Overview of Most Commonly Used Genetic Testing Options for People with Epilepsy

Test Name	Region of Genome Analyzed	PROS	CONS
Next Generation Sequencing (NGS) Multi- Gene Panel (MGP)	Specific genes (currently) recognized to be associated with epilepsy (range in 2024: 20 to >1,000 genes depending on panel)	<ul> <li>A curated and focused set of genes, so least likely to get incidental findings</li> <li>High NGS depth of coverage</li> <li>Easiest for a neurologist without genetics expertise and/or limited access to medical geneticists to interpret and act upon</li> <li>Typically, the least expensive and fast turnaround</li> <li>Easy to order and get covered by insurance</li> </ul>	<ul> <li>Causative gene may not be included (yet)</li> <li>Limited options for reanalysis, so may subsequently undergo repeat WES or WGS testing if high suspicion for genetic etiology</li> <li>Will likely miss actionable</li> <li>secondary findings (e.g., BRCA, Lynch syndrome genes) that are unrelated to epilepsy phenotype, but can profoundly affect medical prognosis &amp; treatment</li> <li>No coverageof non-coding variantsthat have been implicated in generalized genetic epilepsy risk</li> </ul>
Whole Exome Sequencing (WES)	Coding regions (exons) and exon/intron boundaries (~1-2% of genome)	<ul> <li>Comprehensive coverage of coding regions and actionable gene findings</li> <li>Effective for heterogenous neurological conditions &amp; comorbidities</li> <li>Able to identify mutations in novel genes</li> <li>Reanalysis is possible</li> </ul>	<ul> <li>More likely than MGP to result in incidental or secondaryfindings that require interpretation by medical geneticists and/or clinical action</li> <li>Depth of coverage is not uniform</li> <li>Unable to detect non-coding (intronic) variants</li> <li>Limited abilityto identify CNV or structural variants</li> </ul>
Whole Genome Sequencing (WGS)	Entire genome	<ul> <li>Detects coding and noncoding variants (unlike other 2 options)</li> <li>Uniform coverage</li> <li>Able to identify mutations in novel genes as well as non- coding (e.g., presumed regulatory) regions</li> <li>Reanalysis is possible</li> <li>Allows detection of copy number variants (CNV) and some (smaller) structural variants</li> </ul>	<ul> <li>Most expensive and longest turnaround</li> <li>More challenging to get coveredby insurance</li> <li>Most likely to result in incidental findings that are more difficult to interpret</li> <li>Requires medical geneticist for full interpretation</li> </ul>
Chromosomal microarray - comparative genomic	Genome-wide copy number variants (CMV) & structural variants (e.g., deletions, translocations)	<ul> <li>Cost effectivein people with epilepsy PLUS comorbid developmental delay (DD), intellectual disability (ID), or birthdefects</li> <li>Often considered as second line testing if previous testing was unrevealing because it detects structural variants that may be undetectable on other NGS-based tests</li> </ul>	<ul> <li>Not cost-effective as first-line genetic testing unless DD/ID or birth defect comorbidities</li> <li>Cannot detect balanced translocations and certain structural rearrangements, would need chromosome analysis (i.e., karyotype)</li> </ul>
Other genetic testing considerations:	<ul> <li>Trio testing can be done with WES vs WGS if both biological parents are available.</li> <li>Quad testing feasible if there is an affected sibling + above</li> <li>Pros: identifies de novo mutations, Family/pregnancy planning</li> <li>Cons: risk of unexpected familial implications such as consanguinity or non-paternity</li> </ul>		