Self-Assessment of

The False Genotype Rate

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1) There are dozens of single-gene disorders that affect the structure and function of the retina. The most common of them affects only one in people while the rarest ones affect fewer than people in the United States.
2) If we are going to sustainably deliver these treatments to the tens of thousands of people who need them, we will need to be able to do it for less than per patient.
3) To help design a strategy for treating everyone with one of these conditions, investigators at the University of Iowa studied consecutive families diagnosed with inherited retinal disease at the University of Iowa.
4) The most important goal of the project was to devise a way to use clinical information to overcome the huge amount of in the genome.
5) As part of the battle against this under-appreciated, we wanted to come up with a statistic that would make it more understandable to practicing clinicians. We call this statistic the
6) Using a tiered testing approach, we identified mutations in of the families.
7) of these genotypes were found with a focused test that was chosen based on the patients' clinical findings, and of these were mutations that would have been missed by
8) The average cost of the testing was per family despite the fact that some families had multiple tests performed on them. This

s because many of the clinically focused tests are much less expensive than
9)The mutations we found were distributed across more thandifferent genes.
10) Some genes were much more common than others – ABCA4 caused disease in families while of the genes each caused disease in fewer than 1% of the cohort.
11) Most people are relatively unaware that <u>every</u> person's genome is riddled with variants that are rare enough and damaging enough to be a plausible explanation for their disease. The opportunity to observe one or more by chance increases as the number of genes tested goes up.
12) A 305 gene panel is over times more likely to yield one or more than a clinically focused approach. More than half of the families in our family cohort were assigned to a clinical category whose focused test had a false genotype rate of less than% while the average rate for a 305 gene retinal disease panel is% meaning an average patient tested in this way will be found to have false genotypes in addition to their true disease-causing genotype.

This 48 year old woman first had some retinal abnormalities noticed on a routine eye exam at age 33. She is now 20/20 in the right eye and 20/60 in the left. She was diagnosed with diabetes at age 32 and started wearing hearing aids at age 46.

One of the weaknesses of whole exo	<u> </u>	
assess the genome. So, to get the correct		
molecular diagnosis for this lady, you have to know that bilateral atrophic macular lesions in a patient with diabetes and hearing loss		
suggests a cor	dition caused by a specific point	
mutation at position		
genome.		
14)The false genotype rate can <u>only</u> be reduced by		
	– there is no technical	
improvement in the sequencing itse	lf that can do so.	
15) If you encounter multiple possib	ilities despite a narrow	
, you ca	an usually identify the correct one	
by	·	
16) and	the methodical examination of	
your patients'	are both very important factors in	
arriving at a correct molecular diagnosis and will remain so even as the		
cost of next generation sequencing continues to fall.		