New Orleans Summer Cancer Meeting

Cancer Genetic Risk Factors:

What's New and What You Need to Know?





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July 19, 2024

OBJECTIVES

- Identify basics of cancer genetics
- Recognize differences in somatic and germline testing
- Describe possible outcomes in germline testing and interpreting variant of uncertain significance (VUS)
- Demonstrate current NCCN guidelines for germline testing
- Acquire knowledge on ASCO updates for germline testing









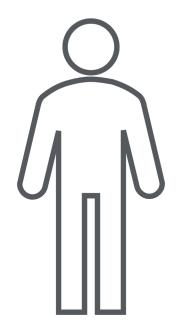


BASICS OF CANCER GENETICS













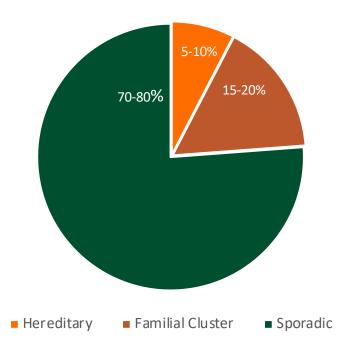








CAUSES OF CANCER



SPORADIC:

Majority of cancers

HEREDITARY:

- >50 single-gene syndromes identified
- Growing number of low/moderate-risk genes

FAMILIAL CLUSTER:

- Possible unidentified single-gene pathogenic variant
- Shared environment or shared genetic





SOMATIC
TESTING
&
GERMLINE
TESTING



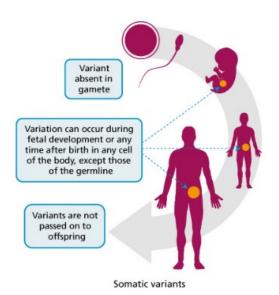




SOMATIC VS GERMLINE

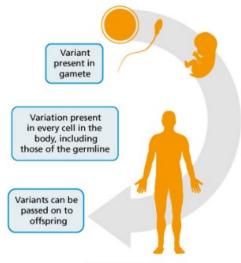
SOMATIC MUTATIONS:

- · Occurs in non-reproductive cells
- Only affecting the tissues derived from the altered cell
- Can be used for prediction, prognosis, and diagnosis

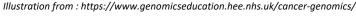


GERMLINE MUTATIONS:

- Occurs in reproductive cells (sperm or egg cells)
- Potentially being passed on to subsequent generations











BASIC INDICATIONS FOR GERMLINE TESTING



- Early onset of cancer(s)
- Multiple family members on the same side with same cancer(s)
- Known genetic mutations (or pathogenic variants) in the family
- Ashkenazi Jewish Ancestry
- Multiple cancers in an individual
- Close degree of affected individual(s) or affected individual with diagnosis at any age (pancreatic cancer, ovarian cancer, metastatic prostate cancer, triple negative breast cancer)
- Rare cancers such as breast cancer in male or retinoblastoma
- Cluster of affected individuals on the same side of the family
- Bilateral cancer in the same organ (such as breast or renal cancer)
- Many colon polyps (>20 adenomas)





INTERPRETING GERMLINE TESTING: VARIANT CLASSIFICATIONS

Pathogenic

Likely Pathogenic

Uncertain Significance Likely Benign

Benign



Alteration which directly contributes to disease development



Alteration which is very likely to contribute to disease development, but evidence is insufficient to conclusively prove



Alteration detected but no evidence to support a classification



Alteration which is not likely to contribute to disease development, but evidence is insufficient to conclusively prove



Alteration which does not cause disease





CONSIDERATIONS FOR VARIANTS OF UNCERTAIN SIGNIFANCE (VUS)

- Are common with use of large multi-gene panels
- Are more common in racial and ethnic minorities compared with non-Hispanic white individuals
- When reclassified, approximately 80%–90% are reclassified as likely benign or benign and 10%–20% as P/LP

While VUS are part of genetic testing results, they should be interpreted cautiously and not used in isolation to dictate medical management.

- Collaborate with genetic specialists
- Consider broader health contexts are essential for making informed decisions about screening and risk reduction strategies





CONSIDERATIONS FOR VUS – TO TEST OR NOT TO TEST?



- Base medical management decisions on personal and family medical histories
- Consider factors like symptoms and age of onset
- TESTING FAMILY MEMBERS FOR VUS
 - Generally, not recommended unless there is clinical suspicion of a genetic condition that could be clarified by additional testing
 - Specific circumstances include cases where the VUS may explain a genetic condition, providing insight into inheritance patterns or phenotypic expression



VUS: RNA ANALYSIS AND RESEARCH STUDIES

RNA CAN BE HELPFUL WITH VUS

- Determine whether a variant affects the expression or function of a gene by analyzing how it influences RNA transcripts
- Useful for variants where the effect on protein function or gene regulation is uncertain based on DNA analysis alone

RESEARCH STUDIES IN VUS

- Consider referral to research studies aimed at defining the functional impact of variants can be beneficial
- Often conducted by clinical laboratories or registries specializing in variant reclassification
- Aim to gather additional data over time to better understand the clinical implications of variants
- Participation can lead to updated classifications of variants as more evidence becomes available

RESOURCES

For current data of classification status such as: https://www.ncbi.nlm.nih.gov/clinvar/,
 https://www.cangene-canvaruk.org/canvig-uk





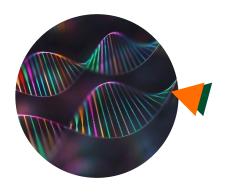
CURRENT NCCN GUIDELINES







FOR HEREDITARY CANCER TESTING- VERSION 3.2024



GENERAL TESTING CRITERIA:

- Individual with any blood relative with a known Pathogenic /
 Likely Pathogenic (P/LP) variant in cancer susceptibility gene
- Individual with previous limited testing
 - I.e.: single gene/absent deletion/duplication) who meets testing criteria for multigene panel
- P/LP variant identified on tumor genomic testing
- To aid in systemic therapy or surgical decisions
- Individual who meets Li-Fraumeni Syndrome (LFS) or Cowden (PTEN) or Lynch Syndrome (LS) testing criteria
- Testing may be considered in:
 - Ashkenazi Jewish ancestry without other risk factors and personal history of serous endometrial cancer





CURRENT NCCN GUIDELINES FOR HEREDITARY CANCER **TESTING- VERSION 3.2024**



OVARIAN:

Epithelial ovarian (including fallopian tube cancer or peritoneal cancer) at any age



PANCREATIC:

 All individuals diagnosed with exocrine pancreatic cancer





FOR HEREDITARY CANCER TESTING- VERSION 3.2024



PROSTATE:

- Metastatic (any age)
- High or Very High-risk group: cT3a to cT4, Grade group 4,
 Grade Group 5, Gleason pattern 5, PSA > 20 ng/mL
- Ancestry: Ashkenazi Jewish ancestry
- Prostate cancer at any age with family history of ≥1 close blood relative with ANY: breast cancer at age ≤50, male breast cancer, triple negative breast cancer, ovarian cancer, pancreatic cancer, prostate cancer with metastatic, or high- or very-high-risk group or ≥3 diagnoses of breast and/or prostate cancer (any grade) on the same side of the family including the patient with prostate cancer





CURRENT NCCN GUIDELINES FOR HEREDITARY CANCER **TESTING- VERSION 3.2024**



COLORECTAL- Lynch Syndrome Criteria

- < 50 at diagnosis
- Known MMR deficiency in tumor at any age
- Synchronous or metachronous CRC
- CRC at any age with family history of : ≥1 close blood relative with Lynch Syndrome (LS) cancer at <50 or ≥2 close blood relatives with LS related cancer at any age

COLORECTAL- Adenomatous Polyposis Criteria

- Personal history of ≥ 20 cumulative adenomas
- Known PV/LP in polyposis gene
- Multifocal/bilateral congenital hypertrophy of retinal pigment epithelium (CHRPE)
- Consider testing if: 10-19 cumulative adenomas, desmoid tumor, hepatoblastoma, cribriformmorular variant of papillary thyroid cancer, unilateral CHRPF





FOR HEREDITARY CANCER TESTING- VERSION 3.2024



BREAST:

- Diagnosis at ≤50 years
- To aid in systemic treatment decisions using PARP inhibitors for breast cancer in the metastatic setting or adjuvant setting in HER2
- Triple Negative Breast, Multiple primary breast cancers (synchronous or metachronous), Lobular breast cancer with personal or family history of diffuse gastric cancer
- Male breast cancer
- Ancestry: Ashkenazi Jewish ancestry
- Breast cancer at any age with family history of ≥1 close blood relative with ANY: breast cancer at age ≤50, male breast cancer, ovarian cancer, pancreatic cancer, prostate cancer with metastatic, or high- or very-highrisk group or ≥3 diagnoses of breast and/or prostate cancer (any grade) on the same side of the family including the patient with breast cancer











Germline Testing in Patients With Breast Cancer: ASCO-Society of Surgical Oncology Guideline

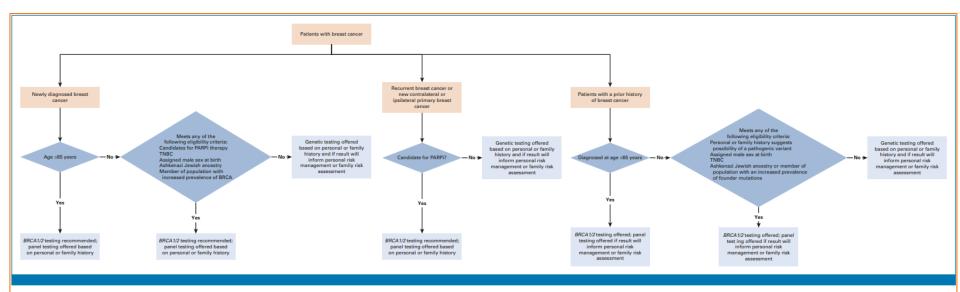


FIG 1. Algorithm for Germline Testing in Patients with Breast Cancer Abbreviations. PARPi, poly(ADP-ribose) polymerase inhibitors; TNBC, triple-negative breast cancer.







ASCO Update: Selection of Germline Genetic Testing Panels in Patients With Cancer

KEY CONSIDERATIONS WITH GERMLINE TESTING:

- Detailed family history taken (details of cancer, first- and seconddegree relatives and ethnicity)
- Multigene panel should be offered if > 1 gene is relevant based on personal or family history
- Patients who meet criteria for germline genetic testing should be offered germline testing regardless of results from tumor testing
- Patients who would not normally be offered germline genetic
 testing based on personal and/or family history criteria but who
 have a pathogenic or likely pathogenic variant identified by tumor
 testing should be offered germline testing





ASCO UPDATE: CONTINUED

WHEN CONSIDERING WHAT GENES TO INCLUDE IN THE PANEL, THE MINIMAL PANEL SHOULD INCLUDE:

- The more strongly recommended genes from Table 1 and may include those less strongly recommended.
- A broader panel may be ordered when the potential benefits are clearly identified, and the potential harms from uncertain results should be mitigated.

TABLE 1. Genes Recommended for Testing and Inclusion in Multigene Panels for Selected Cancers

Cancer Type and Specific Population	More Strongly Recommended (higher relative risk of cancer or highly actionable)	Less Strongly Recommended (moderate relative risk of cancer or potential impact for therapy/change in medical management)
Breast cancer	BRCA1, BRCA2, PALB2 CDH1," PTEN," STK11," TP53°,°	ATM, BARD1, CHEK2, RAD51C, RAD51D NF1 ^{ab}
Colorectal cancer	APC, EPCAM, MLH1, MSH2, MSH6, MUTYH, ⁴ NTHL1, ⁴ PMS2, POLD1, POLE BMPR1A, ⁸ SMAD4, ⁸ STK11, ⁸ TP53 ^{8,6}	AXIN2, CHEK2, MBD4 GREM1," MSH3," PTEN," RNF43"
Endometrial cancer	EPCAM, MLH1, MSH2, MSH6, PMS2 PTEN, ^a STK11 ^a	NA
Gastric cancer	APC, CTNNA1, EPCAM, MLH1, MSH2, MSH6, PMS2 BMPR1A," CDH1," SMAD4," STK11"	NA
Gastrointestinal stromal tumors	KIT, PDGFRA If SDH-deficient or SDH-mutant tumor: SDHA, SDHAF2, SDHB, SDHC, SDHD If NF1-mutated tumor: NF1	If tumor is not SDH-deficient, SDH-mutated, or NF1- mutated: NF1, SDHA, SDHAF2, SDHB, SDHC, SDHD
Medullary thyroid carcinoma	RET	NA
Non-small cell lung cancer—if EGFR tumor pathogenic variant (such as p.T790M) found with no previous EGFR-TKI therapy	EGFR STK11 ^a	TP53**
Adrenocortical tumors	APC, EPCAM, MEN1, MLH1, MSH2, MSH6, PMS2, TP53	NA
Melanoma, cutaneous	CDKN2A, CDK4	BAP1, MC1R, MITF, POT1, TERT PTEN ^a
Melanoma, uveal	BAP1	NA
Ovarian cancer (epithelial)	BRCA1, BRCA2, BRIP1, EPCAM, MLH1, MSH2, MSH6, PALB2, PMS2, RAD51C, RAD51D	ATM
Pancreatic adenocarcinoma	ATM, BRCA1, BRCA2, CDK4, CDKN2A, EPCAM, MLH1, MSH2, MSH6, PALB2, PMS2 STK11, a TP53ac	APC
Phaeochromocytomas and paragangliomas	FH, MAX, RET, SDHA, SDHB, SDHC, SDHD, TMEM127 NF1°, VHL°	EGLN1, EPAS1, KIF1B, MET, SDHAF2
Prostate cancer	BRCA1, BRCA2, EPCAM, HOXB13, MLH1, MSH2, MSH6, PMS2	ATM, CHEK2, PALB2
Renal cell carcinoma	BAP1, FH, FLCN, MET, SDHA, SDHAF2, SDHB, SDHC, SDHD PTEN ^a , VHL ^a	TSC1°, TSC2°
Sarcoma (soft tissue or osteosarcoma)	TP53 ^{a,c}	NF1ª, RB1ª





ASCO UPDATE: CONTINUED

ALL PATIENTS WITH PATHOGENIC VARIANTS IDENTIFIED IN TUMOR TESTING WHICH WARRANT GERMLINE TESTING:

- BRCA1, BRCA2, BRIP1, MLH1, MSH2, MSH6, MUTYH (when biallelic), PALB2, PMS2, RAD51C, RAD51D, RET, SDHAF2, SDHB, SDHD, TMEM127, TSC2, VHL
- Test only if patient <30 years old: APC, PTEN, RB1, TP53 (brain tumors excluded)

PATIENTS WITH PATHOGENIC VARIANTS IDENTIFIED IN TUMOR TESTING MAY BE OFFERED GERMLINE TESTING:

- ATM, BAP1, BARD1, CHEK2, DICER1, FH, FLCN, NF1, POLD1, POLE, SDHA
- Test only if patient < 30 years old: CDKN2A, SMARCA4















Key Points from Universal Germline and Tumor Genomic Testing Needed to Win the War Against Cancer: Genomics is the Diagnosis by Vivek Subbiah et al in the Journal of Clinical Oncology in June 2023

- Updated viewpoint from universal somatic testing to also include universal germline testing to win war against cancer because only somatic testing is insufficient for identifying inherited cancer risks in relatives
- Germline testing allows for proactive management and tailored interventions if predisposition identified and can assist in reducing apprehension about cancer risk in those who are identified as non-carriers
- It transforms outcomes for traditional hereditary syndromes and identifies broader associations and risks from germline variants
- Comprehensive genetic insights are crucial for effective cancer treatment and early detection strategies

<u>Vivek Subbiah et al.</u>, Universal Germline and Tumor Genomic Testing Needed to Win the War Against Cancer: *Genomics Is the Diagnosis. JCO* 41, 3100-3103(2023).DOI: 10.1200/JCO.22.02833

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Key Points from Universal Germline and Tumor Genomic Testing Needed to Win the War Against Cancer: Continued

- CHALLENGES IN IMPLEMENTING UNIVERSAL GENOMIC TESTING (SOMATIC AND GERMLINE) INCLUDE:
 - Logistics
 - Insurance coverage
 - Need for education
- Access to well-trained genetic counselors is crucial for effective family member testing and counseling as part of genomic services
- INNOVATIVE SOLUTIONS OUTLINED IN THE ASCO EDUCATIONAL HANDBOOK INCLUDE:
 - Telegenetics
 - Group genetic counseling
 - Collaboration with non-genetics healthcare professionals
 - Genetic counselor extenders
 - Modifications of traditional counseling models





UNIVERSAL TESTING VS GUIDELINE-DIRECTED TESTING IN CANCER

Multisite study (Interrogating Cancer Etiology Using Proactive Genetic Testing [INTERCEPT] program) within Mayo Clinic (Rochester, Minnesota, Jacksonville and Phoenix) in patients with solid tumors from 4/1/18 to 3/31/20.



POPULATION

- Inclusion:
 - English-speaking adult (18-85 years of age)
 - new or active cancer diagnosis of carcinoma
 - treated at any of the Mayo Clinic Cancer Centers
- Exclusion:
 - · Hematologic malignant cancers
 - Cancer survivors



METHOD

- Patients were unselected for various items such as:
 - cancer type
 - stage of disease
 - Family history of cancer
 - race/ethnicity
 - age



METHOD

- Patients viewed a standardized pretest education video (also offered additional pretest genetic counseling)
- Testing with panel of 83 genes (84 genes as of July 2019) with Invitae Multi-Cancer panel (at no cost)
- All test results were reviewed by a certified genetic counselor, results disclosed to the patient and those with PGVs were invited for genetic counseling.

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- 2984 patients
- PGV were found in 397 patients (13.3%)
 - 282 moderate to high penetrance genes
- VUS were found in 1415 patients (47.4%)
- Clinically actionable findings in 192 patients (6.4%)
 - Would not have been detected if by phenotype or family history testing criteria
 - 42 patients (28.2%) had modifications to treatment



- Universal multigene panel testing in solid tumor patients was noted to have increased detection of PGV over the predicted target testing guidelines alone
- Almost 30% of patients with high penetrant genes had change in therapy











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