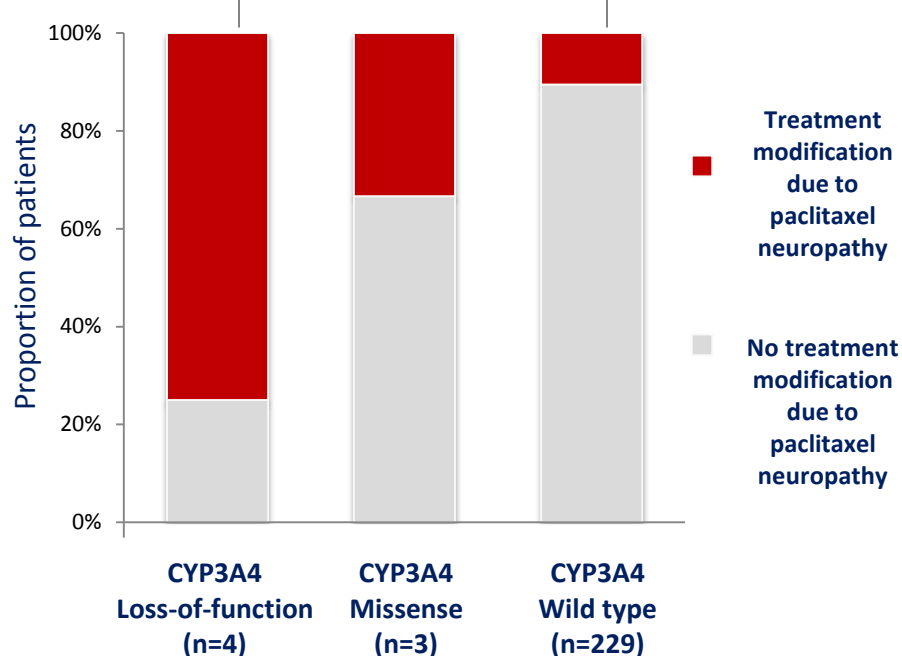
P=0.042



7-fold higher risk of treatment modifications

P=5.9x10⁻⁵

P=5.8x10⁻³



Correction for neuropathy risk factors or tumor type does not change association