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Judging in the Genomic era: judges' genetic knowledge, confidence and need for training

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Abstract

Genetic information is increasingly used in many contexts, including health, insurance, policing and sentencing – with numerous potential benefits and risks. Protecting from the related risks requires updates to laws and procedures by justice systems. These updates depend to a large extent on what the key stakeholders – the judiciary – know and think about the use of genetic information. This study used a battery of 25 genetic knowledge items to collect data from 73 supreme court judges from the same country (Romania) on their knowledge of genetic information. Their responses were compared with those of two other groups: lawyers (but not judges; N = 94) and non-lawyers (N = 116) from the same country. The data were collected at approximately the same time from the three groups. The judges' results were also compared to the results obtained from a general population data collection (N = 5310). The results showed that: 1) judges had overall better knowledge of genetics than the other groups, but their knowledge was uneven across different genetic concepts; 2) judges were overall more confident in their knowledge than the other two groups, but their confidence was quite low; and 3) the correlation between knowledge and confidence was moderate for judges, weak for lawyers and not significant for non-lawyers. Finally, 100% of the judges agreed that information on gene-environment processes should be included in judges' training. Increasing genetic expertise of the justice stakeholders is an important step towards achieving adequate legal protection against genetic data misuse.

Key words: judges, genetic training, genetic data misuse, genetics law, updating laws, genetic discrimination

Introduction

Genetic information is increasingly used in different life contexts, such as health (1), law (2) and reproductive choices (3). This increased application of genetics marks the genomic era, which has brought multiple potential benefits and risks for individuals. In justice, the benefits of genetic information include DNA identification in criminal investigations and the exoneration of the wrongly convicted (4). Genetics have also provided insights into origins of individual differences in human behaviour, including for traits that are relevant to criminal justice, such as impulsivity, aggressiveness and ‘free’ will/control over behaviour. For example, an aetiological approach conceptualises human will (to act and to control actions) as a trait. Therefore, as with virtually all human traits, individual differences in *will* result from complex gene-environment processes (5,6). This contrasts with the well-established view of ‘free’ will as each individual’s ability to control their actions/decisions and the belief that the will of all ‘sane (mentally healthy)’ people is free to the same extent (7). Many genes/genetic markers have already been linked to traits such as psychiatric disorders, criminal behaviour, physical illness and learning disabilities, and many more will be discovered in the future (8–11). This information may be used to aid justice, for example, in taking decisions on the best interventions for criminal behaviour. Conversely, the same information might be used to harm individuals, including through limiting access to health insurance and education, or through surveillance (12).

The justice system has been slow to utilise advances in genetic knowledge. Current laws are not designed to protect from misuses of the vast amounts of information that can be extracted from whole genome sequencing. For example, laws do not provide sufficient protection from misuses of predictive genetic information on health risks (e.g. for determining insurance premiums); on criminal behaviour (e.g. for crime prevention); on intelligence (e.g. for selection or streaming in education); and on career specific skills (e.g. for the military). Updating relevant laws requires that the judiciary has the necessary expertise, as they play a ‘steering’ role in development of the law for novel matters. Moreover, even before laws are updated, the judiciary faces challenges of deciding cases involving genetic information. An increasing number of cases involve genetic information, including in the US (13,14); England and Wales¹ (15); Italy (16); and the Netherlands (17). Taking decisions in such cases without sufficient knowledge of genetics has serious consequences for justice, because these first decisions set precedent – influencing the development of the law.

Considering this important role of the judiciary, it is necessary to explore their knowledge of fundamental genetic concepts. It is also important to explore how prepared judges are to embrace relevant training in genetics. To our knowledge, no previous study explored genetic knowledge of judges. The findings from several recent studies with non-judges suggest that levels of genetic knowledge are generally low (18–22). For example, only 34% of 62 respondents, recruited through a random digit dialling method in the continental United States, knew that genes are stored in every cell of the body (19). Another study, which utilised the same measure used here, identified that participants

¹ *ABC v St George’s Healthcare NHS Foundation Trust* [2017] EWCA Civ 336, 2017.

struggled to answer questions designed to evaluate a basic and functional level of genetic knowledge, with only 1.2% of 5404 participants answering all questions correctly (22).

If judges' genetic knowledge is similarly insufficient, their decisions in cases involving evaluation of genetic information may be affected. Moreover, variability in genetic knowledge among judges may contribute to the wide variability in sentencing decisions (23), for example via affecting views on aetiology of behaviour, immutability of 'genetically determined' traits, and 'free will' (24–26).

Several studies that explored judges' views on the use of genetic information in sentencing found widely mixed views on how this information should be used (24–26). For example, one study explored through phone interviews how knowledge of genetic influences on mental disorders would affect judges' views on sentencing. The study used a sample of 59 Pennsylvania State Court judges, with a response rate of 7.4% out of a sample of 800 judges approached. The judges were asked to describe their thoughts about sentencing in cases where (a) the offender had mental disorders and (b) the offender's mental disorder was known to be genetically influenced (27). The qualitative analyses showed that a high proportion of judges held essentialist beliefs (e.g. that traits are genetically determined); as well as stigmatisation biases associated with such beliefs (e.g. that a person with genetic risk poses a threat to society). The study also suggested that sentencing partly depended on the judges' personal experiences with genetics, personal experiences with mental disorders and other factors. For example, the stereotyping led to more restrictive sentences and support for deterrence and incapacitation in the absence of personal experience with genetics or mental health illness.

Overall, the results of the limited previous research suggest that genetic information can affect the views of judges, and that these effects may differ as a function of multiple factors, such as held beliefs, knowledge and experience with genetics; and jurisdiction.

A key limitation of previous studies is that they did not specifically evaluate judges' knowledge on genetics. Another limitation of most previous studies is the potential selection bias, as participation rates were either very low, or unknown. This may have decreased representativeness of the samples, for example with participants having particular interest in issues related to sentencing of people with psychopathy. Another limitation is that most previous research explored judges' views only in a few jurisdictions (e.g. US, Germany) and more research is needed to understand whether judiciaries' attitudes differ across jurisdictions. In addition, most previous research focused on mental disorders, specifically psychopathy - a diagnosis associated with much stigma. Previous research also used single items or very few items, mostly addressing only what judges would do in a scenario under the current laws, procedure and guidance, and not judges' views on how genetic data should be used in court. Finally, most research employed qualitative analyses, quantitative research is needed to compare judges' knowledge with that of other groups.

The current research addresses some of these limitations. First, 91% of the judges approached in the current study completed the survey. Second, this study is the first to collect data from a non-western sample of judges. Third, the study is the most comprehensive to date - exploring the judiciary's knowledge on a wide range of genetic

concepts; and comparing them with those of non-judge lawyers (from here, ‘lawyers’) and non-lawyers (others). We used the iGLAS – International Genetic Literacy and Attitudes Survey – to collect data on 17 key genetic knowledge items and heritability estimates for 8 traits (28). In addition, we evaluated confidence in own genetic knowledge, and the relationship between knowledge and confidence. Finally, we explored the judges’ views on whether genetics should be included in their training.

We expect that: (a) the judges’ genetic knowledge (GK) will be higher than other groups’ as previous research found that GK is correlated with education; (b) the judges’ confidence in their GK would be higher than that of other groups; (c) knowledge and confidence would be only moderately correlated, as previous research has indicated that people have poor knowledge calibration in many areas (29); (d) many judges will endorse including genetic information in their training. This prediction is based on our previous sessions with lawyers and judges as part of seminars and working groups; e.g. the Legal, Ethical and Societal Implications of Genetics (LESIG) Working Group (30).

Participants and Methods

The study was approved by the Goldsmiths Department of Psychology Ethics Committee (PSY10.10.2016).

This study was conducted as part of an ongoing large scale project by The Accessible Genetics Consortium (TAGC) to collect data from a range of jurisdictions (tagc.world). The International Genetic Literacy and Attitudes Survey (iGLAS) was used to collect the data. Detailed information on validation, construction and use of iGLAS can be found in a previous publication (28). iGLAS is a dynamic instrument which is currently in its 10th version. iGLAS can be completed in 7 languages, including Romanian. All items in iGLAS were developed in English; then the items were translated and back translated - for each of the languages currently available. The translations were additionally checked by a team of experts and piloted with small sample of participants. Translation documentation is available from the authors. Over 13000 participants have completed iGLAS to date.

Participants

The total sample included 283 participants (73 judges, 94 lawyers and 116 non-lawyers). All the judges were supreme court judges and were recruited specifically for this study, with data collection facilitated by two members of the supreme court. The Supreme Court is the highest court in Romania, with approximately 120 judges. Participation rate in this study was 91% (80 judges were approached, 73 provided full data). The samples of lawyers and non-lawyers were composed of all Romanian participants who completed the general iGLAS on-line collection at approximately the same time (August 2017 – January 2018). Non-lawyers included participants who identified themselves as students or working in professions other than law.

The number of participants slightly varied across different analyses as not all questions were answered by every participant. Participants were all at least 18 years old ($M = 42.08$, $SD = 11.09$). In total, 178 females and 102 males completed this study; 2 participants identified as non-binary; and 2 did not disclose their sex. Further descriptive

statistics for each group can be found in Table 1. All participants were educated and living in Romania.

Table 1. Descriptive statistics (age and gender) for each group of participants

Group	Age (in years)			Sex			
	Mean	SD	Range	Male	Female	Non-binary	Prefer not to say
Judges	48.5	6.87	34-66	27 (37.5%)	44 (61.1%)	1 (1.4%)	0 (0.0%)
Lawyers	45.2	6.75	21-62	37 (39.4%)	57 (60.6%)	0 (0.0%)	0 (0.0%)
Non-Layers	35.6	12.57	18-62	38 (33.0%)	77 (67.0%)	0 (0.0%)	0 (0.0%)

Measures and Procedure

Data were collected via Qualtrics software. Informed consent was gathered before the beginning of the survey.

Participants first provided demographic information. They then rated how confident they were in their genetic knowledge and completed 17 genetic knowledge items (See Table 3 for the list of items). The 17 items were summed to give total genetic knowledge scores for each participant. Questions were formatted in various ways: yes/no, Likert scales, dropdowns and multiple choice.

Participants also rated on a scale of 0-100 (zero to full genetic influence) the heritability of 8 human traits: height, weight, IQ, eye colour, clinical depression, motivation, school achievement, sexual orientation. Participants also completed a large number of opinion and attitudes items. Of these, only one is analysed in the current study: ‘Information about gene environment processes should be included in judges’ training (strongly disagree to strongly agree on a 1-7 scale).

Results

Table 2 presents the results for genetic knowledge and confidence for the three groups (judges, lawyers, non-lawyers). The results of an ANCOVA showed that the judges’ genetic knowledge was significantly higher than that of the other two groups, after controlling for age and education level $F(2,269) = 5.24, p = .006$ (Partial Eta Squared .037). The judges’ greater knowledge was not related to differences across the groups in terms of education, $F(1,269) = .50, p = .481$ (η^2 .002). However, their greater knowledge was partially related to age, $F(1,269) = 4.18, p = .042$ (η^2 .015), with older participants scoring on average higher. The judges also showed significantly narrower distribution of scores (Levene’s test = $F(2,271) = 18.75, p < .001$).

Table 2. Overall average Genetic Knowledge and Confidence for the judges, lawyers and non-lawyers.

Average Genetic Knowledge (0-1)						
Group	Mean	Std. Deviation	N	Min	Max	
Judges	.73	.11	73	.29	.94	
Lawyers	.66	.17	94	.12	1.00	
Non-lawyers	.61	.21	116	.24	.94	
Total	.66	.18	274	.12	1.00	

How confident are you in your genetic knowledge? (0-1)					
Group	Mean	Std. Deviation	N	Min	Max
Judges	.55	.10	72	.30	.76
Lawyers	.50	.19	93	.00	.92
Non-lawyers	.41	.23	115	.00	1.00
Total	.48	.20	280	.00	1.00

Note: Genetic knowledge scores are based on each participant's total correct score divided by the total items (17), and so are analogous to percentage correct scores (e.g. .73 = 73% correct). Confidence in genetic knowledge was measured on a scale of 0 – 100, rescaled in this table to 0-1 so that figures can be easily compared with average genetic knowledge scores. Percentages are not presented in this table so that means and standard deviations can be more easily considered together.

We also compared the judges' results with the results obtained from a large sample of unselected participants (N = 5310) reported in Chapman et al, which also collected data using iGLAS (22). The overall GK score of the judges (73%) was higher than that of the sample in Chapman et al. (65.5% correct) (22). In Chapman, data collection was not targeted to a specific group; however, 87.6% of the participants had completed or were working towards at least degree level education (93.8% in the current study). Participants tended to be younger (M = 32.5, SD = 12.8) however, the gender split was very similar (61.1% female) to the present study (62.9% female). The frequencies of responses for the judges and this unselected sample are presented in SOM Table 1.

The proportions for each response option for the knowledge items for the 3 groups are provided in Table 3. Focusing on the judges, the judges' knowledge of different concepts could be split into three categories: excellent knowledge; relatively good knowledge, and poor knowledge.

Table 3. Number of participants and proportions of responses for each of the multiple-choice option in the 17 genetic knowledge items. Correct responses are highlighted in bold. The darker the shading - the higher the proportion of participants selecting that response).

Item	N participants (%participants)			
1. What is a genome?				
	A sex chromosome	The entire sequence of an individual's DNA	All the genes in DNA	Gene expression
Judges	0 (0)	29 (39.7)	44 (60.3)	0 (0)
Lawyers	0 (0)	75 (79.8)	18 (19.1)	1 (1.1)
Non-lawyers	4 (3.4)	78 (67.2)	27 (23.3)	7 (6)
2. Which of the following 4 letter groups represent the base units of DNA?				
	GHPO	HTPR	GCTA	LFWE
Judges	7 (9.6)	12 (16.4)	42 (57.5)	12 (16.4)
Lawyers	15 (16.3)	14 (15.2)	53 (57.6)	10 (10.9)

Non-lawyers	11 (10.1)	11 (10.1)	80 (73.4)	7 (6.4)
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3. How many copies of each gene do we have in each cell?

	1 copy	2 copies	23 copies	5 copies
Judges	0 (0)	71 (97.3)	2 (2.7)	0 (0)
Lawyers	8 (8.5)	74 (78.7)	12 (12.8)	0 (0)
Non-lawyers	22 (19.3)	67 (58.8)	22 (19.3)	3 (2.6)

4. All humans differ in the amount of DNA they share. How much of this differing DNA do siblings usually share?

	75%	50%	0.01%	99.90%
Judges	2 (2.8)	65 (90.3)	1 (1.4)	4 (5.6)
Lawyers	6 (6.5)	58 (62.4)	1 (1.1)	28 (30.1)
Non-lawyers	16 (13.8)	75 (64.7)	11 (9.5)	14 (12.1)

5. What is the main function of all genes?

	Storing information for protein synthesis	To provide energy to the cell	To clear out waste from the cell	To repair damage to a cell
Judges	18 (24.7)	36 (49.3)	8 (11)	11 (15.1)
Lawyers	49 (52.7)	33 (35.5)	4 (4.3)	7 (7.5)
Non-lawyers	77 (67.5)	16 (14.0)	5 (4.4)	16 (14.0)

6. On average, how much of their total DNA is the same in two people selected at random?

	Less 50%	75%	90%	More than 99%
Judges	35 (47.9)	6 (8.2)	4 (5.5)	28 (38.4)
Lawyers	33 (35.5)	9 (9.7)	12 (12.9)	39 (41.9)
Non-lawyers	46 (39.7)	5 (4.3)	7 (6.0)	58 (50.0)

7. Genetic contribution to the risk for developing Schizophrenia comes from:

	One gene	Many genes
Judges	9 (12.5)	63 (87.5)
Lawyers	24 (26.4)	67 (73.6)
Non-lawyers	46 (39.7)	70 (60.3)

8. In humans, DNA is packaged into how many pairs of chromosomes?

	23 pairs	48 pairs	10 pairs	27 pairs
Judges	69 (94.5)	2 (2.7)	1 (1.4)	1 (1.4)
Lawyers	85 (90.4)	7 (7.4)	2 (2.1)	0 (0.0)
Non-lawyers	99 (87.6)	12 (10.6)	2 (1.8)	0 (0.0)

9. An Epigenetic change is:

	A change in gene expression	A change of the genetic code itself	A process by which human beings can consciously change their DNA	Gene splicing
Judges	47 (65.3)	13 (18.1)	3 (4.2)	9 (12.5)

Lawyers	45 (47.9)	28 (29.8)	11 (11.7)	10 (10.6)
Non-lawyers	60 (52.2)	25 (21.7)	19 (16.5)	11 (9.6)

10. Approximately how many genes does the human DNA code contain?

	2,000	1 million	3 billion	20,000
Judges	4 (5.5)	2 (2.7)	1 (1.4)	66 (90.4)
Lawyers	12 (12.8)	15 (16.0)	10 (10.6)	57 (60.6)
Non-lawyers	12 (10.5)	21 (18.4)	15 (13.2)	66 (57.9)

11. Genetic contribution to the risk for developing Autism comes from:

	One gene	Many genes
Judges	2 (2.8)	70 (97.2)
Lawyers	23 (24.7)	70 (75.3)
Non-lawyers	64 (55.7)	51 (44.3)

12. What are polymorphisms?

	Building blocks of the DNA	Proteins found in the brain	Points of genetic variation	Deoxyribonucleic Acid
Judges	10 (13.9)	4 (5.6)	56 (77.8)	2 (2.8)
Lawyers	21 (22.6)	4 (4.3)	66 (71)	2 (2.2)
Non-lawyers	25 (21.7)	7 (6.1)	79 (68.7)	4 (3.5)

13. The DNA sequence in two different cells, for example a neuron and a liver cell, of one person, is:

	Entirely different	About 50% the same	More than 90% the same	100% identical
Judges	1 (1.4)	0 (0.0)	1 (1.4)	70 (97.2)
Lawyers	7 (7.4)	5 (5.3)	13 (13.8)	69 (73.4)
Non-lawyers	16 (13.8)	18 (15.5)	23 (19.8)	59 (50.9)

14. "Non-coding" DNA describes DNA that:

	Is removed when passed from parent to offspring	Does not lead to the production of proteins	Is non-human DNA	Is not composed of nucleotides
Judges	22 (30.1)	21 (28.8)	19 (26)	11 (15.1)
Lawyers	27 (29.3)	37 (40.2)	13 (14.1)	15 (16.3)
Non-lawyers	24 (21.2)	53 (46.9)	19 (16.8)	17 (15.0)

15. Genetic modification is:

	Selective breeding	Genetic engineering	Both of the above	Neither of the above
Judges	5 (6.8)	8 (11.0)	54 (74)	6 (8.2)
Lawyers	19 (20.4)	31 (33.3)	36 (38.7)	7 (7.5)
Non-lawyers	22 (19.1)	50 (43.5)	40 (34.8)	3 (2.6)

16. Can we fully predict a person's behaviour from examining their DNA sequence?

	Yes	No
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Judges	3 (4.1)	70 (95.9)
Lawyers	16 (17.0)	78 (83.0)
Non-lawyers	17 (14.8)	98 (85.2)

17. At present in many countries, new born infants are tested for certain genetic traits

	TRUE	FALSE
Judges	70 (95.9)	3 (4.1)
Lawyers	88 (93.6)	6 (6.4)
Non-lawyers	97 (83.6)	19 (16.4)

Note. The numbers represent N participants choosing each response option. Proportions (%) of participants choosing each option are presented in brackets. Conditional formatting has been applied to the proportion of responses. Darker cells indicate a higher proportion of responses. Formatting is applied across all items so that both inter and intra comparisons are possible.

Excellent knowledge was demonstrated for 8 of 17 items. For example, over 90% of the judges knew that: each cell contains 2 copies of each gene; that there are approximately 20000 genes in the human genome; that siblings share on average 50% of the variable DNA (DNA that can differ across people); and that DNA sequence in two different cells is identical. They also correctly stated that Autism results from many (rather than one) genes. Slightly fewer judges (87.5%) answered correctly a similar question about Schizophrenia.

Participants were overall accurate in knowing that we cannot fully predict someone's behaviour from looking at their DNA (Table 3: Item 16) and that infants are tested for certain genetic traits in many countries (Table 3: item 17). The results of a Chi-squared analyses, comparing the three groups, showed that significantly more judges (95.9%) and lawyers (93.6%) than non-lawyers (83.6%) knew that in many countries infants are tested for certain genetic traits ($\chi^2(2, N = 283) = 9.51, p = .009$). Significantly more judges (95.90%) than lawyers (83%) and non-lawyers (85.20%) also correctly identified that we cannot fully predict a person's behaviour from examining their DNA sequence ($\chi^2(2, N = 282) = 6.86, p = .032$).

Relatively good knowledge was demonstrated on 3 of the 17 items. A substantial proportion of judges (65.3%) knew that an epigenetic change is a change in gene expression; that polymorphisms are points of genetic variation (77.8%); and that genetic modification includes both selective breeding and genetic engineering (74%).

Poor knowledge was found for the 5 remaining items that tapped into fundamental genetic concepts. First, the question 'what is a genome?' was correctly answered only by 39.7% of the judges; the majority (60.30%) selected an incorrect answer: 'all the genes in DNA'. The responses for this item were better for lawyers (74.8%) and non-lawyers (67.2%).

Second, only 57.5% chose the correct combination of the 4 letter groups that represent the base units of the DNA. The rest of the responses were distributed across the other 3 incorrect response options – demonstrating a high degree of guessing. The response rates for this item were similar for lawyers (57.6%) and better for non-lawyers (73.4%).

Third, fewer than 25% of the judges answered correctly that the main function of all genes is storing information for protein synthesis. Almost 50% chose the incorrect answer

‘To provide energy to the cell’. A greater proportion of lawyers (52.7%) and non-lawyers (67.5%) than judges chose the correct response for this item.

Fourth, only 38% of the judges knew that on average more than 99% of the total DNA is the same in two people selected at random. 48% selected an incorrect response of ‘less than 50%’. The response rates for this item were similar for lawyers (41.4%) and non-lawyers (50%).

Fifth, only 28.8% of the judges knew that “non-coding” DNA describes DNA that does not lead to the production of protein. A higher proportion of lawyers (40.2%) and non-lawyers (46.9%) than judges chose the correct response for this item. The judges’ answers were distributed across all 4 response options – suggesting high degree of guessing.

Table 2 in SOM presents participants’ estimates of genetic influence (heritability) for 8 complex traits. Results show that the judges were overall relatively accurate in estimating the heritability of these traits, providing similar estimates to those reported in the scientific studies (22). The estimates were also overall accurate for the other two groups, with a tendency to underestimate in some cases (e.g., height; weight).

Confidence

The average judges’ confidence in their genetic knowledge was 55.6 out of 100, ranging from 30 to 76 (see Table 2). This is significantly higher than that found in the other two groups (non-lawyers, showing the lowest). It is also higher than the confidence level (35.95 out of 100) found in a group of undergraduate Psychology students in the UK (N = 153) (31). The ANCOVA on genetic knowledge confidence, indicated significant group differences between the judges, lawyers and non-lawyers when controlling for education level and age, $F(2,266) = 6.39$, $p = .002$, $\eta^2 = .046$. Age did not have a significant effect on confidence $F(1,266) = 1.55$, $p = .215$, $\eta^2 = .006$. Education level also did not have a significant effect $F(1,266) = .201$, $p = .654$, $\eta^2 = .001$. Levene’s test indicated unequal variances, $F(2,268) = 19.73$, $p < .001$, with judges showing a narrower distribution than the other two groups.

Moderate positive correlations between genetic knowledge and confidence were found in the samples of judges ($r = .43$, $N = 72$, $p < .001$); and lawyers ($r = .34$, $N = 93$, $p < .001$). There was no significant correlation for non-lawyers ($r = .12$, $N = 115$, $p = .206$).

Training

100% of the judges agreed that information about gene-environment processes should be included in judges’ training: 74% - agreed, 16.4% - somewhat agreed, and 9.6% - strongly agreed.

Discussion

The judges’ average genetic knowledge was relatively good but uneven. For some items, the judges’ average knowledge was much higher than that of the lawyers and non-lawyers; and for other items, substantially lower (see Table 2). The observed pattern of results shows that the average good knowledge shown by the judges reflects partly their

ability to apply common sense to the multiple-choice options – selecting the most plausible answers based on their general knowledge and perhaps school biology. It also shows that their knowledge of some of the key genetic concepts is poor.

When compared to the results of Chapman et al., (22) the judges particularly underperformed on knowledge items related to molecular genetics, especially: the function of genes, the definition of the genome, the nature of non-coding DNA and the constituent units of DNA. For example, over 60% of the judges selected an incorrect answer for the question of ‘what is a genome’ - selecting ‘all the genes in DNA’. Understanding the difference between genes and genome is important, for example, for decisions to undergo genetic testing or interpreting the results of such testing. In sentencing, ‘predictive’ information (from single genes vs. polygenic risk scores vs. epigenetic profiles) may be incorrectly interpreted or given an inappropriate weight.

Less than 40% of the judges knew that on average more than 99% of the total DNA is the same in two people selected at random. At the same time, the judges correctly identified sibling genetic similarity. These results suggest that many judges do not distinguish between ‘total DNA’ and ‘variable/differing/segregating’ DNA – the portion (less than 1%) of the total DNA that differs across people. These misconceptions may lead to other misconceptions, such as viewing individuals from different groups as being genetically very different; or having deterministic and essentialist biases.

The judges were overall accurate in estimating heritability. In fact, they did not show a pattern of overestimation and underestimation previously found in Chapman et al. with the same items (22). In that study, heritability of traits viewed as ‘fixed’, such as height, eye colour and IQ were overestimated; and heritability of traits viewed as ‘malleable’, such as motivation, school achievement and weight, were underestimated.

Confidence (self-evaluation of their knowledge) was significantly higher in the group of judges, compared to the other two groups, as well as to the results of a study that utilised this same measure with a cohort of undergraduate psychology students in the UK (31). This was expected as the judge’s knowledge was also higher than that of the other groups. However, the correlations between knowledge and confidence for judges ($r = .43$) and lawyers ($r = .34$) were only moderate; and correlation was not significant for non-lawyers. This suggests that people, including judges, are not precise in the estimates of their own genetic knowledge. For example, many judges whose knowledge was high did not think so, and some of those whose knowledge was very poor reported high knowledge.

Summary and conclusion

Overall, the results demonstrate that without specific training even most highly educated people, at the top of their profession lack much of the essential genetic knowledge. This is of course not surprising as genetic science is rapidly developing, amassing vast amounts of complex continuously updated information. The 100% endorsement by the judges of the need for gene-environment training attests to their recognition of the importance of such knowledge and is a positive outcome for justice.

The 3 main findings of this study are:

1. Judges showed higher genetic knowledge than other groups. This relatively good *overall* genetic knowledge masked poor knowledge of 5 of the most fundamental genetic concepts that are important for successful application of genetic knowledge in the genomic era.
2. The judges' confidence in their genetic knowledge, although higher than that of the other groups, was quite low and showed only a moderate correlation with their knowledge.
3. 100% of the judges agreed that information about gene-environment processes should be included in judges' training – endorsing the importance of genetic knowledge for justice.

The study addressed some limitations of previous research, exploring knowledge on a wide range of topics in a sample of the judiciary from a non-western country with a very high response rate. However, a range of socio-cultural factors and country-specific context of the legal system may mean that the results are not fully applicable across all jurisdictions. For example, Romanian judges participate at least once every three years in continuous training programmes organized by National Institute of Magistracy or other institutions. The continuous training might have contributed to their unanimous endorsement of the need for training in gene-environment processes. The representativeness of the non-selected sample (non-lawyers) is likely to have been limited by the method of data collection. Participants needed the economic and educational resources to access the internet in order to engage with this study. This is supported by the fact that 79.7% of the non-lawyers were either working towards or had completed degree level studies. Further work is underway to collect data from judiciary and non-lawyers in other countries to examine generalisability of the results.

To conclude, judges have significant weight in the development of laws. It is clear that the first step towards achieving adequate laws in this area is to increase genetic expertise of the justice stakeholders. The study identified specific weaknesses in judges' knowledge, and this information can be used in designing training programmes. Over the past ten years genetics has begun to penetrate curricula across the social sciences, including degrees in psychology, sociology, anthropology and economics. We hope that the findings of the present study will encourage this trend in training of lawyers.

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Conflict of interest:

The authors declare no conflict of interest.

References

1. Oliveri S, Masiero M, Arnaboldi P, Cutica I, Fioretti C, Pravettoni G. Health Orientation, Knowledge, and Attitudes toward Genetic Testing and Personalized Genomic Services: Preliminary Data from an Italian Sample [Internet]. *BioMed Research International*. 2016 [cited 2019 Jun 10]. Available from: <https://www.hindawi.com/journals/bmri/2016/6824581/>
2. Catley P, Claydon L. The use of neuroscientific evidence in the courtroom by those accused of criminal offenses in England and Wales. *J Law Biosci*. 2015 Jul 14;2(3):510–49.
3. Archibald AD, Smith MJ, Burgess T, Scarff KL, Elliott J, Hunt CE, et al. Reproductive genetic carrier screening for cystic fibrosis, fragile X syndrome, and spinal muscular atrophy in Australia: outcomes of 12,000 tests. *Genet Med* [Internet]. 2017 Oct 26 [cited 2017 Nov 7]; Available from: <https://www.nature.com/gim/journal/vaop/ncurrent/full/gim2017134a.html>
4. Innocence Project. DNA Exonerations in the United States [Internet]. Innocence Project. [cited 2019 Jul 14]. Available from: <https://www.innocenceproject.org/dna-exonerations-in-the-united-states/>
5. Plomin R, DeFries JC, Knopik VS, Neiderhiser JM. Top 10 Replicated Findings From Behavioral Genetics. *Perspectives on Psychological Science*. 2016 Jan 1;11(1):3–23.
6. Polderman TJC, Benyamin B, Leeuw CA de, Sullivan PF, Bochoven A van, Visscher PM, et al. Meta-analysis of the heritability of human traits based on fifty years of twin studies. *Nature Genetics*. 2015 Jul;47(7):702–9.
7. Jones M. Overcoming the myth of free will in criminal law: the true impact of the genetic revolution. *Duke Law J*. 2003 Mar;52(5):1031–53.
8. Hill WD, Marioni RE, Maghzian O, Ritchie SJ, Hagenaars SP, McIntosh AM, et al. A combined analysis of genetically correlated traits identifies 187 loci and a role for neurogenesis and myelination in intelligence. *Molecular Psychiatry*. 2018 Jan 11;1.
9. Howard DM, Adams MJ, Shirali M, Clarke T-K, Marioni RE, Davies G, et al. Genome-wide association study of depression phenotypes in UK Biobank identifies variants in excitatory synaptic pathways. *Nature Communications*. 2018 Apr 16;9(1):1470.
10. Okbay A, Beauchamp JP, Fontana MA, Lee JJ, Pers TH, Rietveld CA, et al. Genome-wide association study identifies 74 loci associated with educational attainment. *Nature*. 2016 May;533(7604):539–42.
11. Zhang-James Y, Fernández-Castillo N, Hess JL, Malki K, Glatt SJ, Cormand B, et al. An integrated analysis of genes and functional pathways for aggression in human and rodent models. *Molecular Psychiatry*. 2018 Jun 1;1.
12. Selita F. Genetic data misuse: risk to fundamental human rights in developed economies. *Legal Issues Journal*. 2019 Jan 15;7(1):53–95.
13. Denno DW. Courts' Increasing Consideration of Behavioral Genetics Evidence in Criminal Cases: Results of a Longitudinal Study. *Michigan State Law Review*. 2011;2011:967–1047.
14. Farahany NA. Neuroscience and behavioral genetics in US criminal law: an empirical analysis. *J Law Biosci*. 2015 Nov 1;2(3):485–509.
15. Catley P, Claydon L. The use of neuroscientific evidence in the courtroom by those accused of criminal offenses in England and Wales. *J Law and the BioSci*. 2015 Jul 14;lsv025.

16. Forzano F, Borry P, Cambon-Thomsen A, Hodgson SV, Tibben A, de Vries P, et al. Italian appeal court: a genetic predisposition to commit murder? *European Journal of Human Genetics*. 2010 May;18(5):519–21.
17. de Kogel CH, Westgeest EJMC. Neuroscientific and behavioral genetic information in criminal cases in the Netherlands. *J Law and the BioSci*. 2015 Jun 23;lsv024.
18. Bowling BV, Huether CA, Wang L, Myers MF, Markle GC, Dean GE, et al. Genetic Literacy of Undergraduate Non–Science Majors and the Impact of Introductory Biology and Genetics Courses. *BioScience*. 2008 Jul 1;58(7):654–60.
19. Lanie AD, Jayaratne TE, Sheldon JP, Kardia SLR, Anderson ES, Feldbaum M, et al. Exploring the Public Understanding of Basic Genetic Concepts. *Journal of Genetic Counseling*. 2004 Aug 1;13(4):305–20.
20. Miller JD, Scott EC, Okamoto S. Public Acceptance of Evolution. *Science*. 2006 Aug 11;313(5788):765–6.
21. Shaw KRM, Horne KV, Zhang H, Boughman J. Essay Contest Reveals Misconceptions of High School Students in Genetics Content. *Genetics*. 2008 Mar 1;178(3):1157–68.
22. Chapman R, Likhanov M, Selita F, Zakharov I, Smith-Woolley E, Kovas Y. New literacy challenge for the twenty-first century: genetic knowledge is poor even among well educated. *J Community Genet*. 2018 Mar 28;1–12.
23. United States Sentencing Commission, editor. Intra-city differences in federal sentencing practices: federal district judges in 30 cities, 2005-2017. Washington, DC: United States Sentencing Commission; 2019. 1 p.
24. Aspinwall LG, Brown TR, Tabery J. The double-edged sword: does biomechanism increase or decrease judges’ sentencing of psychopaths? *Science*. 2012 Aug 17;337(6096):846–9.
25. Fuss J, Dressing H, Briken P. Neurogenetic evidence in the courtroom: a randomised controlled trial with German judges. *J Med Genet*. 2015 Nov;52(11):730–7.
26. Cheung BY, Heine SJ. The double-edged sword of genetic accounts of criminality: causal attributions from genetic ascriptions affect legal decision making. *Pers Soc Psychol Bull*. 2015 Dec;41(12):1723–38.
27. Berryessa CM. Judicial Stereotyping Associated with Genetic Essentialist Biases toward Mental Disorders and Potential Negative Effects on Sentencing: Judicial Stereotyping & Genetic Essentialist Biases. *Law & Society Rev*. 2019 Mar;53(1):202–38.
28. Chapman R, Likhanov M, Selita F, Smith-Woolley E, Kovas Y. Genetic Literacy And Attitudes Survey (Iglas): International Population-Wide Assessment Instrument. In 2017 [cited 2017 Dec 19]. p. 45–66. Available from: <http://www.futureacademy.org.uk/files/images/upload/ICPE2017F6.pdf>
29. Alba JW, Hutchinson JW. Knowledge Calibration: What Consumers Know and What They Think They Know. *J Consum Res*. 2000 Sep 1;27(2):123–56.
30. TAGC.world. Working Group on Legal, Ethical and Societal Implications of Genetics (LESIG) [Internet]. TAGC. [cited 2020 Jan 26]. Available from: <https://tagc.world/lesig/>
31. Gallop L, Chapman R, Selita F, Kovas Y. Effects of Education and Media Framing on Genetic Knowledge and Attitudes. *The European Proceedings of Social & Behavioural Sciences EpSBS*. 2017 Dec 12;33:121–41.