WEBVTT

- NOTE duration:"00:02:22.4850000"
- NOTE language:en-us
- NOTE Confidence: 0.86357

 $00:00:00.000 \rightarrow 00:00:01.865$  The evolution has been extraordinary

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 $00:00:01.865 \longrightarrow 00:00:04.499$  and just over the past 1050 years.

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 $00{:}00{:}04{.}500 \dashrightarrow 00{:}00{:}06{.}612$  So we started from the inexpensive

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 $00{:}00{:}06{.}612 \dashrightarrow 00{:}09{.}184$  test where we were guessing what the NOTE Confidence: 0.86357

 $00{:}00{:}09{.}184 \dashrightarrow 00{:}00{:}11.739$  gene could be with the defective gene

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 $00{:}00{:}11.811 \dashrightarrow 00{:}00{:}14.457$  could be according to what the patient

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 $00{:}00{:}14.457 \dashrightarrow 00{:}00{:}16.340$  and their families were showing,

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 $00{:}00{:}16.340 \dashrightarrow 00{:}00{:}18.930$  and then if that test was negative,

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00:00:18.930 --> 00:00:21.352 we were considering about going to a

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00:00:21.352 --> 00:00:23.926 different test to check for another gene

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 $00{:}00{:}23.926 \dashrightarrow 00{:}00{:}26.700$  that could be responsible for that process.

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 $00{:}00{:}26.700 \dashrightarrow 00{:}00{:}28.884$  So that was expensive and often

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 $00:00:28.884 \dashrightarrow 00:00:30.340$  time consuming because we're

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 $00:00:30.402 \rightarrow 00:00:32.038$  not finding the mediations.

- NOTE Confidence: 0.86357
- $00:00:32.040 \longrightarrow 00:00:33.548$  And the initial tribe.

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 $00{:}00{:}33.548 \dashrightarrow 00{:}00{:}36.319$  So this has evolved to having more

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 $00:00:36.319 \longrightarrow 00:00:38.494$  jeans that are responsible for

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 $00{:}00{:}38{.}494 \dashrightarrow 00{:}00{:}41{.}120$  diseases will learn from and those

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 $00{:}00{:}41.120 \dashrightarrow 00{:}00{:}43.556$  genes package within tests are now

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 $00{:}00{:}43.556 \dashrightarrow 00{:}00{:}45.962$  encompass a number of genes that

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 $00:00:45.962 \rightarrow 00:00:48.852$  are being tested at the same time

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 $00:00:48.852 \rightarrow 00:00:51.360$  we call multi gene panel tests.

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 $00{:}00{:}51{.}360 \dashrightarrow 00{:}00{:}53{.}826$  These are now the ones that

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 $00:00:53.826 \longrightarrow 00:00:55.470$  we are commonly using.

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 $00:00:55.470 \longrightarrow 00:00:57.834$  They allow us to really test

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00:00:57.834 --> 00:01:00.433 for different genes that can be

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00:01:00.433 --> 00:01:02.317 responsible for similar cancer.

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 $00{:}01{:}02{.}320 \dashrightarrow 00{:}01{:}03{.}484$  Susceptibilities and therefore

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 $00:01:03.484 \dashrightarrow 00:01:06.704$  they will let us to be much more NOTE Confidence: 0.86357

00:01:06.704 --> 00:01:08.879 efficient in terms of diagnostics,

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 $00:01:08.880 \longrightarrow 00:01:10.930$  so that really has revolutionized

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 $00:01:10.930 \longrightarrow 00:01:12.980$  how we do genetic testing.

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 $00:01:12.980 \longrightarrow 00:01:16.049$  An it has it has allowed us to really NOTE Confidence: 0.86357

 $00{:}01{:}16.049 \dashrightarrow 00{:}01{:}19.127$  be much more efficient when there,

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00:01:19.130 --> 00:01:21.590 when it comes to genetic testing,

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 $00{:}01{:}21.590 \dashrightarrow 00{:}01{:}23.465$  so changes are happening there

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 $00{:}01{:}23.465 \dashrightarrow 00{:}01{:}25.851$  happening fast and in the capacity

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 $00:01:25.851 \rightarrow 00:01:28.467$  of these panels to incorporate knew NOTE Confidence: 0.86357

 $00{:}01{:}28.467 \dashrightarrow 00{:}01{:}30.725$  genetic defects that we're learning NOTE Confidence: 0.86357

00:01:30.725 - 00:01:32.930 every day that are responsible.

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 $00:01:32.930 \rightarrow 00:01:35.100$  For cancer susceptibility are easily

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00:01:35.100 --> 00:01:38.000 incorporated and that also let us

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 $00{:}01{:}38{.}000 \dashrightarrow 00{:}01{:}40{.}310$  re check on patients who were tested

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 $00:01:40.310 \longrightarrow 00:01:42.771$  several years ago and some of those

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 $00:01:42.771 \rightarrow 00:01:45.570$  jeans were not discovered by that time yet.

- NOTE Confidence: 0.86357
- $00{:}01{:}45{.}570 \dashrightarrow 00{:}01{:}48{.}260$  So we can go back to this.

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 $00:01:48.260 \dashrightarrow 00:01:49.904$  Individuals who tested negative

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 $00{:}01{:}49{.}904 \dashrightarrow 00{:}01{:}52{.}859$  at that time and double check see

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00:01:52.859 --> 00:01:55.367 those new mutations that have been

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00:01:55.367 --> 00:01:58.054 discovered are actually the ones that

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 $00{:}01{:}58.054 \dashrightarrow 00{:}02{:}00.329$  are causing their cancer predisposition.

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00:02:00.330 --> 00:02:01.266 And so again,

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00:02:01.266  $\operatorname{-->}$  00:02:03.138 I think that whoever got information

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 $00:02:03.138 \longrightarrow 00:02:04.090$  two years ago,

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 $00:02:04.090 \rightarrow 00:02:05.354$  it's already different nowadays

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 $00:02:05.354 \longrightarrow 00:02:07.250$  and probably in two years is

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 $00{:}02{:}07{.}304 \dashrightarrow 00{:}02{:}08{.}779$  still going to be different.

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00:02:08.780 --> 00:02:10.586 Therefore it's an active field that

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00:02:10.586 $-\!\!>$ 00:02:12.876 we really need to make sure that

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00:02:12.876 --> 00:02:14.581 our patients do understand that NOTE Confidence: 0.86357

4

00:02:14.581 --> 00:02:16.461 our knowledge keeps evolving and we NOTE Confidence: 0.8635700:02:16.461 --> 00:02:18.511 need to really keep in touch with

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00:02:18.511 --> 00:02:20.557 our patients so they can actually

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 $00{:}02{:}20.557 \dashrightarrow 00{:}02{:}22.484$  benefit from their new knowledge.