

Ovarian Cancer in the 'Omics Era TRACO lecture Christina M. Annunziata, MD, PhD



NATIONAL CANCER INSTITUTE Center for Cancer Research

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- Most lethal gynecologic malignancy in the US
 - >16,000 deaths/yr
 - 5th most common cancer death for women
- 70% diagnosed with advanced disease
- < 35% of advanced stage patients alive at 5y

Ovarian Cancer Stages

Ovarian Cancer

Stage	Description	Incidence	Survival
1	Confined to ovaries	20%	90%
н	Confined to pelvis	5%	65%
	Spread IP or nodes	58%	45%
IV	Distant metastases	17%	<5%



Treatment for Newly Diagnosed Ovarian Cancer

- Complete surgical staging
- Optimal reductive surgery
- Chemotherapy
- Clinical Trials



The State of Treatment for Newly Diagnosed Ovarian Cancer

- Complete surgical staging
- Optimal reductive surgery
- Chemotherapy
 - Platinum = cisplatin or carboplatin AND
 - Taxane = paclitaxel or docetaxel
 - Intraperitoneal if Stage III, optimal reduction
- Clinical Trials

Ovarian cancer treatment



Treatment evolution for Ovarian Cancer

LKYLATORS	1970	CISPLATIN COMB	OS 1990	ANGIOGENESIS INHIBITION	2010
1960	CISPLATIN	1980	CARBO/TAX	2000	DNA REPAIR
OVARIAN	CANCERS				
		CISPLATIN & CTX	CARBO/TAX	BEV	PARPis
5-year sur	vival, advar	nced disease			
0%	5%	15%	35%	40%	

Treatment paradigm



Treatment paradigm for Ovarian Cancer



Treatment paradigm



Treatment paradigm for Ovarian Cancer



Prevalence

- Serous 80%
- Endometrioid 10%
- Clear cell 5%
- Mucinous 3%
- Other 2%



Ovarian Cancer

Prevalence

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Tissue of origin

- Fallopian tube?
 - Serous
- Endometriosis?
 - Endometrioid and clear cell
- Mullerian epithelium
 - Extra-uterine





- Increasing our understanding about the biological and biochemical events underlying ovarian cancer progression will create avenues for new treatments
- Can we use Genomics?

Clear cell, Endometrioid



Clear Cell cancers



- 5-10% of all cases (serous = 70%)
- Worse response to standard chemotherapy
- Associated with endometriosis (up to 40%)

Clear cell ovarian cancer

Clear cell OC – genomics

- Sequenced RNA from 18 clear cell ovarian cancers, and one cell line (discovery)
- Sequenced DNA exons from 210 samples
 - 101 more clear cell, 33 endometrioid, 76 serous, 1 more clear cell line (validation)
- Immunostain 455 more samples
 - 132 clear cell, 125 endometrioid, 198 serous





ARID1A



- SWI-SNF chromatin remodeling complex
- Mutated in breast cancer, lung cancer
- 1p36: deleted 6% of all cancers
- Tumor suppressor gene?

ARID1A mutations







Clear cell and endometrioid cancer

- ARID1A mutated or lost in
 - Over 40% clear cell
 - 30% endometrioid
 - Less than 1% serous
- Unknown oncogenic mechanism
 - No indication of which resulting pathways affected
 - Unclear therapeutic utility
- Diagnostic utility?
 - Not a 'functional' experiment

Mucinous





Mucinous ovarian cancer





K-ras mutations

KRAS mutations - mucinous

Table 2: KRAS mutation frequencies observed in borderline malignancies

borderline						
histotype	n	mutated	% mutated			
serous	20	7	35.00			
endometroid	1	0	0.00			
mucinous	6	3	50.00			
unknown	2	0	0.00			
total	29	10	34.48			



Low grade serous



KRAS and **BRAF** mutations

KRAS and BRAF mutations

- BRAF codon 599
- KRAS codon 12 or 13
- 15 of 22 (68%) of low grade serous cancers
- 31 of 51 (61%) precursor lesions (SBT)
- None of 72 high grade serous cancers



KRAS and **BRAF**

KRAS and BRAF mutations





RAS signaling pathway - a potential driver?





MEK inhibitor

Clinical trial: MEK inhibitor

- Recurrent Low Grade Serous ovarian cancer
- Selumetinib 50 mg twice daily
- 52 patients
 - 8 responses
 - 34 stable disease >4mo



Farley, Lancet Oncol 2013





Selumetinib responses

mutations

	Number	No tumour response	Tumour response	p value*	
Total	34	27 (79%)	7 (21%)		
BRAF mutat	ion				
No	32	25 (78%)	7 (22%)	1.000	
Yes	2	2 (100%)	0		
KRAS mutation					
No	20	15 (75%)	5 (25%)	0.672	
Yes	14	12 (86%)	2 (14%)		
BRAF or KRAS mutation					
No	18	13 (72%)	5 (28%)	0.405	
Yes	16	14 (88%)	2 (13%)		
Data are number (%), unless otherwise indicated. *Fisher's exact test.					



Farley, Lancet Oncol 2013



High grade serous



High grade serous cancers

High grade serous cancers

- The Cancer Genome Atlas (TCGA)
 - Clinically annotated HGS-OvCa samples
 - Identify molecular abnormalities that
 - influence pathophysiology,
 - affect outcome and
 - constitute therapeutic targets.
 - Microarray analyses: 489 HGS-OvCa tumours,
 - mRNA expression,
 - microRNA (miRNA) expression,
 - DNA copy number and
 - DNA promoter methylation for and
 - Whole exome DNA sequence: 316 samples.







High grade serous cancers

Sample inclusion criteria

- Newly diagnosed patients
- ovarian serous adenocarcinoma
- no prior treatment
- companion normal tissue specimen
 - adjacent normal tissue,
 - peripheral lymphocytes,
 - or previously extracted germline DNA



Genome copy number

Genome copy number abnormality

Copy number profiles of 489 HGS-OvCa, compared with profiles of 197 glioblastoma multiforme (GBM) tumours.

Copy number increases (red) and decreases (blue) are plotted as a function of distance along the normal genome (vertical axis, divided into chromosomes).



Deletion

Neutral

Amplification

Mutated genes

Table 2 | Significantly mutated genes in HGS-OvCa

Gene	No. of mutations	No. validated	No. unvalidated
TP53	302	294	8
BRCA1	11	10	1
CSMD3	19	19	0
NF1	13	13	0
CDK12	9	9	0
FAT3	19	18	1
GABRA6	6	6	0
BRCA2	10	10	0
RB1	6	6	0

Validated mutations are those that have been confirmed with an independent assay. Most of them are validated using a second independent whole-genome-amplification sample from the same tumour. Unvalidated mutations have not been independently confirmed but have a high likelihood to be true mutations. An extra 25 mutations in *TP53* were observed by hand curation.



Altered pathways in HGS-OvCa



TCGA – what next?



- New therapeutic approaches?
 - 50% with HR defects : **PARP inhibitors**
 - commonly deregulated pathways: RB, RAS/PI3K, FOXM1, NOTCH, provide opportunities for therapeutic treatment
 - Inhibitors exist for 22 genes in regions of recurrent amplification
- aberrant genes or **networks**: targeted therapies selected to be effective ...

Targeting deficient Homologous Recombination

PARP inhibitors

BRCA mutations

• Hall...King, Science, 1990



High grade serous cancers **BRCA1** germline 8% **BRCA2** germline BRCA1 somatic 6% 4% Other BRCA2 somatic 31% 3% **BRCA1** methylation 11% MMR germline 2% Rb1 loss **EMSY** amplification 4% 6% PTFN loss CCNE1 amplification. Other HRD 6% 14% 5% * HRD, homologous recombination defect

High grade serous cancers

DNA repair

How is DNA repaired?

- Homologous recombination (HR)
- Undamaged DNA is the guide.
- Replaces damaged part with the "correct" code
- Uses BRCA

- Base excision repair (BER)
- Cuts out damaged DNA
- Joins cut end with another piece
- Uses PARP





PARP inhibitors



PARP inhibitors

- Olaparib (Lynparza)
- Rucaparib (Rubraca)
- Niraparib (Zejula)

PARP inhibitors and clinical trials

PARP inhibitors clinical trials

- Initial treatment
 - VELIA veliparib with carboplatin + paclitaxel
- Maintenance treatment
 - First line
 - SOLO1 olaparib in women with BRCA mutation
 - PRIMA niraparib in women with high risk cancer
 - After platinum-sensitive relapse
 - SOLO2 olaparib after response to 2nd line platinum
 - ARIEL rucaparib in women with HR deficiency
- Relapsed ovarian cancer
 - Not currently recommended

PARP inhibitors use



PARP inhibitors - when to use

- First-line maintenance
 - BRCA mutation germline (hereditary) or somatic (tumor only)
 - HR deficient mutations in particular genes or changes in DNA
- Second-line maintenance
 - Response to second round of carboplatin/cisplatin
 - If no prior PARP inhibitor...
- Treatment
 - Not currently recommended

ASCO guideline



PARP inhibitors in clinical practice – ASCO guideline



HR deficiency testing

HR deficiency testing

- Molecular testing
- Ex: MyRisk panel
 - Germline 36 genes with evidence for hereditary cancer
- Tumor testing
 - Somatic BRCA mutations



ASCO guideline: Konstantinopoulous, et al. J Clin Oncol. 2020





Exploration of new targets

• Functional analysis



High grade serous cancers

High grade serous cancers



New targets



High throughput drug screen for new targets in ovarian cancer



SMAC mimetic and HDAC inhibitor



SMAC mimetic and HDAC inhibitor are highly synergistic in vitro



Survival curve



SMAC mimetic + HDAC inhibitor prolongs survival in mice



Mechanism of synergy

Mechanism of synergy

- Differential regulation of NF-kB classical and alternative pathways.
- Pleatropic effects of TNFα.
- Shifting balance between survival and apoptosis.

TNF upregulation





NF-KB activity







TNF and SMAC mimetic



Phase 1 trial



SMACm + HDACi - phase 1 clinical trial under development

	Doce	Entinostat	4 STY660	Subjects
Oral Agents:	Level	(mg, orally)	(mg, orally)	(n)
ASTX660 (SMAC minietic, Astex)	-1	3, every other week	90 once daily	3-6
Entinostat (HDAC inhibitor, Syndax)	1	3, once weekly	90 once daily	3-6
	Z	5, once weekly	90 once daily	3-6
 Clinical visit and labs weekly Restaging scans q8 weeks Expansion cohort at MTD 	з	5, once weekly	120 once daily	3-8
	4	5, once weekly	150, once daily	3-6
	MTD	MTD, once weekly	MTD, once daily	15

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	MTD	MTD, once weekly	MTD, once daily	15
Day 1 8 15 22	1	8 15 O	22 cle 2	
ASTX660++++++	2*	*****	*****	
📥 Tumor biopsy Jexpansion cohort)	A		[at progress	ion] 📥

Studies for exploratory aims (expansion cohort): TNF upregulation, Target inhibition (cIAP level, H3 histone acetylation), CODEX immune cell assay

Ovarian cancer genomicsAcknowledgements

Ovarian cancer genomics



NCI CCR





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