

4^a Jornada de Actualización en Cáncer Ginecológico

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ASONMEC

Utilidad del ctDNA en cáncer de ovario

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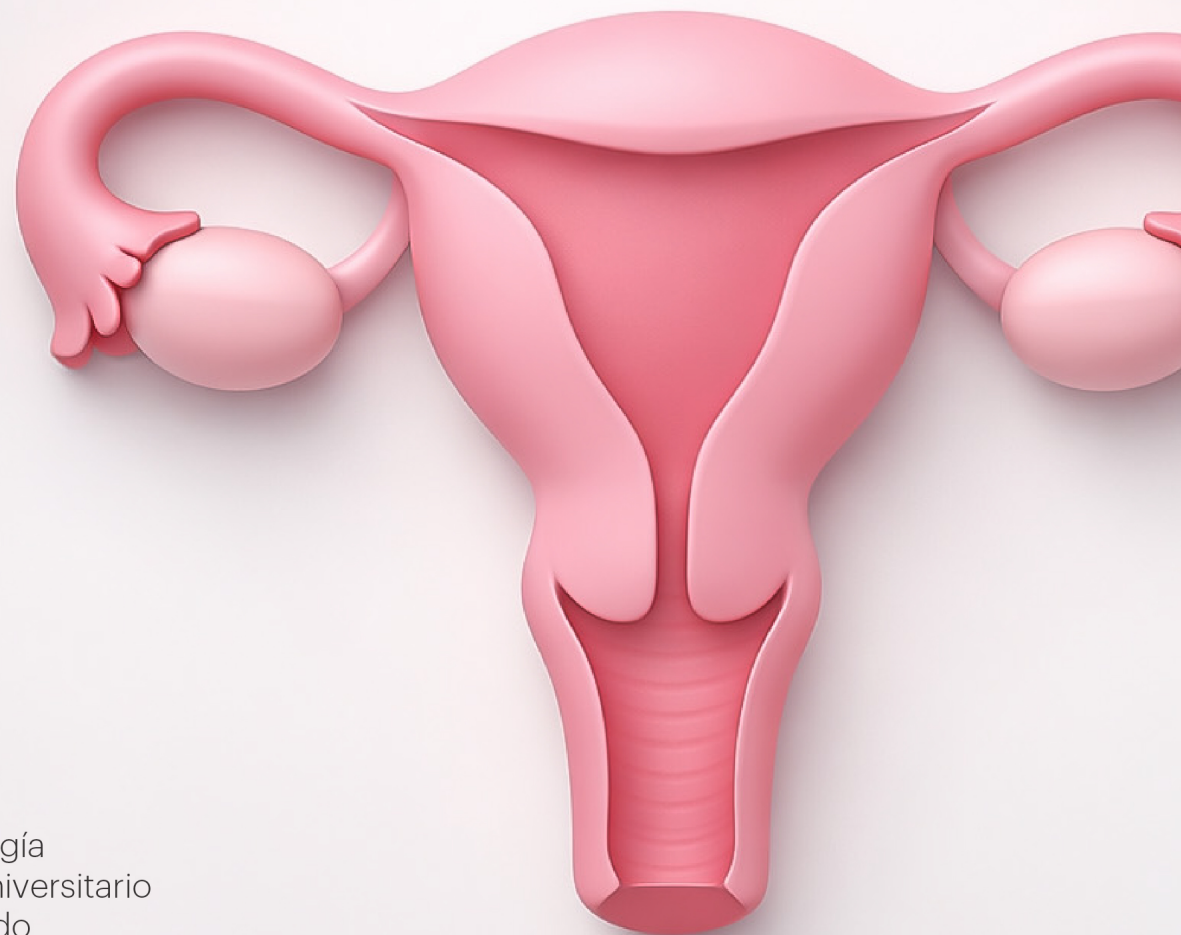
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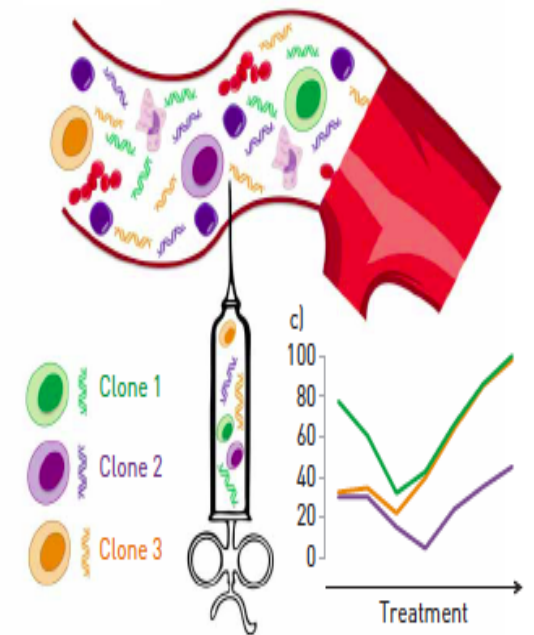
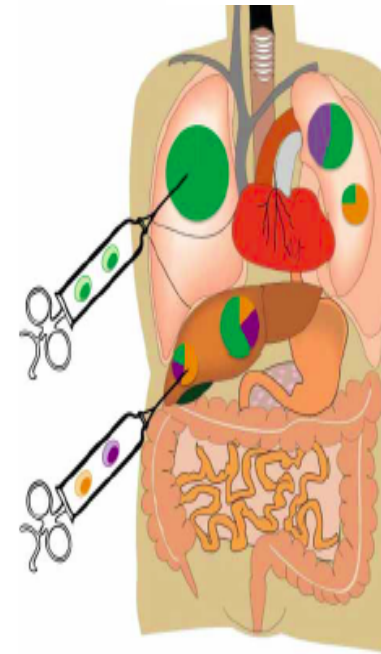
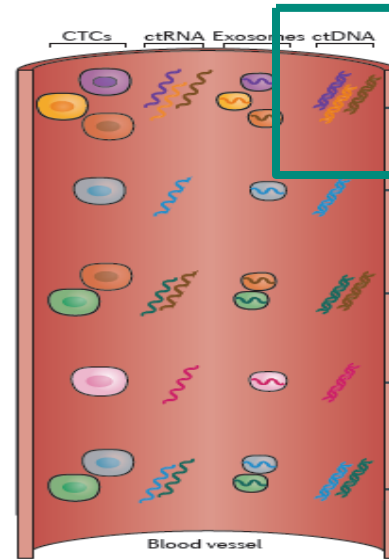
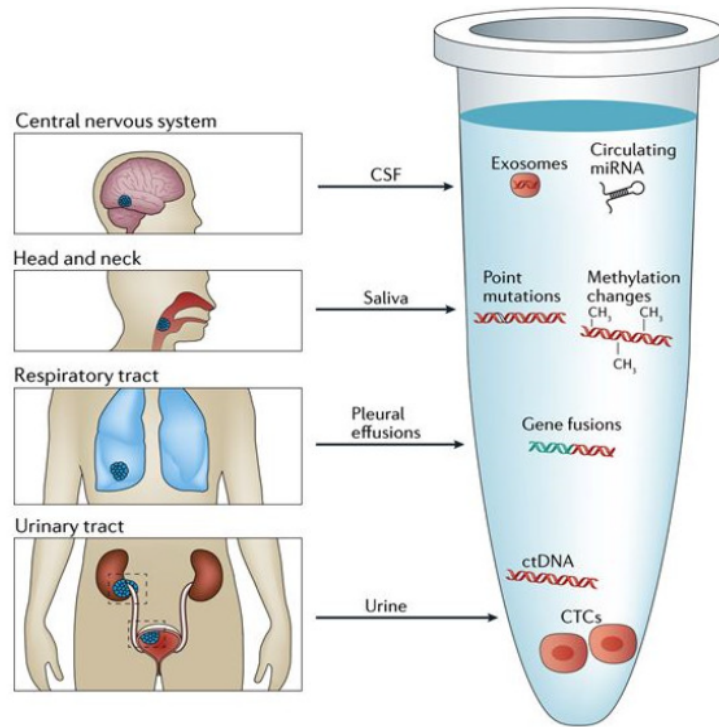
Disclosure Information

- Consultant or Advisory Role: AstraZeneca, GSK, Gemmab, MSD, BMS, Pierre Fabre, Immunocore, Abbvie.
- Speaking: Pharmamar, AstraZeneca, MSD, GSK, BMS, Pierre Fabre, Abbvie.
- Attending scientific meetings: AstraZeneca, MSD, GSK, Pierre Fabre.

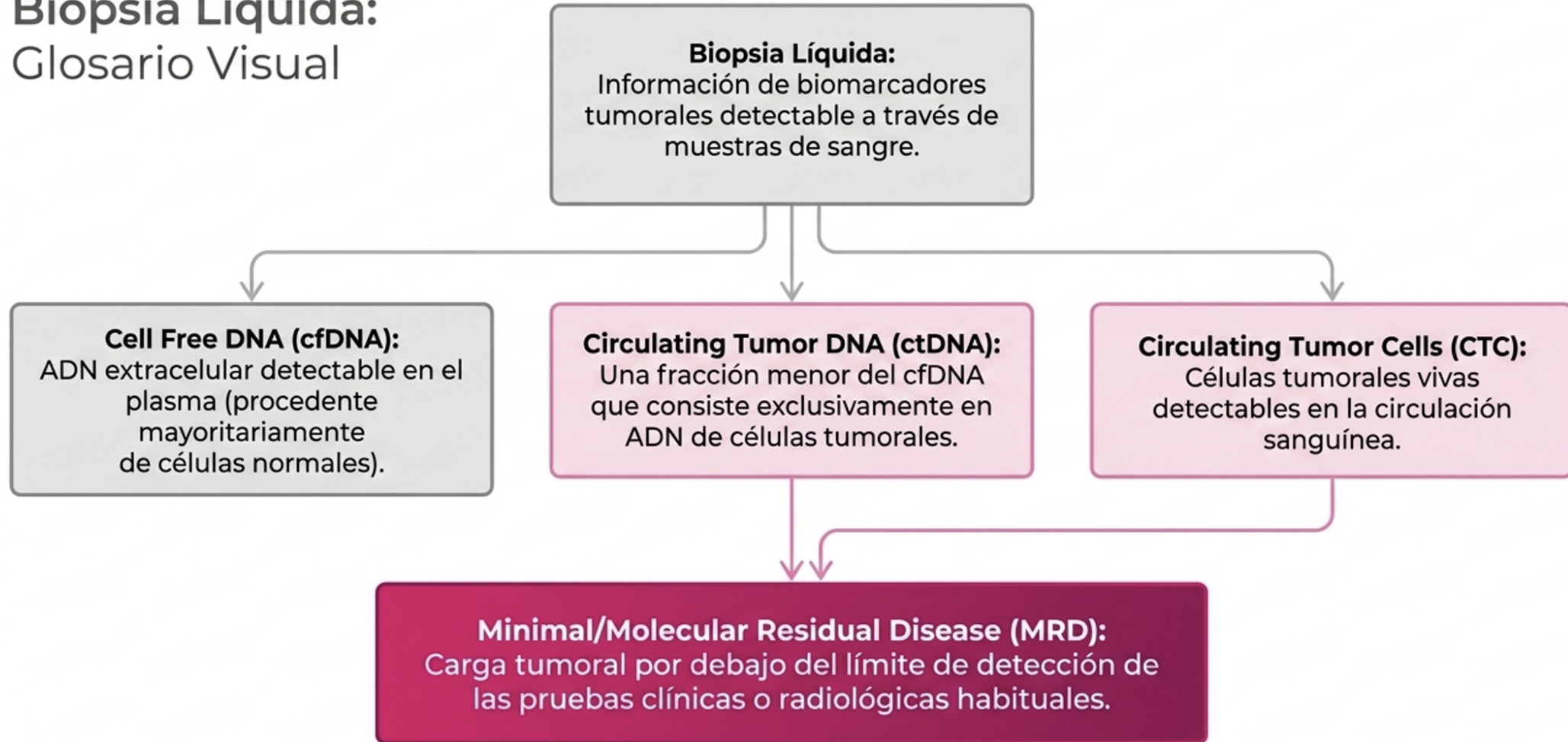
Liquid biopsy, source of tumor information

Any biological fluid contains genetic material, cell-free DNA

Peripheral blood remains the most studied liquid biopsy
ctDNA assesses spatial and temporal tumor heterogeneity



El Ecosistema de la Biopsia Líquida: Glosario Visual



Liquid biopsy in Ovarian Cancer:ctDNA

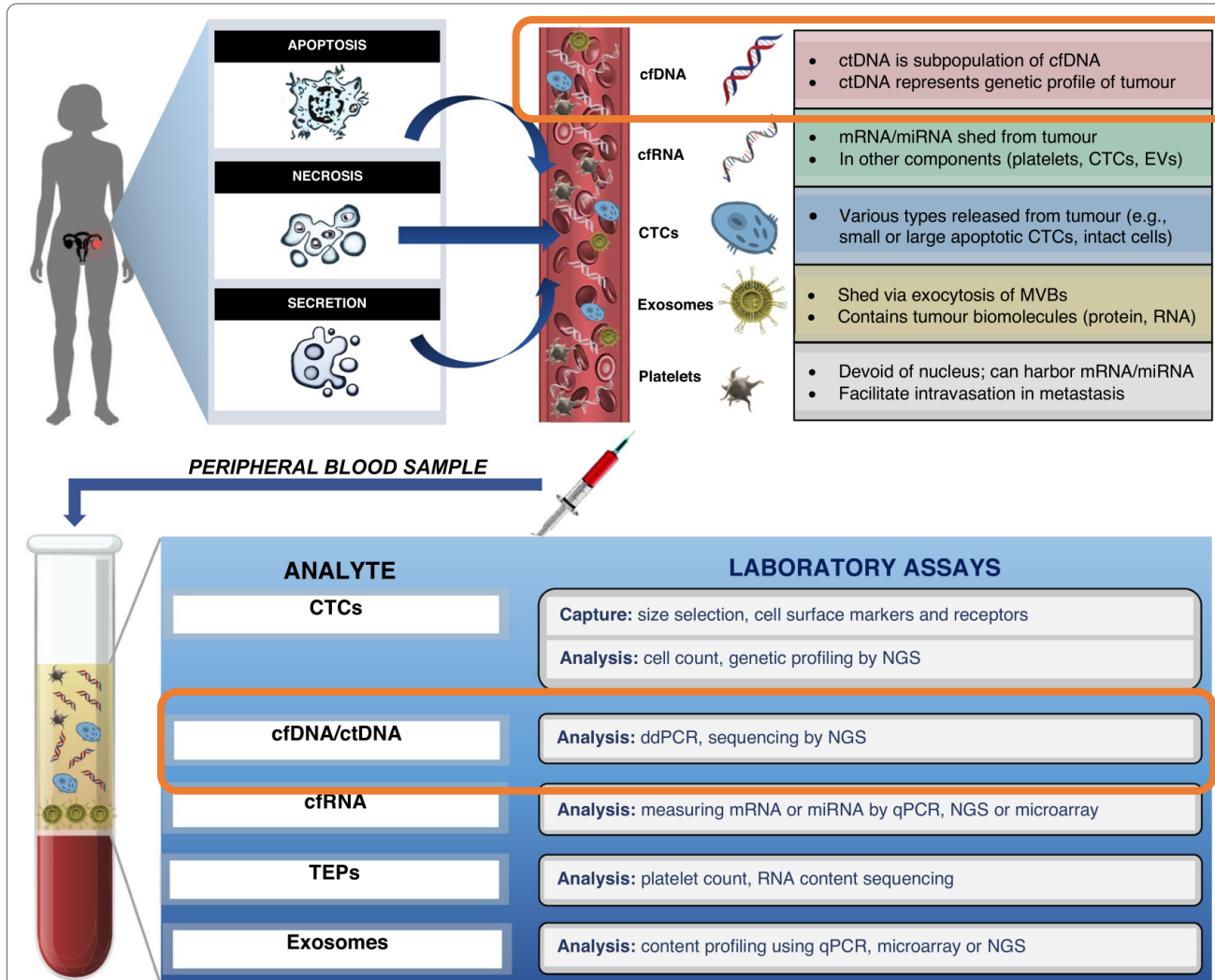
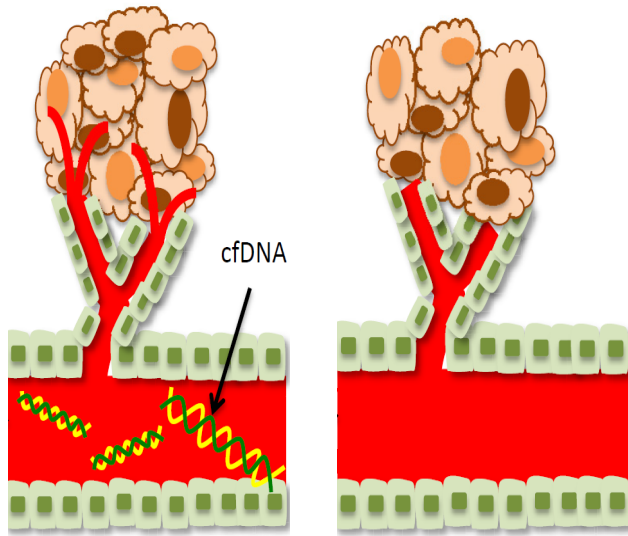


Fig. 2 Overview of the liquid biopsy process, from hypothesized mechanisms of tumour release of liquid biopsy components, to laboratory analysis techniques. Tumour biomarkers are first released and enter the circulation via one of three main mechanisms: apoptosis, necrosis, or secretion. Liquid biopsy involves the collection and analysis of five distinctive tumour components from peripheral blood samples: cell-free nucleic acids (cfDNA/ctDNA, cfRNA), CTCs, exosomes and tumour educated platelets. Tumour components in peripheral blood samples are then captured and analyzed using their corresponding laboratory assays. cfDNA: circulating free DNA, ctDNA: circulating tumour DNA, cfRNA: cell-free RNA, CTCs: circulating tumour cells, TEPs: tumour educated platelets, NGS: next generation sequencing, qPCR: quantitative polymerase chain reaction

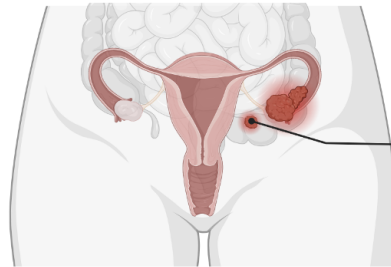
- Las células tumorales liberan/desprenden ctDNA al torrente sanguíneo mediante apoptosis, necrosis y secreción.
- El ctDNA puede diferenciarse por su menor longitud en comparación con el ADN libre circulante (cfDNA), que procede de células normales.
- La fracción tumoral de ctDNA mide el porcentaje de ctDNA en relación con el ADN total presente en sangre (ctDNA + cfDNA). El ctDNA está presente en pequeñas cantidades (0,1–10% del ADN circulante total).
- La detección de ctDNA requiere métodos de detección altamente sensibles, generalmente secuenciación de nueva generación (NGS).
- No todos los tipos tumorales liberan suficiente ctDNA como para ser detectado. En tumores con alta liberación (“high shedding”), el ctDNA puede servir como herramienta para:
 - diagnóstico del cáncer,
 - monitorización,
 - pronóstico,
 - y detección de mutaciones

Factors that may influence sensitivity and specificity of ctDNA detection

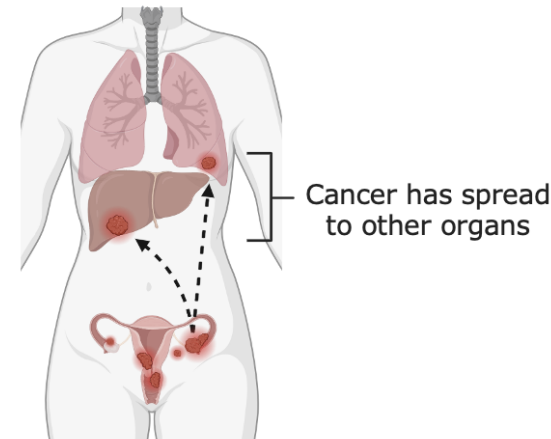
Shedding vs. Non-shedding



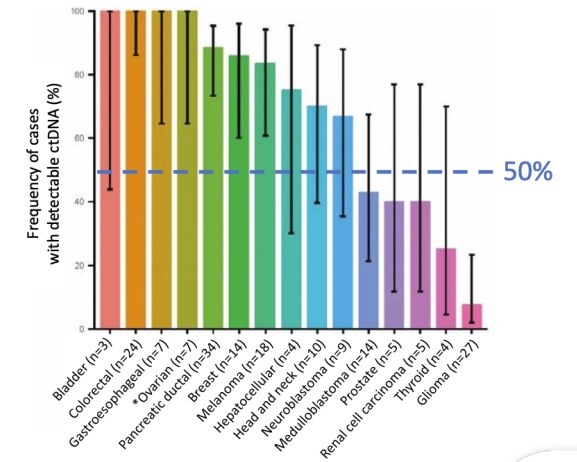
Stage



Inter-metastatic heterogeneity



Tumor type



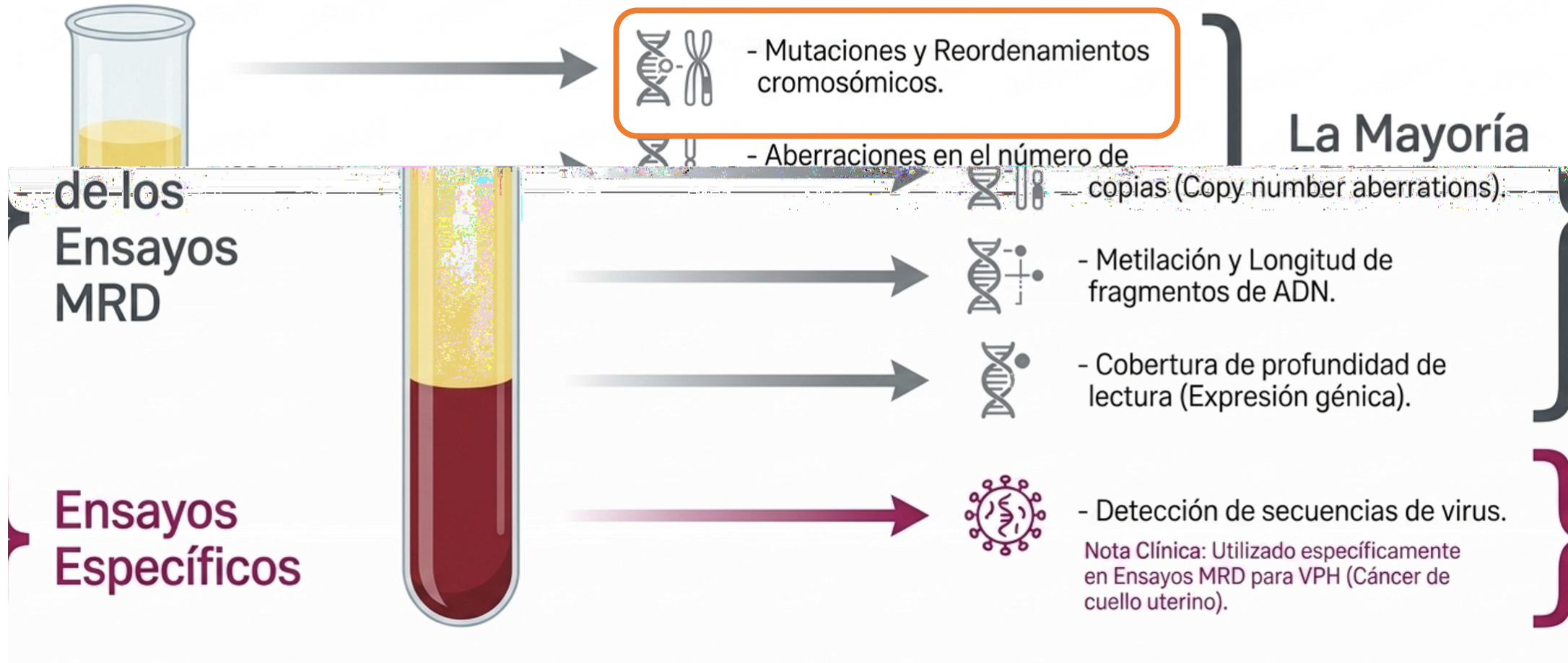
- ctDNA accounts for 0.4% (median) of cfDNA
- cfDNA exists as very short fragments of DNA (150-200 base pairs)
- There is a correlation between Disease burden and amount of tumour derived DNA (ctDNA) in the blood
- The higher disease stage, the greater the chance to detect ctDNA

- Requires more sensitivity than tissue analysis
 - ◆ Circulating tumor derived (ct)DNA is $\leq 0.5\%$ (can vary) of total cell free (cf)DNA versus $\geq 10\%$ in tissue
 - ◆ Short half-life (~2 hours)

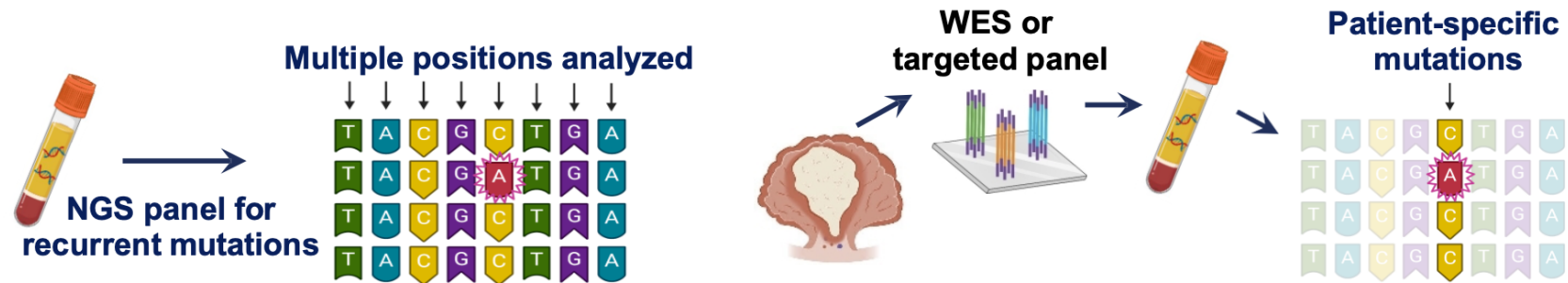
Biological and pathological factors affecting ctDNA levels:

- Tumor burden
- Anatomical site of the tumor Histology
- Proliferation index
- Necrosis
- Type of biological fluid

Arquitectura del ctDNA: ¿Qué Estamos Midiendo Exactamente?



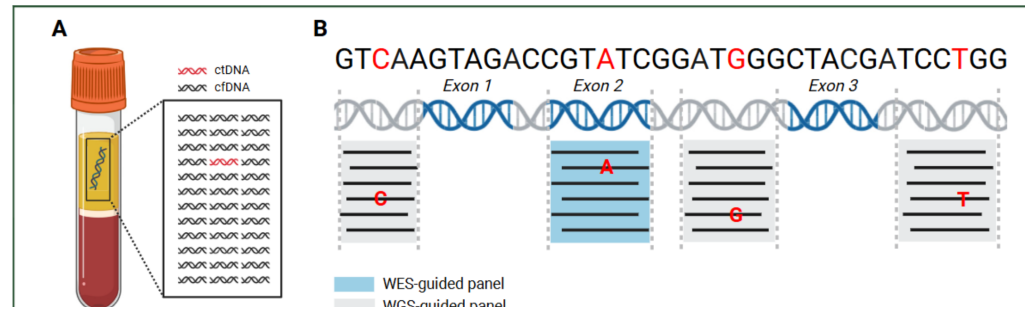
ctDNA Analysis: Tumor-Naïve vs Tumor-Informed Approach



	Tumor-Naïve	Tumor-Informed
Method	Detect mutations de novo from <u>plasma</u> (same panel for all patients)	Identify mutations in <u>tumor</u> tissue → track mutations in <u>plasma</u> (personalized panel)
Key Advantage	Does not require tumor tissue	Higher Sensitivity
Key Disadvantage	Lower sensitivity	Requires tumor tissue
Applications	Non-invasive genotyping (metastatic) Detect emerging resistant mutations Cancer screening	Minimal residual disease detection Surveillance – monitor recurrence Response monitoring

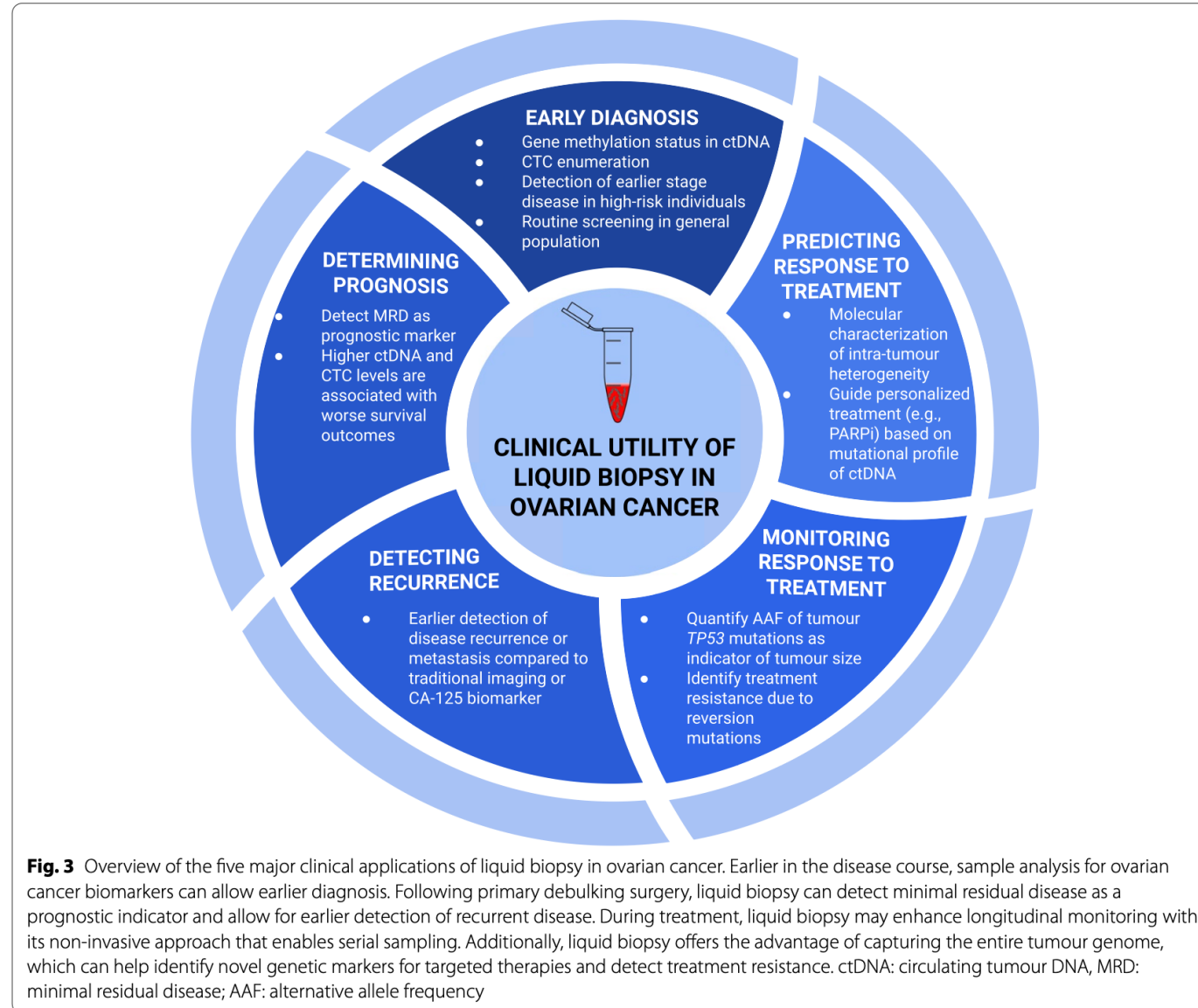
Técnicas de detección de ctDNA

Tumor Informed (Bespoke) ctDNA Assays: WES vs. WGS








	Tumor-naïve	Tumor-informed (WES)	Tumor-informed (WGS)
Variant source	Targeted NGS panel of cancer-associated genes	Top somatic variants from whole exome sequencing	WGS-derived patient-specific variants
Variants tracked	~10-100 genes	16 variants	Up to 1,800 variants
Limit of detection (tumor fraction)	0.1-1%	0.01-0.02%	< 0.01%
Tissue requirement	None	Tumor + matched normal	Tumor + matched normal

Utilidad de la biopsia líquida en cáncer de ovario



ctDNA en cáncer de ovario: aplicaciones clínicas, ventajas y limitaciones

Liquid Biopsy Component	Circulating Tumour Cells (CTCs)	Circulating Tumour DNA (ctDNA)	Cell-Free RNA (cfRNA)	Tumour Educated Platelets (TEPs)	Exosomes
					
Main Clinical Application	Diagnosis and prognosis	Diagnosis, prognosis, predicting response to treatment, monitoring response to treatment and detection of recurrence	Diagnosis and prognosis	Diagnosis	Diagnosis, prognosis, and prediction of response to treatment
Advantages	<ul style="list-style-type: none"> • Earlier detection of recurrence or metastasis • Predicting recurrence • Accessible source of tumour RNA/DNA/proteins • Detecting CTCs originating from both primary tumour and metastatic sites • Non-invasive 	<ul style="list-style-type: none"> • Higher available concentrations in bloodstream • Availability of laboratory techniques for analysis (e.g., NGS, ddPCR) • Higher stability compared to other liquid biopsy components • Capturing tumour heterogeneity • Available in a variety of body fluids • Non-invasive 	<ul style="list-style-type: none"> • Providing information on tumour's genetic expression profile • Monitoring tumour expression changes over time • Non-invasive 	<ul style="list-style-type: none"> • Potential use for earlier diagnosis • Routinely available clinical tests for quantification (e.g., CBC) • Non-invasive 	<ul style="list-style-type: none"> • Genomic contents protected from degradation • Accessible and variable source of tumour components • Available in a variety of body fluids • More abundant • Non-invasive
Limitations	<ul style="list-style-type: none"> • Low plasma counts • Difficulty differentiating CTCs from other cells in bloodstream 	<ul style="list-style-type: none"> • Low concentration (ctDNA:cfDNA ratio) in early stages make detection difficult • Difficulty differentiating ctDNA from cfDNA 	<ul style="list-style-type: none"> • More difficulty with isolation compared to cfDNA • Unstable molecule • No reliable methods for reproducible and practical application in clinical setting 	<ul style="list-style-type: none"> • Limited research • Lack of reliable methods for reproducible and practical application in clinical setting 	<ul style="list-style-type: none"> • Lack of standardized isolation methods • Lack of reliable methods for clinical application
Future Directions	<ul style="list-style-type: none"> • Improving methods for detection (e.g., low EpCAM expression settings) • Higher quality studies with larger sample sizes for determining prognostic applications 	<ul style="list-style-type: none"> • Improving methods for enrichment of ctDNA • Optimizing sensitivity for analysis techniques for detection at low allele frequencies • Further studies with larger sample sizes 	<ul style="list-style-type: none"> • Optimal combination of RNA candidates using machine learning methods • Improving methods for stabilizing cfRNA and extraction of cfRNA from plasma • Further studies with larger sample sizes 	<ul style="list-style-type: none"> • More evidence on the diagnostic sensitivity and specificity in different cancers • More standardized methods for analyzing platelet content • Further studies with larger sample sizes 	<ul style="list-style-type: none"> • More evidence on the diagnostic sensitivity and specificity in different cancers • More standardized methods for extraction of exosomes • Further studies with larger sample sizes

- ✓ **Non-invasive**
- ✓ **Reflects tumour heterogeneity**
- ✓ **Real-time monitoring is feasible**

- ✗ **Lack of standardization**
- ✗ **Need for sensitive techniques**

Fig. 4 Comparison of five liquid biopsy components and the main advantages, disadvantages, and future directions of their clinical application in ovarian cancer management

SPECIAL ARTICLE

ESMO recommendations on the use of circulating tumour DNA assays for patients with cancer: a report from the ESMO Precision Medicine Working Group

J. Pascual¹, G. Attard², F.-C. Bidard^{3,4}, G. Curigliano^{5,6}, L. De Mattos-Arruda^{7,8}, M. Diehn⁹, A. Italiano^{10,11,12}, J. Lindberg¹³, J. D. Merker¹⁴, C. Montagut¹⁵, N. Normanno¹⁶, K. Pantel¹⁷, G. Pentheroudakis¹⁸, S. Popat^{19,20}, J. S. Reis-Filho²¹, J. Tie^{22,23}, J. Seoane^{24,25}, N. Tarazona^{26,27}, T. Yoshino²⁸ & N. C. Turner^{19,20*}

<https://doi.org/10.1016/j.annonc.2022.05.520>

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J. Pascual et al.

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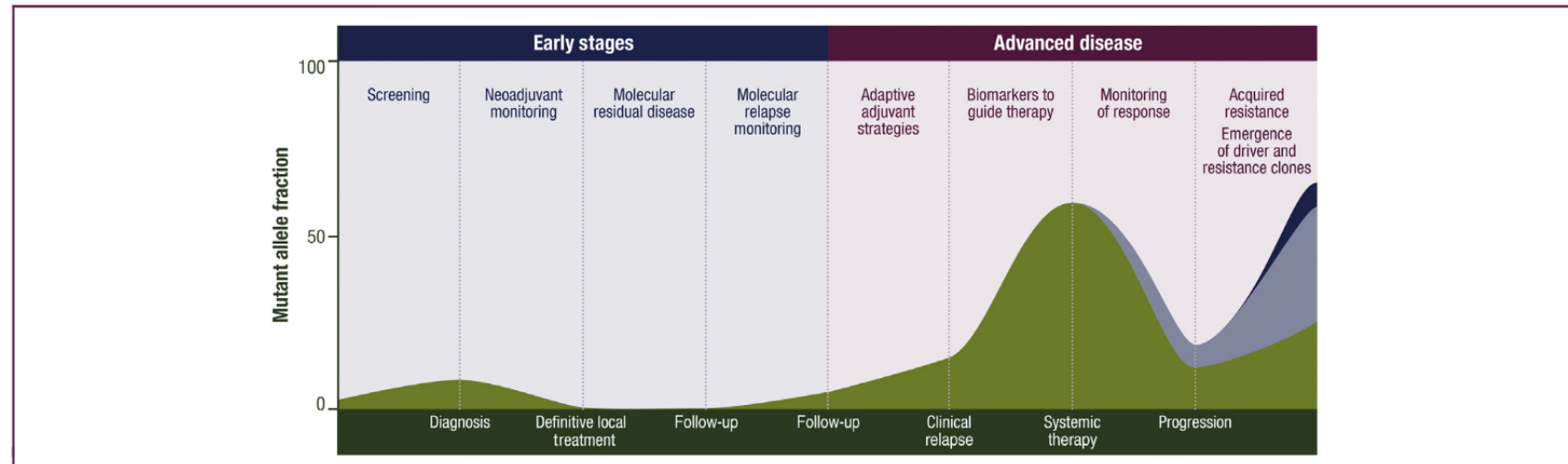
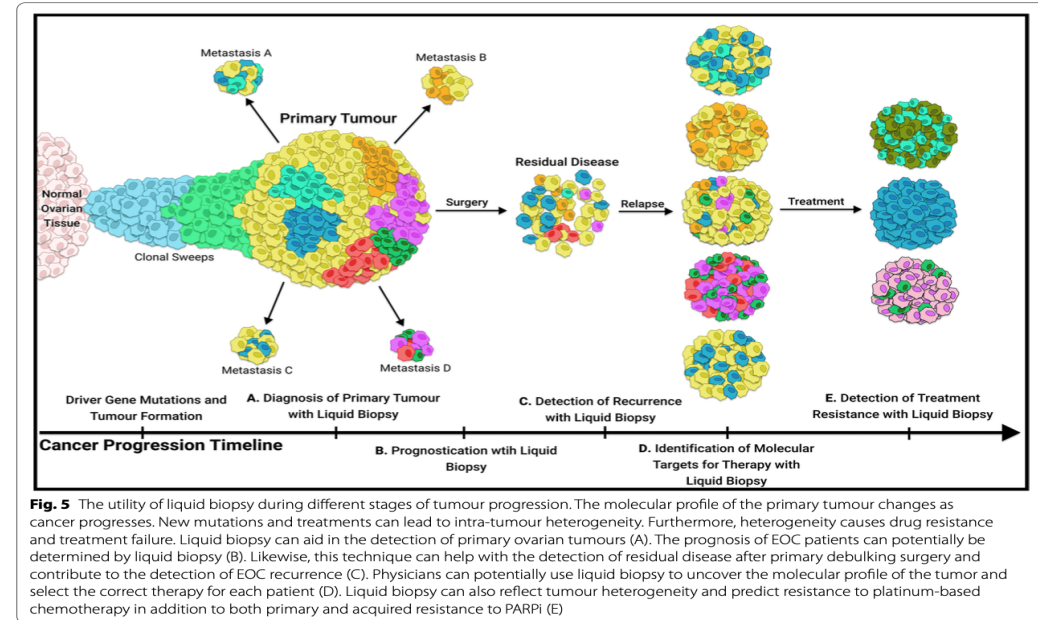
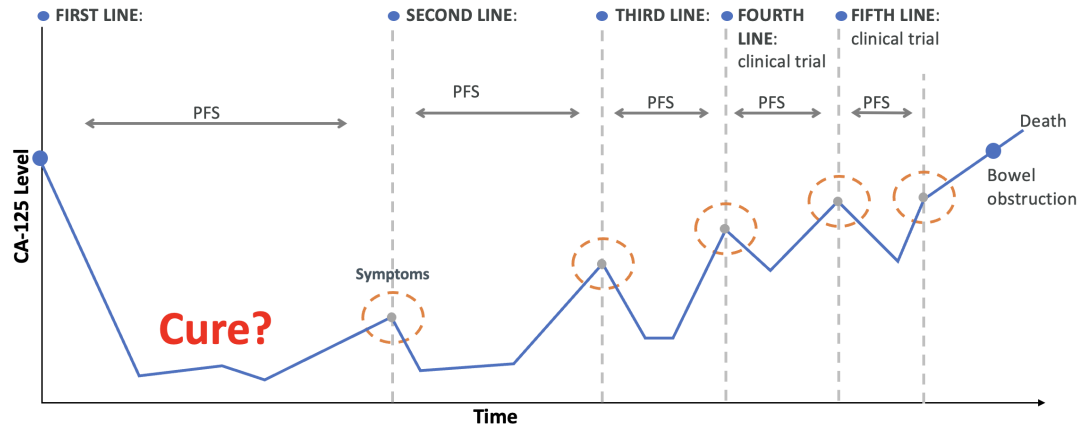


Figure 1. Clinical applications of ctDNA assays for patients with cancer and expected DNA levels in different phases of the disease. ctDNA, circulating tumour DNA.

Advanced cancer ctDNA dynamics for cancer monitoring

In ovarian cancer, pretreatment ctDNA levels and the extent of ctDNA decrease after chemotherapy initiation were significantly associated with time to progression, and were more informative than CA 125 levels

¿Puede ser útil el ctDNA en Cáncer de ovario?



¿Qué herramientas tenemos en práctica clínica para diagnóstico precoz, monitorizar respuesta a tratamiento y detectar recaídas?

CA-125

Naturaleza del Biomarcador

Proteína genérica del epitelio.

Sensibilidad a la Recurrencia Temprana

Baja (A menudo se eleva solo en progresión macroscópica).

Rendimiento bajo PARPi

Pobre (Alta tasa de falsos negativos).

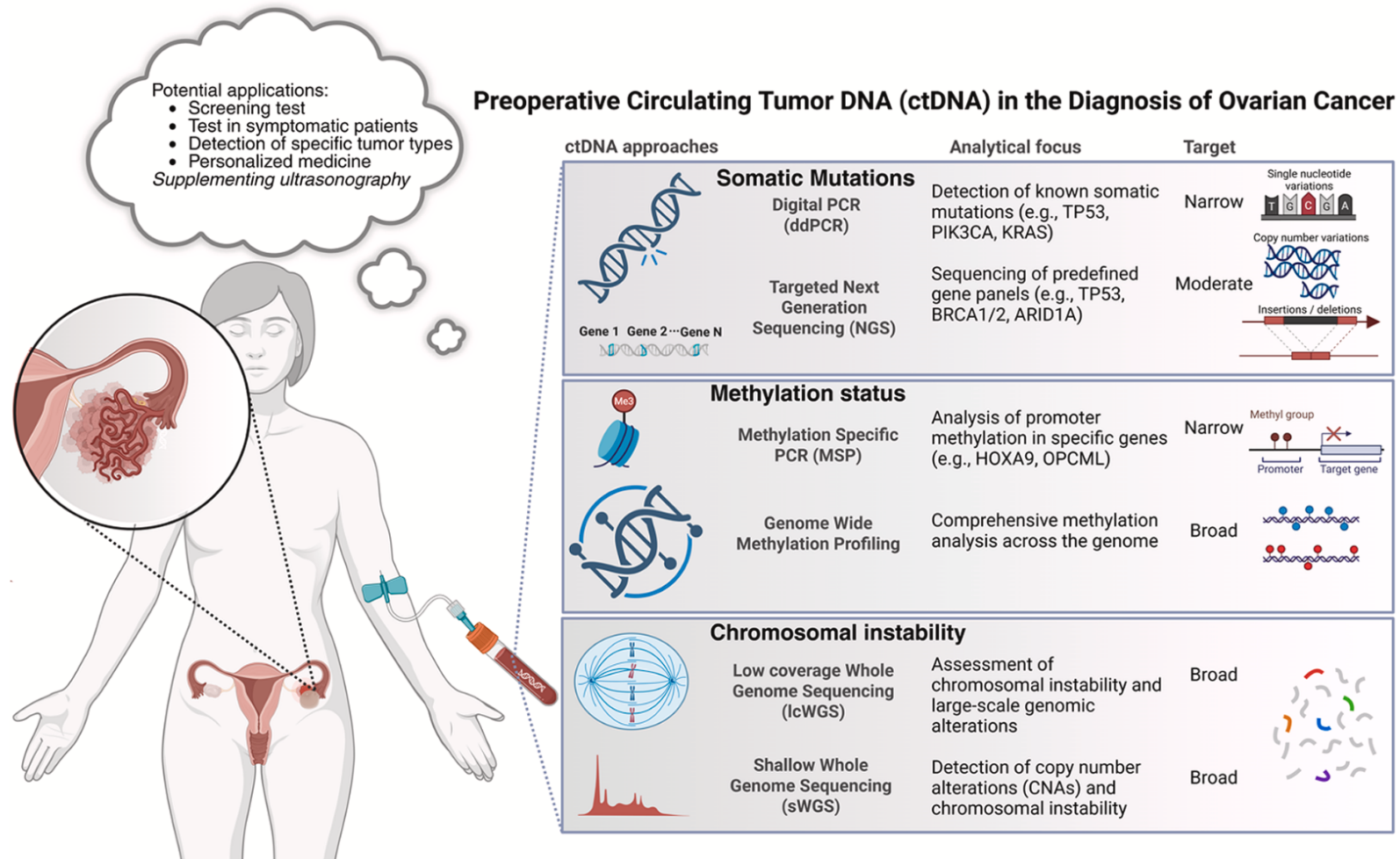
Capacidad Predictiva

Reactiva.

Las herramientas actuales para diagnóstico inicial, detectar recaídas, monitorizar la respuesta al tratamiento, como las pruebas de imagen y el CA-125, a menudo son inconsistentes con los hallazgos clínicos y los resultados de las pacientes.



Utilidad de ctDNA: diagnóstico precoz del cáncer de ovario

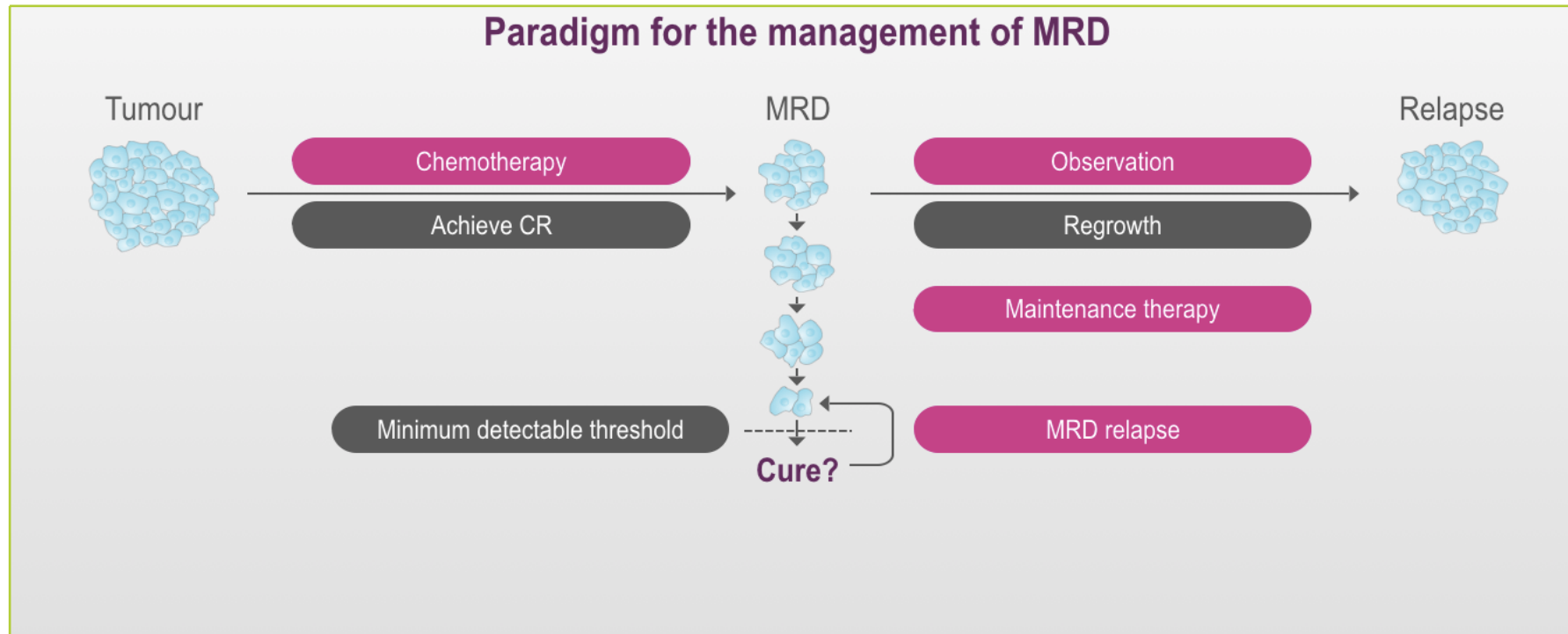


ctDNA is emerging as a highly promising diagnostic biomarker for ovarian cancer. Most studies have focused on the analysis of promoter methylation profiles of various tumor suppressor genes, identifying a strategy that has shown great potential, particularly for the early detection. However or the clinical implementation of liquid biopsy through ctDNA analysis, continued research is necessary to identify the most effective approach for a tumor as highly heterogeneous as ovarian cancer

Figure 3 Preoperative circulating tumor DNA in the diagnosis of ovarian cancer. Schematic overview of circulating tumor DNA-based approaches and their potential clinical applications. CAN, copy number alteration; ctDNA, circulating tumor DNA; ddPCR, droplet digital polymerase chain reaction; lcWGS, low-coverage whole genome sequencing; MSP, methylation-specific polymerase chain reaction; NGS, next-generation sequencing; sWGS; shallow whole genome sequencing.

Importancia de la MRD en el Cáncer de ovario avanzado

Maintenance therapy with PARPis have brought forward a paradigm shift, altering the natural course of disease in ovarian cancer by extending PFS



Goals of maintenance therapy

- 1 Prolong benefit following surgery and chemotherapy
- 2 Improve survival (PFS and hopefully OS)
- 3 Manageable toxicity and no negative effects on QoL

“The essential is invisible to the eyes”

El Principito. Antoine de Saint Exupery



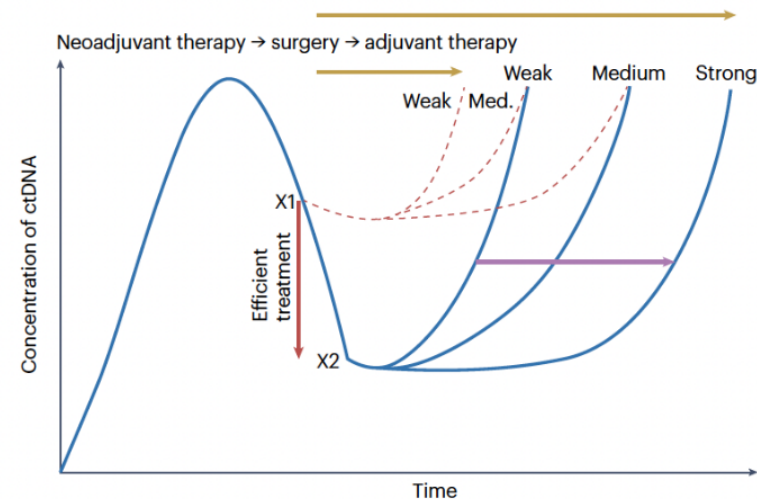
Utilidad de ctDNA: detectar recurrencias

Aplicaciones clínicas del ctDNA en la MRD

Clinical applications – Minimal Residual Disease (MRD)

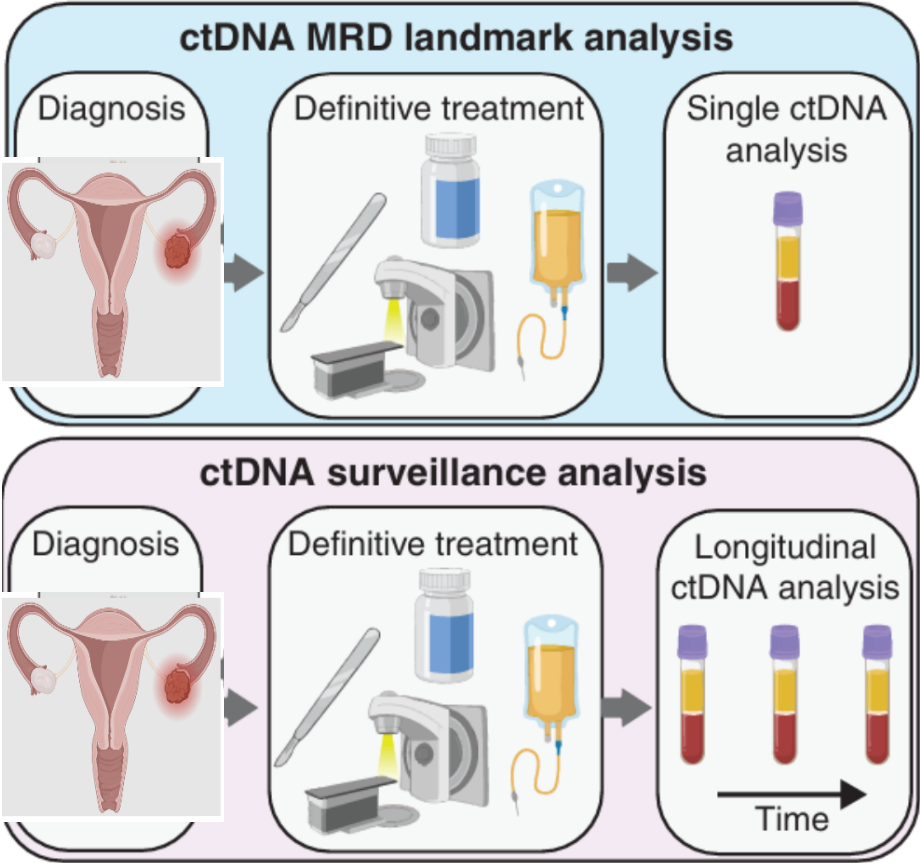
- *Identifying small traces of residual cancer post-treatment*
- *Detecting relapse earlier than imaging, especially at early stages*

- **Role in recurrence prediction:** ctDNA positivity post-surgery predicts relapse risk.
- **Potential for therapy escalation or de-escalation:** Personalizing adjuvant therapy based on MRD status.



Evolution of MRD patients with solid tumors

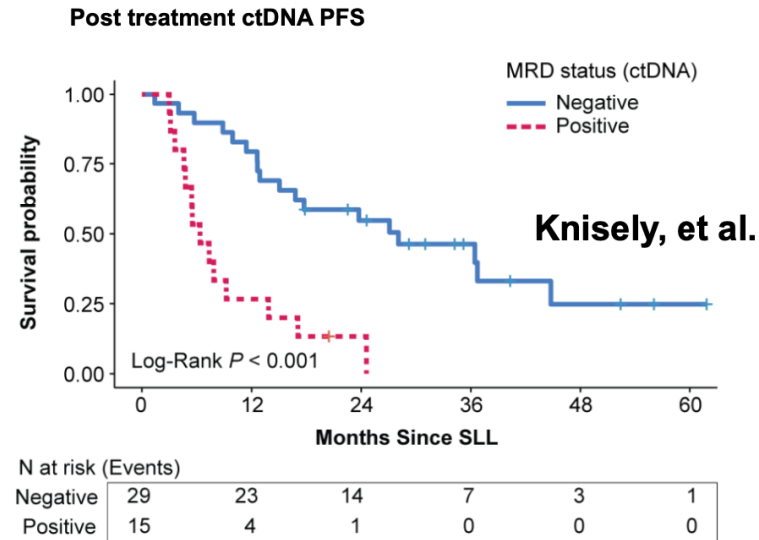
Estrategias de evaluación de ctDNA: landmark vs longitudinal



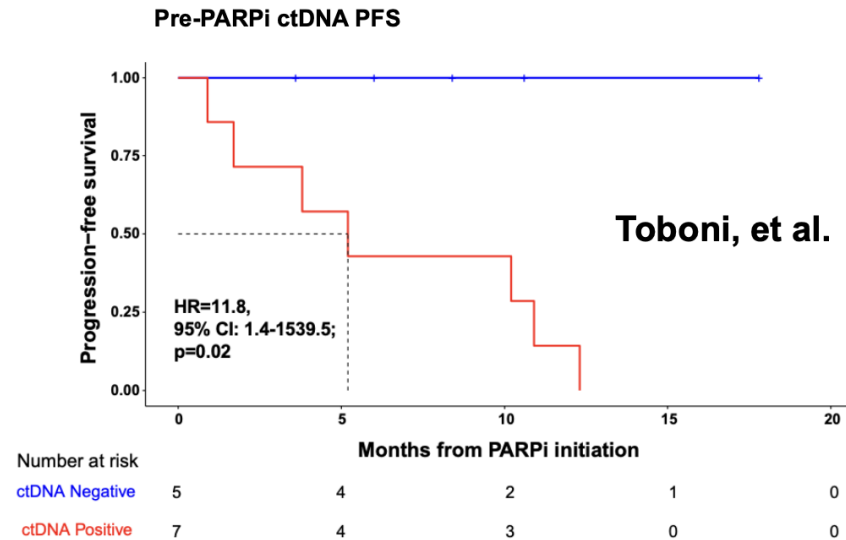
Feature	Landmark Assessment	Longitudinal Assessment
Primary Purpose	Early MRD detection at a fixed time point	Continuous monitoring for recurrence and early relapse detection
Sensitivity	Moderate	Higher due to repeated sampling
Specificity	High when positive	High but may detect transient fluctuations
Logistics	Simpler	Requires repeated draws
Limitations	Timing-dependent, may miss late MRD	More complex interpretation, potential noise

Utilidad de ctDNA: determinar pronóstico

Tumor-informed ctDNA status is highly prognostic



ctDNA negativity in NACT OVCA patients was associated with prolonged PFS, while positivity identified early progression in post-ACT samples.



ctDNA negativity in OVCA patients on PARPi was associated with prolonged PFS.

1. Toboni MD, Gyn Onc 2026.
2. Knisely A, Clin Cancer Res 2025.

Utilidad de ctDNA: monitorizar respuesta y recurrencia al tratamiento



Clinical Performance of a ctDNA Genome Assay to Predict Treatment Response in Patients with Advanced-Stage Ovarian Cancer Receiving Neoadjuvant Chemotherapy

Emily E. O'Brien, MD
University of Alabama at Birmingham
Division of Gynecologic Oncology
O'Neal Comprehensive Cancer Center

Objective

To investigate the utility of ctDNA levels both at baseline and throughout therapy for treatment response and recurrence monitoring in advanced-stage ovarian cancer patients who received NACT

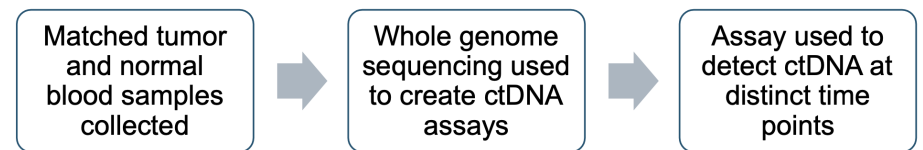
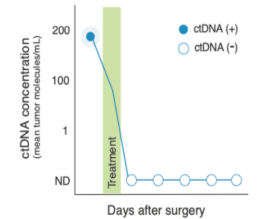
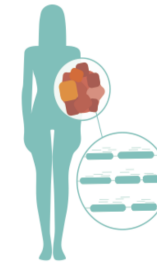
Study Design

Tissue and plasma samples from newly diagnosed, advanced ovarian cancer patients managed with neoadjuvant chemotherapy (NACT) were prospectively banked.

Longitudinal blood samples were collected across four timepoints:



ctDNA assay creation and analysis

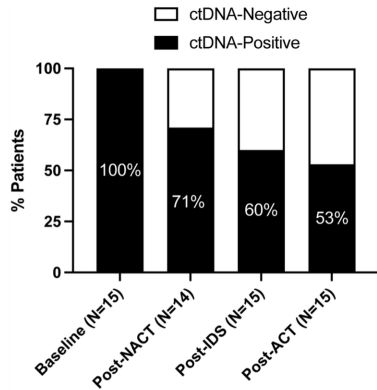


Utilidad de ctDNA: monitorizar respuesta y recurrencia al tratamiento

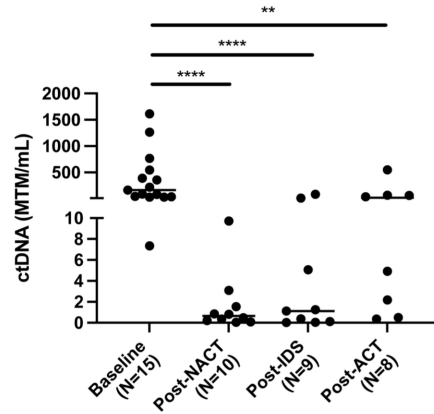
Patient Demographics (N=15)

Variable	Patient N (%)
Median age (years)	65 (46-86)
Race	
White	9 (60%)
African American	6 (40%)
Stage at Diagnosis	
III	11 (73%)
IV	4 (27%)
Debulking Status	
Optimal	15 (100%)
Suboptimal	0 (0%)
Disease Recurrence	
Yes	6 (40%)
No	9 (60%)
Platinum Status at Recurrence	
Sensitive	1 (17%)
Resistant	4 (66%)
Refractory	1 (17%)

ctDNA detection rates and MTM/mL

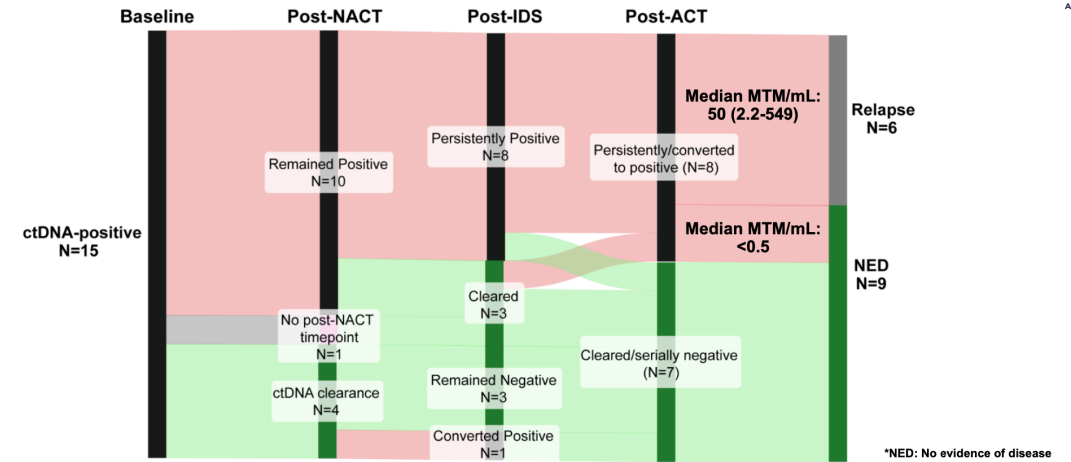


- Baseline ctDNA detection rate was 100%
- Post-ACT ctDNA positivity rate was 53%



- Baseline ctDNA median MTM/mL was 165
- Post-NACT ctDNA detection median MTM/mL was 0.6

Longitudinal ctDNA dynamics across treatment timepoints



All recurrences had a ctDNA-positive result prior to radiographic finding; while ctDNA negativity correlated with 0% recurrence rate. (median follow up: 17.3 months from end of ACT)

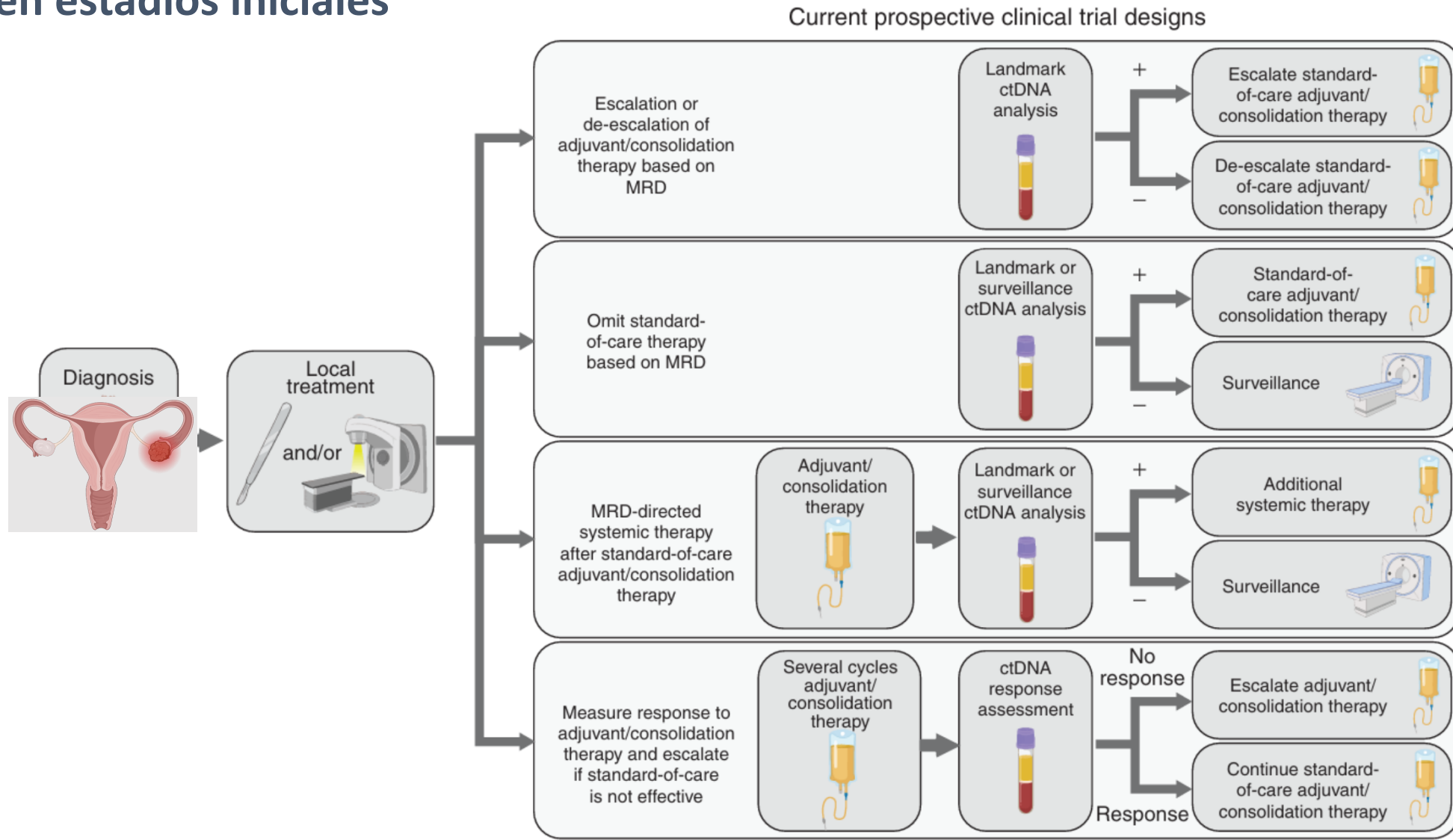
Utilidad de ctDNA: monitorizar respuesta y recurrencia al tratamiento

Evaluación de ctDNA en Cáncer de ovario: herramienta para predecir recurrencia y eficacia

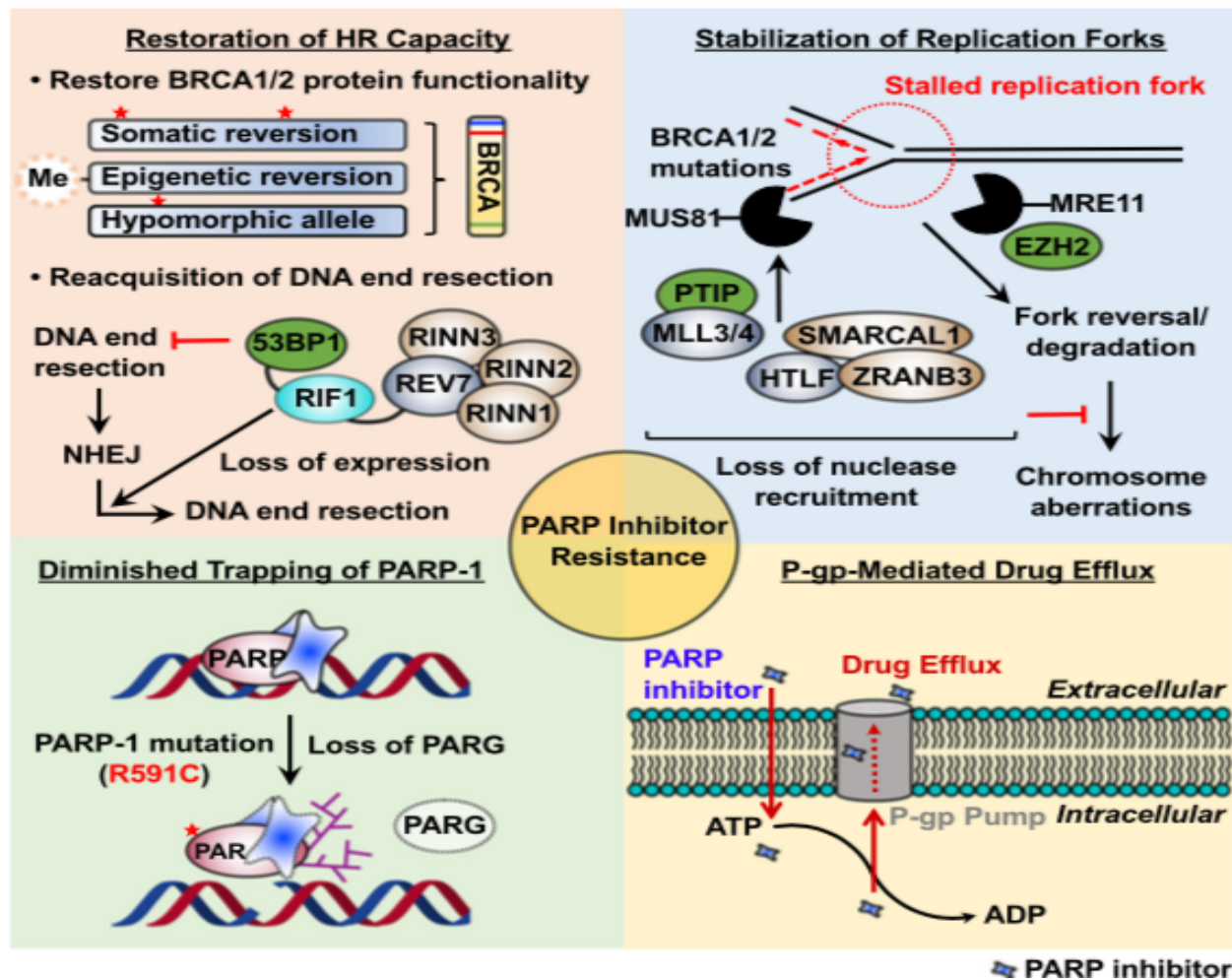
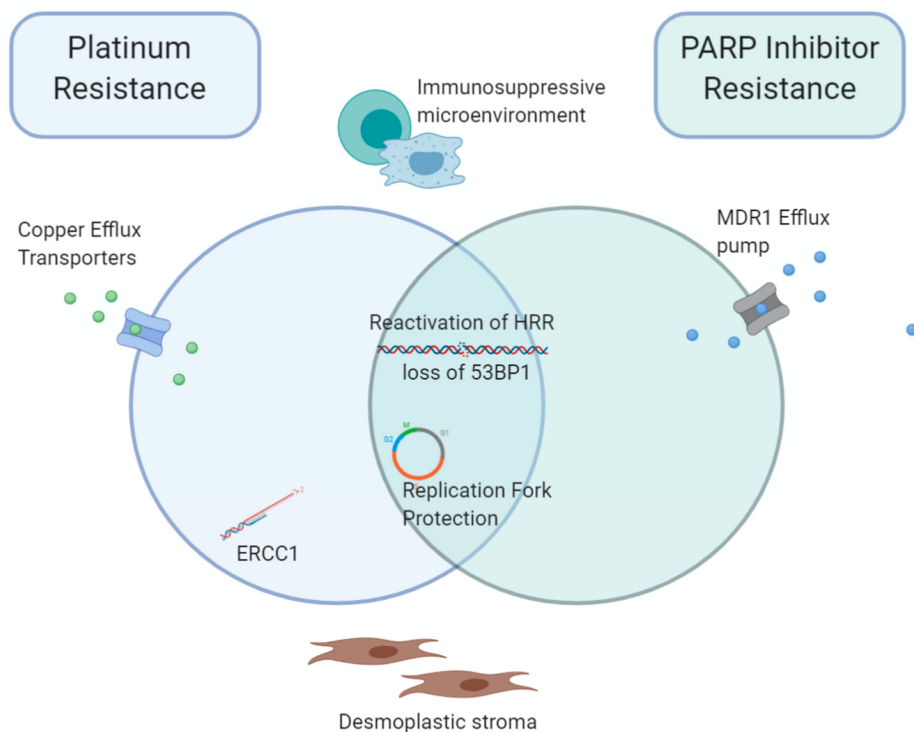
APRIL 10-13, 2026

Study	Setting	Assay	Headline MRD / monitoring signal
Hou 2022	69 Pre-op, postop, surveillance subsets	Tumor-informed panel ctDNA (Signatera)	Detected all 7 relapses in the serial surveillance subset (HR 17); ~10-month average lead over imaging; CA-125 elevation not predictive
Zhang 2024	51 epithelial ovarian cancer after PDS and ACT	ctDNA MRD assay of 1021 sequenced genes	Post-surgery MRD independently associated with relapse-free survival (HR 3.4); all post-ACT + MRD relapsed, outperformed CA 125
Kallio 2024	63 EOC patients undergoing upfront treatment; serial plasma	Tumor guided plasma ctDNA (479-1,856 variants)	Positive last on-treatment sample - shorter progression interval (HR 5.6) and OS (8.2); ctDNA anticipated progression with median lead time 5.9 months.
Glueck 2025	27 advanced ovarian cancer postop after PDS	Personalized tumor-informed dPCR based on WGS	Day-10 postop ctDNA was higher with residual disease (367.38 vs 0.92 copies/mL) and moved in the expected direction with incomplete vs complete resection.
Knisely 2025	Complete clinical response with second-look laparoscopy	Tumor-informed ctDNA	ctDNA positivity separated PFS (6.4 vs 28.1 months), but ctDNA detected only 11 of 22 surgically MRD-positive patients.
Paracchini 2026	172 OVCA post PDS, post chemo, post maintenance bev (MITO16a/ManGO-OV2)	Multimodal ctDNA WGS based tumor fraction	Early postop tumor fraction detectable in 97% outperformed residual tumor (captures MRD); fragmentomics independently stratified PFS/OS risk
Toboni 2026	53 ovarian cancer patients on PARPi maintenance after response to platinum	Personalized tumor-informed Signatera	Pre-PARPi ctDNA 58% (7/12); early persistent or converted + on PARPi marked shorter PFS; no ctDNA-negative patient recurred at last follow-up; ctDNA outperformed CA-125 / BRCA-HR status.

Futuro.. Incorporación del análisis de ctDNA en el diseño de los ensayos clínicos en estadios iniciales



Mecanismos de resistencia a iPARP y platino



Los principales mecanismos descritos hasta la fecha se relacionan con la restauración de la reparación de la recombinación homóloga y la estabilización de las horquillas de replicación.

Utilidad de ctDNA: Predecir /monitorizar respuesta al tratamiento

Mutaciones de reversión de BRCA en ctDNA: predicción de resistencias primarias y adquiridas a iPARP.

Múltiples mutaciones de reversión pueden presentarse en un paciente individual.

BRCA Reversion Mutations and Resistance to PARP Inhibitor

RESEARCH BRIEF

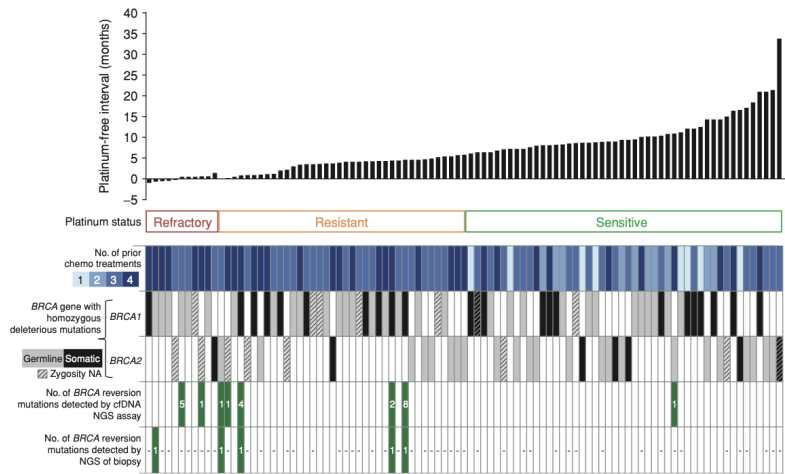
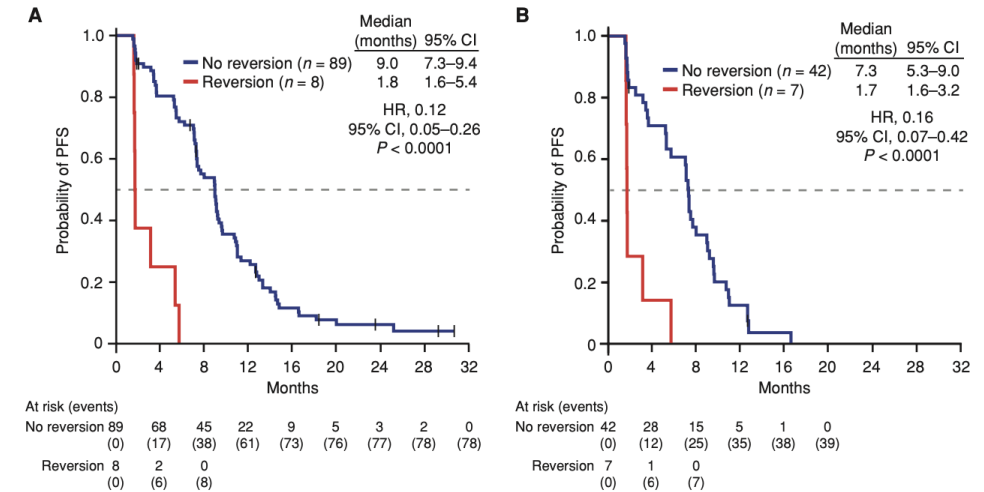


Figure 1. Detection of *BRCA* reversion mutations in pretreatment cfDNA and tumor biopsy. The platinum-free interval and platinum status is based on the patient's most recent platinum-based treatment. The primary deleterious *BRCA* mutations are categorized based on their germline or somatic origin. All tumors with evaluable zygosity of the *BRCA* mutation were found to be homozygous; tumors with indeterminate zygosity are indicated with hatching. The number of *BRCA* reversion mutations detected by each assay is indicated; an empty cell denotes that no reversion mutation was detected. A dash within a cell denotes a pretreatment tumor biopsy sample was not available for sequencing.

BRCA Reversion Mutations and Resistance to PARP Inhibitor

RESEARCH BRIEF



ABSTRACT

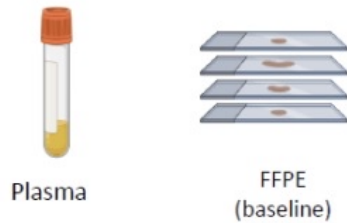
A key resistance mechanism to platinum-based chemotherapies and PARP inhibitors in *BRCA*-mutant cancers is the acquisition of *BRCA* reversion mutations that restore protein function. To estimate the prevalence of *BRCA* reversion mutations in high-grade ovarian carcinoma (HGOC), we performed targeted next-generation sequencing of circulating cell-free DNA (cfDNA) extracted from pretreatment and postprogression plasma in patients with deleterious germline or somatic *BRCA* mutations treated with the PARP inhibitor rucaparib. *BRCA* reversion mutations were identified in pretreatment cfDNA from 18% (2/11) of platinum-refractory and 13% (5/38) of platinum-resistant cancers, compared with 2% (1/48) of platinum-sensitive cancers ($P = 0.049$). Patients without *BRCA* reversion mutations detected in pretreatment cfDNA had significantly longer rucaparib progression-free survival than those with reversion mutations (median, 9.0 vs. 1.8 months; HR, 0.12; $P < 0.0001$). To study acquired resistance, we sequenced 78 postprogression cfDNA, identifying eight additional patients with *BRCA* reversion mutations not found in pretreatment cfDNA.

SIGNIFICANCE: *BRCA* reversion mutations are detected in cfDNA from platinum-resistant or platinum-refractory HGOC and are associated with decreased clinical benefit from rucaparib treatment. Sequencing of cfDNA can detect multiple *BRCA* reversion mutations, highlighting the ability to capture multiclonal heterogeneity.

LIBINI (GEICO 155-T)

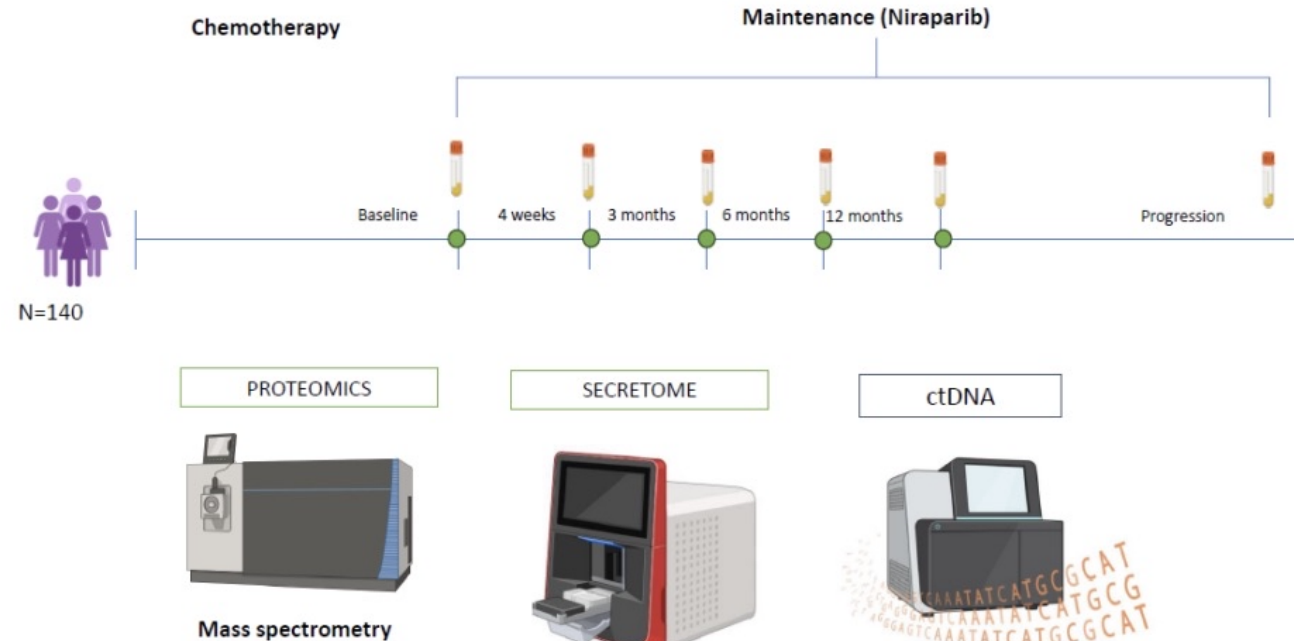
Liquid Biopsy for predicting Niraparib benefit in 1st line

Samples and storage



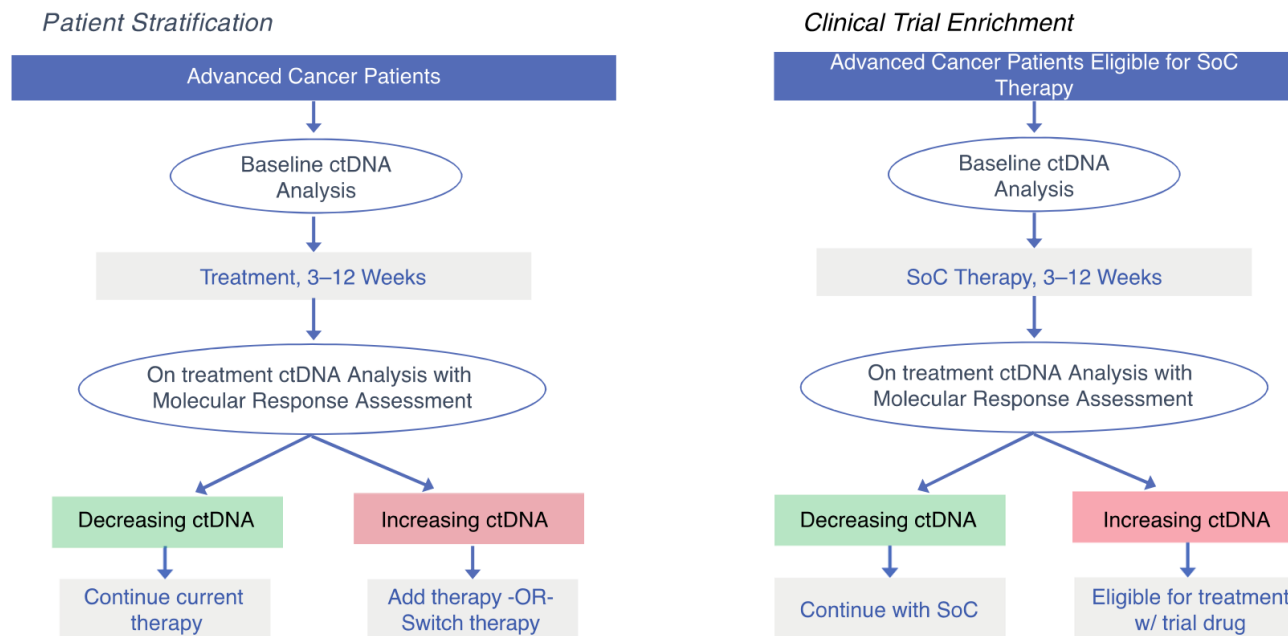
Biobanco Universidad de Navarra

Sample schedule

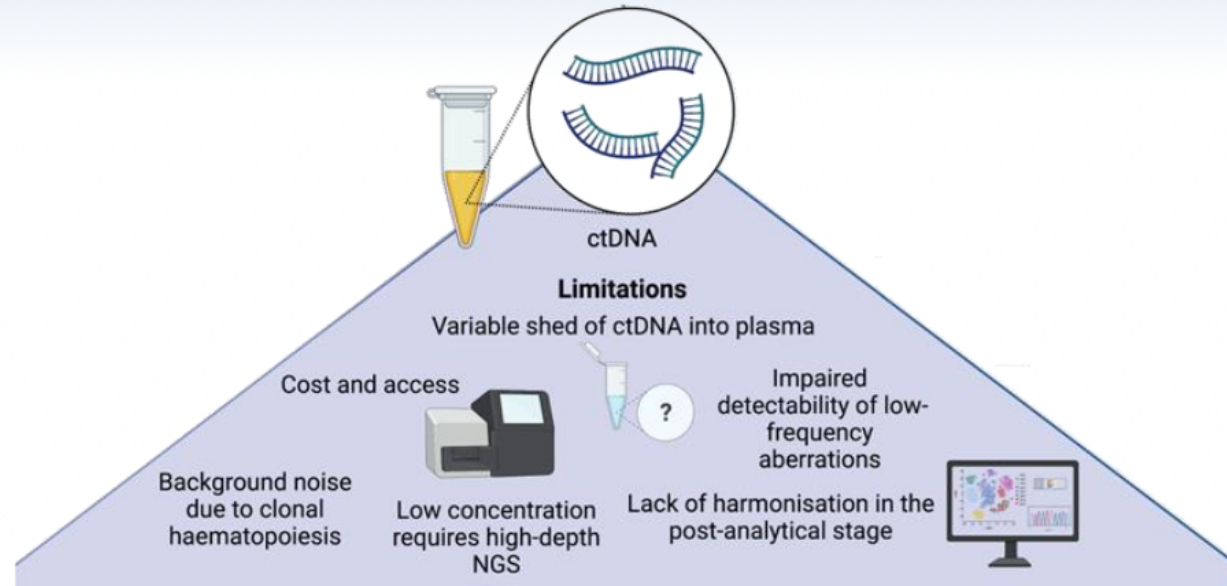


Futuro.. Incorporación del análisis de ctDNA en el diseño de los ensayos clínicos en estadios avanzados

Making clinical decisions based on ctDNA results



Pitfalls and Challenges



Technical challenges

- Sensitivity of detection method – due to low abundance
- False Positive/Negatives – non-tumor-derived cfDNA mutations
 - Standardization of (pre)-analytical protocols → **ELBS**

Biological limitations

- Low ctDNA levels in Early-Stage Cancers & MRC
- Tumor Heterogeneity and ctDNA shedding

Cost and Accessibility

- High cost – Sequencing technologies and assays can be expensive
 - Limited accessibility



Future Directions

- **Future improvements in sequencing technologies** - aim to enhance the sensitivity and specificity of ctDNA detection



- ✓ Ultra-sensitive next-generation sequencing (NGS)
- ✓ Whole-genome sequencing (WGS),
- ✓ Single-molecule sequencing



- **Exploration of ctDNA biological roles beyond a biomarker**

- **Integration with AI and multi-omics approaches**



- ✓ Integrating AI with ctDNA analysis facilitates the interpretation of complex genomic data.



- ✓ Machine learning algorithms can identify patterns and predict treatment responses, thereby personalizing cancer therapy

Take home message in 2026

Lo que el ctDNA puede hacer ahora

- ✓ Identificar pacientes de alto riesgo después de la cirugía o terapia de primera línea.
- ✓ Detectar la recurrencia molecular antes que la confirmación estándar en algunos pacientes.
- ✓ Complementar el CA-125 y las imágenes cuando las decisiones de vigilancia son inciertas.
- ✓ Monitorear potencialmente el riesgo molecular durante el mantenimiento con PARPi (Toboni 2026).

Lo que el ctDNA aún no puede hacer

- ✗ Reemplazar las imágenes o la evaluación clínica como estrategia de vigilancia única.
- ✗ Descartar enfermedad peritoneal microscópica con una sola muestra de plasma.
- ✗ Justificar la intensificación o desintensificación rutinaria del tratamiento fuera de protocolos basados en evidencia.
- ✗ Aplicarse por igual en todas las histologías ováricas con la misma confianza.

El desarrollo de ensayos posoperatorios más sensibles, la aplicación de enfoques multimodales de fracción tumoral / fragmentómica, y la incorporación de estudios de mantenimiento guiados por ctDNA o intervenciones basadas en EMR son los pasos lógicos a seguir.

CONCLUSIONES

ctDNA en cáncer de ovario



1. El ctDNA es una herramienta prometedora para avanzar hacia una monitorización más dinámica y personalizada del cáncer de ovario.



2. Supera las limitaciones actuales Frente al CA-125 y la imagen, el ctDNA ofrece una evaluación en tiempo real de la carga tumoral, la respuesta al tratamiento y la evolución clonal.



3. Monitorización longitudinal = información clave

- Identificar precozmente resistencia.
- Detectar recaídas moleculares antes de la progresión clínica.
- Mejorar la estratificación pronóstica.



4. El ctDNA y la MRD: el escenario con mayor potencial

- Detectar enfermedad mínima residual.
- Guiar decisiones en mantenimiento.
- Vehículo hacia estrategias de escalada/desescalada terapéutica.



5. Comprender la resistencia para anticiparnos

- El ctDNA permite detectar mecanismos de resistencia, como las mutaciones de reversión BRCA y la restauración de la recombinación homóloga.
- Información clave para orientar decisiones futuras.



6. Retos importantes por superar

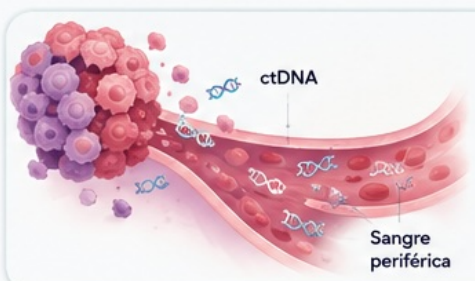
- Sensibilidad en tumores con bajo shedding.
- Estandarización de plataformas y puntos de corte.
- Validación prospectiva.
- Demostración de utilidad clínica real.



7. ¿Dónde estamos hoy?
El ctDNA tiene gran validez biológica y pronóstica, pero aún necesitamos estudios prospectivos que demuestren que actuar sobre esta información mejora los resultados clínicos.



8. Hacia una nueva oncología
Estamos pasando de una oncología basada en la anatomía a una oncología **dinámica, molecular y evolutiva**.



MENSAJE FINAL

“ El ctDNA no solo nos permite observar el tumor; nos permite seguir su evolución en tiempo real y comprender cómo cambia bajo presión terapéutica. ”



★ Mucho camino por recorrer, pero el futuro es prometedor.
El ctDNA puede convertirse en un cambio de paradigma en el manejo del cáncer de ovario.





Muchas Gracias



SERVIZO
GALEGO
de SAÚDE

Complexo Hospitalario Universitario
A Coruña



instituto de
investigación biomédica
de a coruña

**4^a Jornada
de Actualización en
Cáncer Ginecológico**
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