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Genetic Knowledge within a National Australian Sample: Comparisons with Other Diverse Populations

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Genetic knowledge · Public understanding of science · Temporal and cross-cultural comparisons · Social categorisations

Abstract

Background: Genetic knowledge, which plays important functions in our understanding of science, health, social groupings, and even behaviour, has been evaluated in past studies with various populations. This wide reach of genetics means that different types of items are used to assess genetic knowledge, which restricts meaningful comparisons across time- and locale-based studies. ***Aim:*** The present study addresses this limitation by recruiting an Australia-wide sample and evaluating their genetic knowledge using items sourced from four diverse samples. ***Method:*** Seven hundred and eighty Australians completed a variety of items assessing their genetic knowledge as well as several demographic indicators. ***Results:*** The results show superior overall genetic knowledge in the current sample compared with previous samples. Additionally, the study finds that genetic knowledge about health and illness seems to be the most accurate, whereas such knowledge about social categorisations and behaviours seems to be the most error-prone. In the current sample, being a female and having interest in genetics were positive predictors of genetic knowledge; surprisingly educational attainment was not a significant predictor. ***Conclusion:*** Compared with previous surveys, the current sample showed significantly better genetic knowledge. However, certain areas that relate to public understating still indicate rampant misperceptions.

In recent years, there has been a rapid advancement in scientific knowledge of genetics within various fields such as healthcare, research, policy, and education. We can now directly probe into our genetic code to better understand where our ancestors came from, which diseases we are at risk of developing, and what kind of physical and psychological attributes we are predisposed to have [1]. As such, the public is required to integrate new genetic information and make important life choices based on their genetic understanding [1–3]. While behavioural geneticists are uncovering the fascinating way in which our genes influence our behaviour (e.g., [4–6]), the psychological and philosophical literature has focused on the

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way in which people's understanding of genetics influences their beliefs, behaviours, and lifestyle choices [7–9]. It has been argued that the sophistication of an individual's genetic knowledge is an important indicator of the way people attribute social categories and human conditions to genetics [1, 8]. Surprisingly, current awareness and potential misconceptions of genetic concepts within the general public have received limited attention in the literature. Whereas some attempts to document levels of genetic knowledge (the ability to identify correct facts about genetics) within populations have been made [10–13], only few studies explore variations in such knowledge over time and across geographical divides [14].

Genetic Essentialism and Genetic Knowledge

Why is it important to assess genetic knowledge among individuals? Psychological literature has identified genetic essentialist biases that often arise when arguments about genetic causation are encountered. Genetic essentialism refers to the tendency to over-attribute a person's characteristics and behaviours, in all of their complexity, to their genetic makeup. In particular, Dar-Nimrod and Heine [7] argue that genetic essentialist thinking leads people to believe that traits are caused by genes in a determined and immutable sense, discounting other causal influences such as the environment. They are viewed as hard to change, natural, and embodying a typicality or identifying feature to members who share the same underlying gene or genes [7, 8]. These beliefs are at odds with our current scientific understanding of human genetics, where most traits are thought to be the product of a complex set of influences, including multiple genes and the environment, throughout development, which vary within and between groups (e.g., [15, 16]). Instead of genes determining particular behaviours or characteristics, single genes often provide probabilistic information about these elements. For most human characteristics, a large number of genes are thought to contribute towards trait variation through complicated intractable biological pathways, and via interactions with other genes, regulatory factors, and the environment [1].

Genetic essentialist thinking may be minimised by providing individuals with relevant knowledge. Adequate genetic knowledge helps health-related decisions such as determining genetic testing needs [17] as well as understanding of ethics and privacy issues related to genetics research [18]. For example, data on genetic diseases are largely lacking in diverse samples, which subsequently limits what is known about genetic diseases in heterogeneous populations [19]. Knowing this gap may lead minority groups to seek policy changes for increased funding and differentially weigh current genetically derived medical advice. The potential variations in genetic knowledge are particularly important for public health campaigns when attempting to identify and address knowledge gaps disproportionately affecting specific demographic groups.

Population-Based Studies of Genetic Knowledge

Several studies have attempted to quantify the knowledge of human genetic concepts among general populations around the world including within the United States [10, 11], Finland [12], and Western Australia [13]. With the exception of Molster et al. [13], the bulk of research within Australia has investigated genetic knowledge within clinical groups [20–22]. The genetic literacy of the Australian-wide population, accounting for key demographic variables such as age and gender, has yet to be reported.

Population-based studies have found large discrepancies in levels of genetic knowledge. For example, data suggest that knowledge of genetics was overall poor in countries like Russia, the UK, and the US [14], whereas it was considered moderate in Western Australia [13]. Furthermore, substantial variation in accuracy has been found between individual items within a specific study, with differences as large as 60% across items [10–12]. Taken together, this variability may be in part due to item selection (discussed in more detail below) and/or sample characteristics. In terms of key demographic variants, higher levels of education [10–13], greater affinity with genetics [13], greater exposure, as measured by professional involvement within genetics [12], and employment in white-collared professions in comparison to blue-collared or business owners [12], have all been implicated in predicting higher genetic knowledge to a small degree. However, the roles of age, gender, and country of origin are less clear. In some instances younger people showed better knowledge than older respondents [10, 12], but age does not always predict differences on specific genetic knowledge items [11, 14]. Some studies showed females as scoring higher on genetic knowledge than males [11, 13] or vice versa [14], whereas no gender differences were detected in others [12].

Inconsistencies between studies could indicate interstudy sample differences, potentially linked to demographic variables such as those listed above. However, many studies have generated their own items to measure genetic knowledge, with items selected to address specific aims of individual studies. As a consequence, there is a lack of consistency between studies and comparisons between them are complicated by item selection. The present survey is designed to address this vagueness. More broadly, an adequate measure of genetic knowledge is useful when attempting to identify cross-cultural, country-level factors (e.g., availability of genetic testing, uptake of such services, the use genetics technologies, and policy advancements) that also influence genetic knowledge.

Measures of Genetic Knowledge

Researchers have begun to look at subcategories of genetic knowledge [13, 23, 24]. Some emerging categories have included basic physiology of genetics [24], applied knowledge of the relationship between genes, health, and disease [13, 24], the complex mechanisms underlying genetics [13, 23], and procedural/skills relating to genetics and health [23]. A recent study by Fitzgerald-Butt et al. [24] conducted a psychometric analysis on an updated version of 18 items often used within clinical groups in the genetic knowledge literature [25–27], first presented by Jallinoja and Aro [12]. Following the removal of two items that did not fit neatly into categories, two underlying latent factors were identified that mapped to categories labelled basic (e.g., characteristics of genes, chromosomes, and gene function) and applied (e.g., the relationship of genes, health and disease) knowledge about genetics. This analysis, however, required the removal of two items, and the counterintuitive inclusion of the item "A gene can be seen with the naked eye" into the applied category. Furthermore, other population-based studies have included items that are unrelated to those within Fitzgerald-Butt et al. [24] and that may better map onto alternative categories [10, 11, 13]. Thus, it is unclear if the items used by Fitzgerald-Butt et al. [24] were diverse enough to capture all potential subtypes of genetic knowledge.

The attempt of Fitzgerald-Butt et al. [24] to identify the structure of genetic knowledge indicates that the literature is in need of consolidation and standardised methods of categorisation to allow between study comparisons of genetic knowledge. These categories should be derived from theoretical frameworks that may emphasise rounded education and/or a reduction in genetic essentialism [28, 29]. In this way, categorisation will present researchers with valuable information into what particular areas of genetic knowledge are in need of further education.

On examination of the items across population-based studies of genetic knowledge, it appears that individuals may have better knowledge of certain subtypes of items. In line with the adult population from Fitzgerald-Butt et al. [24], respondents in both Jallinoja and Aro [12] and Molster et al. [13] scored higher on questions about genetic inheritance and disease. This pattern, however, was not found by Ashida et al. [10] who discovered wide variation in accuracy for items relating to genetics and disease (approximately 20–80% accuracy on different items). There were notable inconsistencies between studies when focusing on both biology/physiology of genes (see [11, 13]) and the relationship between genes, family, and inheritance (see [12, 13]). Given these inconsistencies, it is important that future research use comparable items to allow for meaningful comparisons, such that conclusions about variations in genetic knowledge across time, context, and demographics can be drawn. As with overall genetic knowledge, subcategories of genetic knowledge may vary across different demographic groups. For instance, Fitzgerald-Butt et al. [24] found generational differences in knowledge related to different factors; parents showed better accuracy on applied genetics relating to health and disease, whereas adolescents showed a better understanding of the underlying physiology and biology of genetics. This variability means that to improve genetic knowledge of the population, research must first understand what area of genetic knowledge is lacking and for whom. This information can then be used to tailor educational programs and target specific groups.

The Current Study

The current study builds on past research in an attempt to document genetic knowledge in a national sample to address the following aims. First, the paper aims to measure overall genetic knowledge in an Australian-wide sample through a collation of items sourced from 4 past genetic knowledge population studies [10–13]. More specifically, it aims to document genetic knowledge variations across key demographics. In line with previous research, it is expected that those with more education [10–13], greater affinity with genetics [13], and greater exposure to genetics [12], will also have greater genetic knowledge. As there are inconsistencies in the literature regarding the difference in genetic knowledge based on age and gender [10–12], it is unclear if genetic knowledge will significantly vary across these groups.

Second, the study aims to compare the current sample's overall genetic knowledge to past samples using identical items. It is unclear if genetic knowledge in the population is changing over time, and the distinctly different items used to assess genetic knowledge across studies has made direct comparisons between them difficult, limiting conclusions that can be drawn about genetic knowledge changes.

Third, the current paper aims to compare the current sample with the source samples on each individual item. This comparison may assist in understanding the difficultly levels of each of the individual items while controlling for between sample differences.

Finally, the current study aims to test whether participants' knowledge differs based on subcategories of genetic knowledge including disease/health, family/inheritance, biology/physiology, social categorisation, and behaviour. In line with past research [12, 13, 24], it is expected that participants are more likely to score higher on items about genes and disease compared to items regarding the physiology and biology of genetics. It is also expected that they score lower on items about genetics and social categorisation, and genes and behaviour [11].

Method

Participants

Of the 957 individuals who were recruited by the research marketing company Qualtrics, 807 attempted the survey. Participants were required to be over 18 years old and fluent in English, so that they could adequately understand and respond to the questions. Of the attempted surveys, 13 cases were excluded for failing to attempt any items on the genetic knowledge questionnaire and 15 cases were excluded for failing to report age or reporting an age under 18. A difference score of the average of all the non-reversed scored items on the genetic knowledge scale and the reverse scored items on the genetic knowledge scale was calculated. If the difference score exceeded 3 standard deviations, the response was excluded from the analysis. Fifty-nine cases were identified and excluded based on these calculations. Of the remaining 720 cases that were analysed, 695 completed the full survey, whereas 25 partially completed the survey. Their ages ranged from 18 to 87 (mean age = 49.32, SD = 16.09). Preliminary analysis did not indicate systemic patterns of missing data either within or between individuals on the genetic knowledge questionnaire; thus, missing data were assumed to be missing at random; these data were estimated using maximum likelihood estimation for the general knowledge items [30].

Although the sampling procedure was not designed to obtain a representative sample, the sample is largely representative of the Australian population on most key demographic aspects (based on census data sourced from the Australian Bureau of Statistics [ABS]: [31], for regionality, and [32–34] for the rest), with a few exceptions. The sample has an over-representation of young adults (at the expense of the 55–64 age bracket), Anglo-Australians (at the expense of Euro-Australians and small minority groups), university graduates (at the expense of high school graduates and non-university trained), and non-religious (at the expense of non-Christians believers). A detailed comparison between the sample's demographics and census data can be found in Table 1.

Relevant Materials

Demographic Background

Demographic items included participants' age, gender, ethnicity, postcode (from which regionality information was derived), education, political orientation, religious background, and level of religiosity. Political orientation and religiosity were measured on a 7-point Likert scale (political orientation: 1 = strongly conservative to 7 = strongly progressive; religiosity 1 = not at all to 7 = extremely). In line with the Australian Bureau of Statistics (ABS, 2005), postcodes were coded based on the Accessibility/Remoteness Index of Australia (ARIA) and summarised into the following Remoteness Areas (RAs): major cities, inner regional, outer regional, remote, and very remote.

Exposure to Genetic Information and Genetic Affinity

Participants were asked whether their study and work involved genetics and inheritance, how well they felt they understood genetics and inheritance, and how interested they were in the topic. Two items assessed specific genetic professional or educational background (see online suppl. materials – henceforth OSM, for more information; see www.karger.com/doi/10.1159/000496381 for all online suppl. material). The items were correlated ($r = 0.38$, $p < 0.001$) and were combined into a single measure of genetic exposure, with lower scores indicating increased exposure. Genetic affinity was calculated by averaging two items ($r = 0.39$, $p < 0.001$) that assessed level of interest in and perceived understanding of genetic information (see OSM, online suppl. material). Lower scores on these combined variables indicate increased exposure/affinity.

Genetic Knowledge

At the time of the current study, validated scale items that measure genetic understanding were undeveloped. Thus, 30 statements were taken from the genetic knowledge questionnaires used by 4 previous studies: Ashida et al. [10] recruited a convenience sample from community health centres in a suburban county in New York State in 2008; in 2001, Christensen et al. [11] recruited a national US sample using random-digit dialling with oversampling of Black participants; Jallinoja and Aro [12] recruited a random national sample of Finish-speaking Finns in late 1996 to early 1997; in 2006, Molster et al. [13] recruited a random sample of residents of Western Australia using randomisation of the latest telephone directory. More detailed information about the characteristics of these four samples can be found in online supplementary Table S1. A few minor modifications were made to items due to outdated information, misleading language/information or significant overlap of meaning due to slightly different use of language between studies. For example, to represent current scientific literature, an item was updated from "it has been estimated that a person has about 70,000 genes" [12] to "it … 20,000–25,000 genes." Participants were presented with the thirty statements about genetics and inheritance, one at a time in randomised order. For each statement, they were asked to indicate whether or not the statement was correct (0 = not correct; 1 = correct). Participants were not given feedback on their performance. Percentages of the correct responses were calculated across all thirty items to create an overall genetic knowledge score for each participant. To compare overall genetic knowledge with results from past papers, percentages of correct responses were calculated separately based on the relevant items, corresponding to each of the source papers such that four alternative overall genetic knowledge scores were produced.

Procedure

The survey was hosted online, on the Qualtrics website. After providing consent, participants completed the demographics and genetic background questions. This was followed by the thirty genetic knowledge questions followed by additional measures that are beyond the scope of this article.

Results

Sample Demographics and Overall Genetic Knowledge

Sample characteristics and their correspondence to overall genetic knowledge scores are presented in Table 1. For descriptive purposes, political orientation was recoded into the following three categories: conservative (1–3), centre (4), and liberal (5–7), and religiosity was coded into the following three categories: low (1–3), somewhat (4), and high (5–7). As interpretations of groups may not be meaningful for small cell sizes, when possible, categories were collapsed when less than 24 responses fell within a single category (see OSM).

Comparisons of Overall Genetic Knowledge

The average overall genetic knowledge of the current sample was 75.8%. Overall genetic knowledge was compared between the current paper and the source papers by calculating the average scores of the items in the current sample, relevant to each source paper, to ensure accurate comparisons across papers. Based on these alternating overall genetic knowledge scores, independent t tests were used to compare the overall genetic knowledge of the current sample with the samples of past studies (mean difference ranged from 8.4 to 25.7%), see Table 2. The criterion for significance was adjusted (Bonferroni) to account for the number of statistical tests simultaneously performed on the data (4) leading to an adjusted critical p value of 0.0125. The sample surveyed for the current paper had significantly greater overall genetic knowledge than samples in all source papers when compared across common items ($p < 0.001$).

Table 1. Sample demographics and relevant percentage of correct overall genetic knowledge

	n	% of sample[a]	Nation wide %	Overall genetic knowledge, % correct responses (SD)[b]
Gender				
Female	379	52.6	50.7	77.1 (8.9)
Male	337	46.8	49.3	74.4 (9.7)
Other[c]	3	0.4		80.0 (10.0)
Age				
18–34	167	23.2	33.8	76.0 (10.3)
35–44	120	16.7	18.4	76.8 (8.8)
45–54	120	16.7	17.9	76.2 (9.8)
55–64	170	23.6	8.5	75.6 (9.1)
65+	143	19.9	21.3	74.9 (8.5)
Ethnicity				
Anglo/Celtic	453	62.9	83.6	76.2 (9.0)
European	123	17.1	10.2	75.8 (9.7)
East/Southeast Asian	48	6.7	7.8	73.6 (10.9)
South Asian	24	3.3	5.2	72.8 (10.6)
Other	69	9.7	0	76.2 (9.2)
State/territory				
New South Wales	252	35	31.9	75.7 (9.8)
Queensland	133	18.5	20	76.8 (8.8)
South Australia	63	8.8	7	72.3 (10.0)
Victoria	172	23.9	25.7	76.0 (8.8)
Western Australia	64	8.9	10.4	77.1 (7.6)
ACT, NT, and Tasmania	33	4.6	4.8	76.4 (11.4)
Regionality				
Major city	558	77.5	70.4	75.5 (9.5)
Inner regional	95	13.2	18.3	76.7 (9.2)
Outer regional	51	7.1	9	77.8 (8.7)
Remote/very remote	9	1.3	2.3	75.9 (9.5)
Education				
Completed year 10	134	18.6	15.7	74.6 (8.7)
Completed year 12	210	29.2	40.3	75.9 (8.3)
Completed an undergraduate degree	211	29.3	15.1	76.9 (10.2)
Completed a postgraduate degree	82	11.4	6.8	75.7 (10.7)
Other	83	11.5	22	74.8 (9.0)
Political orientation				
Conservative	154	21.4		75.2 (9.1)
Liberal	291	40.4		76.2 (8.9)
Centre	275	38.2		75.7 (9.9)
Religion				
Agnosticism/no religion	281	39.0	30.1	77.4 (8.6)
Christianity	362	50.3	52.1	75.4 (9.1)
Other religion	76	10.6	17.8	72.1 (11.6)
Religiosity				
High	155	21.5		74.7 (11.3)
Medium	128	17.8		73.7 (8.7)
Low	437	60.7		76.8 (8.6)
Exposure to genetics				
High/medium	30	4.2		74.1 (15.6)
Low	690	95.8		75.9 (9.0)
Genetic affinity				
High	261	36.3		77.6 (9.6)
Medium	409	56.8		75.1 (9.1)
Low	50	6.9		72.1 (8.4)

[a] Percentage indicates the actual percentage of the sample; missing values for demographic variables were removed using case-wise deletion (<1% of the sample). [b] Overall genetic knowledge is the average of all 30 genetic knowledge items. "Nationwide %" information reflects Australian census data. [c] Did not identify as either male or female.

Genetic Knowledge Subgroups

Items of genetic knowledge were categorised and averaged to create five subgroups based on context in line with relevant categorisations based on items' content and empirical and theoretical accounts (e.g., [13, 23, 24]): *disease* (knowledge about the role of genetics in disease), *social*

Table 2. Comparisons of overall genetic knowledge between the current paper and past papers

	Original paper mean % (SD)	Current paper mean % correct items (SD)	Between-paper difference		
			mean diff.	SE	*t*
Current paper (*n* = 720)	–	75.8 (9.4)			
Jallinoja and Aro [12] (*n* = 1,216)	64.6 (22.6)	82.7 (11.9)	18.1	0.91	$t(1,934) = 19.9$***
Molster et al. [13] (*n* = 1,009)	72.9 (14.0)	81.3 (13.5)	8.4	0.67	$t(1,727) = 12.5$***
Ashida et al. [10] (*n* = 971)	54.0 (28.0)	79.7 (18.2)	25.7	1.20	$t(1,689) = 21.5$***
Christensen et al. [11] (*n* = 1,200)	42.2 (20.4)	54.8 (20.6)	12.6	0.92	$t(1,918) = 13.6$***

*** $p < 0.001$. Overall genetic knowledge within the current paper was calculated based on the 30 genetic knowledge (GK) items. The current paper's GK scores were calculated by taking the average of items only sourced from the specific past paper such that a direct comparison between the past papers could be made. Overall GK for past papers were calculated manually from individual items with the exception of Ashida et al. [10], which was taken directly from the original paper. The total number of items used to calculate the alternate overall genetic knowledge scores were as follows: 13 items for Jallinoja and Aro [12], 12 items for Molster et al. [13], 5 items for Ashida et al. [10], and 6 items for Christensen et al. [11]. Six items overlapped across sources. For more details on individual items and their sources, see Table 1 in the OSM.

group (knowledge about genetic attributions to social group categorisation), *family* (knowledge about inheritance and family genetics), *physiology/biology* (knowledge about the physiology and biology of genes), and *behaviour* (knowledge about the role in genes determining behaviour). Based on these groupings, subtotals of genetic knowledge from the current paper and past papers were calculated. The source papers varied in items used to measure the subgroups of genetic knowledge. Thus, average scores of the items in the current sample, relevant to each source paper, were calculated to ensure unbiased comparisons across papers (Table 3). The percentage of correct genetic knowledge answers within the current study varied widely. In the current sample, respondents scored highest on items relating to disease and genetics (84.9% correct) and worst on items relating to understanding genetics and social groups (42.1% correct).

Subgroup totals of genetic knowledge were compared between the current paper and the source papers using nine independent samples *t* tests and one χ^2 test (Table 3), with a critical *p* value of 0.005 (adjusted for the 10 comparisons). The sample in the current paper demonstrated significantly greater genetic knowledge about disease, social group, family, and physiology/biology than all of the past papers ($p < 0.001$), except one comparison – [13]. Large variations in various areas of genetic knowledge, as demonstrated in the source papers, were found; these differences are also reflected in the current sample, indicating the importance of standardisation of measures.

Item by Item Comparisons of Genetic Knowledge

For a description of the number of correct responses to the individual genetic knowledge items in the current paper and the source papers, see online supplementary Table S2. Across the 30 items, the percentage of correct answers in the current sample ranged from 19 to 98%. χ^2 tests of independence were conducted to test for differences in the percentage of correct responses between the current paper and the source papers. Some items appeared in more than one source paper leading to 36 comparisons. Bonferroni-adjusted *p* values took into account the number of comparisons (36) to attain adjusted critical *p* value of 0.0013. Of these comparisons, 26 (72%) were significant; in each, the current sample had a greater percentage of correct responses ($p < 0.001$).

Current Study's Predictors of Genetic Knowledge

To assess group differences in overall genetic knowledge within the current sample, a multiple regression analysis was conducted. Overall genetic knowledge was regressed on gender, age, regionality, educational attainment, political orientation, and genetic affinity. Exposure to genetics was omitted as a predictor as only 4% of the sample indicated more than low exposure to genetics.

All included predictor variables were continuous with the exception of gender. Given the minimal endorsement of "other" for gender, these responses were not included in the analysis, such that, the variable was dummy coded

Table 3. Comparison between subgroups of genetic knowledge questions between past papers and the current paper

Subgroups of genetic knowledge (number of items)	Current paper mean (SD)	Past paper mean (SD)	Between-paper difference		
			mean diff.	SE	t
Disease					
Total (11)	84.9 (13.5)	–			
Jallinoja and Aro [12] (6)	90.7 (14.4)	81.0 (10.5)	9.7	0.57	$t(1{,}934) = 17.05^{***}$
Molster et al. [13] (5)	85.7 (17.3)	82.4 (9.0)	3.3	0.64	$t(1{,}727) = 5.16^{***}$
Ashida et al. [10] (4)	76.2 (21.3)	54.3 (31.2)	21.9	1.35	$t(1{,}689) = 16.24^{***}$
Social group					
Total (3)	42.1 (28.4)				
Christensen et al. [11] (3)	42.1 (28.4)	37.3 (10.7)	4.8	0.91	$t(1{,}918) = 5.27^{***}$
Family					
Total (10)	81.0 (13.4)	–	–	–	–
Jallinoja and Aro [12] (3)	88.0 (19.4)	76.0 (13.9)	12.0	0.76	$t(1{,}934) = 15.79^{***}$
Molster et al. [13] (5)	81.5 (18.3)	74.0 (15.5)	7.5	0.81	$t(1{,}727) = 9.19^{***}$
Ashida et al. [10] (1)[a]	93.6 (n.a.)	88 (n.a.)	$\chi^2 = 41.2^{***}$		
Christensen et al. [11] (2)	70.5 (32.0)	58.5 (30.4)	12.0	1.46	$t(1{,}918) = 8.21^{***}$
Physiological/biological					
Total (9)	76.8 (15.3)	–	–	–	–
Jallinoja and Aro [12] (7)	75.9 (16.7)	50.6 (20.7)	25.3	0.91	$t(1{,}934) = 27.91^{***}$
Molster et al. [13] (4)	80.1 (23.3)	67.8 (16.8)	12.3	0.96	$t(1{,}727) = 12.75^{***}$
Behaviour					
Total (1)	61.5 (n.a.)				
Christensen et al. [11] (1)[a]	61.5 (n.a.)	24 (n.a.)	$\chi^2 = 261.5^{***}$		

* $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$. [a] A single item of genetic knowledge constituted all items within the subscale and shared between the current paper and source paper.

into males = 0 and females = 1. During assumption checks, 4 cases in which studentised deleted residuals were greater than ±3.29 standard deviations were detected and removed. All other assumptions appeared to have been met. The regression model significantly predicted overall genetic knowledge $F(6{,}698) = 6.01$, $p < 0.001$, adj. $R^2 = 0.05$. Regression coefficients and standard errors can be found in Table 4.

When controlling for the other predictors in the model, gender ($\beta = 0.13$, $t(698) = 3.42$, $p = 0.001$), and genetic affinity ($\beta = -0.15$, $t(698) = -4.08$, $p < 0.001$) significantly predicted overall genetic knowledge. Specifically, females appeared to have greater genetic knowledge than males, and genetic affinity was associated with higher levels of genetic knowledge controlling for other variables. Education attainment, regionality, and political orientation did not appear to predict overall genetic knowledge above and beyond the other predictors ($p > 0.05$).

Table 4. Regression coefficients and standard errors predicting overall genetic knowledge from gender, age, regionality, educational attainment, political orientation, and genetic affinity

Variable	b	SE_b	B
Gender	0.023	0.007	0.129^{***}
Age	<0.001	<0.001	–0.031
Regionality	0.004	0.003	0.056
Educational attainment	0.001	0.003	0.013
Political orientation	0.001	0.002	0.012
Genetic affinity	–0.024	0.006	-0.153^{***}

b, unstandardised regression coefficient; SE_b, standard error; *B*, standardised regression coefficient. *** $p < 0.001$.

Discussion

The current study provides a contemporary snapshot of genetic-related knowledge among an Australian national sample, using a collation of items from 4 past population studies of genetic knowledge [10–13]. The Australian-wide sample, on average, responded correctly to 76% of the 30 genetic knowledge items in which they were asked to choose the correct answer from two provided options. Furthermore, the current paper detailed overall genetic knowledge of specific demographic groups based on gender, age, ethnicity, state of residence, regionality, education level, religion, religiousness, political orientation, and genetic affinity (genetics' understanding and interest). Surprisingly, overall genetic knowledge was relatively stable across the various subgroupings (based on gender, regionality, and education) whose scores on the genetic knowledge test reflected a relatively narrow band of accuracy that ranged from 72 to 80%. This finding is in line with the small amount of variability in genetic knowledge that the present variables (various demographics and genetic affinity) were able to explain and may reflect the importance of future search of explanatory variables that were not included in the current study.

In past papers, items used to assess genetic knowledge had been inconsistent. The current study aimed to pool together items from previous studies, such that individual items and overall genetic knowledge could be compared across samples, controlling for item selection. When compared based on similar items, the current sample scored significantly higher than all four of the source paper samples on overall genetic knowledge. This consistent increase in genetic knowledge suggests that genetic knowledge may have increased in the Western population over time. While speculative, this potential rise in genetic knowledge may be a result of a general increase in genetic information availability through academic and clinical settings as well as health campaigns, mainstream media, and internet resources [8, 28]. This difference, however, may be accounted for by confounding factors such as geographical location, participant characteristics, and sampling methods. That said, the relatively large number of participants in each study reduces the likelihood that such demographics and individual differences may have been the main difference makers, whereas the comparison with one previous Australian sample (which was regional – Western Australia [13]) suggests that the sample's geographical origin is likely not to be the reason (or the sole reason) for the noticeable improvement in knowledge. Further research is needed to explore potential mechanisms of the apparent change in genetic knowledge over time. Furthermore, longitudinal studies are recommended to document genetic knowledge over time to control for confounding issues that arise when comparing multiple studies, especially geographically diverse ones.

There was substantial variability in the overall scores, as summed in the current sample based on items relevant to each of the 4 source papers separately. That is, the scores ranged from an average of 54 to 81% in overall genetic knowledge depending on the source of the items. These variations within the current sample mirrored the differences originally found in the data from the source paper samples, suggesting that the differences in genetic knowledge between past papers may be, at least in part, a result of items' selection rather than true genetic knowledge.

The current paper also aimed to compare subcategories of genetic knowledge based on their categorisations into disease/health, family/inheritance, physiology/biology, social group and behaviour. The current sample scored highest on items relating to health and disease followed by knowledge about family and inheritance, genes' physiology and biology, genes and behaviour, and lastly, genetics and social groups. These results are consistent with past research that found better knowledge on items about the relationship between genetics and disease compared to items about the physiology/biology of genetics [12, 13, 24, 25]. This pattern may not generalise to genetic knowledge among youth [24]. Until such time that the psychometric properties of the genetic knowledge measure can be ascertained, further studies intending on using the items in this study may consider focusing on (1) items that participants showed moderate-to-low knowledge – physiology and biology, behaviour, and social group, (2) items that significantly differed across populations (see OSM), or (3) items that target specific knowledge that is particularly relevant to important outcomes in the area studied.

The finding that the Australian public showed larger misunderstandings on items relating to genetics, behaviour, and social grouping is consistent with previous research documenting genetic knowledge in the general public in other countries [10, 11]. These findings suggest that the lay population may be misattributing social grouping (e.g., gender and/or race) to greater genetic similarity and thus, may have a deterministic understanding of how genes relate to behaviour and social categorisation. These findings seem to be in line with theoretical (e.g., [7, 35]) and empirical findings on various social categorisations (e.g., [36–41]) that demonstrate the role of genetic attributions in essentialising social categories and in biasing perceptions of such groups. Alternatively, information about genetics, disease, and health is commonly presented through mainstream media, health campaigns, and on the internet [28, 42]. Furthermore, general information about inheritance and the physiology/biology of genes is readily available through internet sites and is delivered within the curriculum of secondary school science. Access to information, rather than biases, may thus be a potential explanation to the variability in errors.

The apparent misattributing of social grouping to greater genetic similarity is of concern, as it has been argued that such misunderstanding of genetics may be associated with genetic essentialist biases that underpin discrimination and eugenic ideologies [7, 8]. Improving these areas of genetic knowledge may aid combatting prejudice towards stigmatised groups. Nonetheless, this should be interpreted with caution as there was a limited number of items used to assess genetic knowledge as it relates to social groupings. Relatedly, the lack of variability in items and categories, as sourced from past research, may be indicative of prioritisation of other areas of genetic knowledge within the literature. Future research should aim to assess what categories and items are needed to adequately account for the different facets of genetic knowledge in understudied areas (e.g., social grouping and behaviour) and to explore the link between these subcategories of genetic knowledge, genetic essentialism, and discrimination.

The hypothesis that overall genetic knowledge may vary based on key demographic variables was partially supported. Specifically, genetic knowledge was predicted by genetic affinity; however, it was not predicted by genetic exposure or educational attainment when demographics and genetic affinity were simultaneously entered. The unexpected finding that overall genetic knowledge did not vary with educational attainment is out of step with previous research that consistently indicated that more education is associated with greater overall genetic knowledge [10–13]. Instead, consistent with previous research [13], genetic affinity (as measured by indicating greater interest in and understanding of genetics) predicted higher levels of genetic knowledge. Therefore, in the current sample, it appears that interest and understanding of genetics are better independent predictors of genetic knowledge than educational attainment. This finding falls in line with previous findings [14], which found poor genetic knowledge even among educated individuals across different cultures. This finding may be explained by the accessibility of genetic information from multiple sources. That is, as people look to mainstream media and the internet for genetic information [28], the impact of formal education may, at this time, be less important in predicting overall levels of genetic knowledge. As such, the attainment of higher education does not necessitate the study of genetic content, particularly since most higher education programs only provide minimal (or no) training in the field of genetics.

Contrary to predictions, genetic exposure (measured by the amount of genetics involved in one's studies and work) did not significantly predict genetic knowledge. This finding should be interpreted cautiously as those with medium and higher exposure to genetics were considerably underrepresented, with 96% of respondents indicating they had low exposure to genetics. Research has indicated that while individuals tend to seek advice about inheritance and risk factors from their primary care physicians rather than a geneticist, these healthcare providers may not have the knowledge to competently fulfil that role [28, 43, 44]. By investigating the genetic knowledge of healthcare providers, who would be considered as having medium exposure to genetics through their study and work, the gaps in professional knowledge of such individuals can be identified and addressed. Interestingly, despite this low exposure to genetics, 93% of the sample reported having moderate to high genetic affinity and may reflect reduced representativeness of the current sample in that regard. This paradox of being confident in one's understanding of genetics despite having low day-to-day exposure to genetics is an avenue for future research to explore, especially in addressing the consequences of such conflicting beliefs. Thus, future research should investigate the association between genetic exposure and genetic knowledge in a sample that adequately represents high, medium, and low exposure and affinity to genetics as well as seek to explain the discrepancy between exposure and affinity.

Lastly, females appear to have greater genetic knowledge than males in Australia at this time. Past research on gender differences has produced inconsistent findings. Christensen et al. [11] and Molster et al. [13] found that on some items females scored higher than males, whereas, Jallinoja and Aro [12] did not detect gender differences. To the best of our knowledge, no theoretical account has targeted gender differences in genetic knowledge or the specific areas that such differences should be expected. Research in broader areas of health knowledge, however, suggests that women are more knowledgeable than men, particularly regarding information concerning reproductive and childhood health [45]. Furthermore, American women are more likely to be a household's healthcare decision maker (US Department of Labor, 2013 [46]), potentially resulting in higher exposure to genetic information related to reproductive health and family planning. Future studies can examine whether this trend extends to Australian women's genetic knowledge particularly in areas concerning reproductive and developmental health.

In summary, there appears to be an increase in overall genetic knowledge in the current sample compared to samples in past surveys. However, given the use of cross-study comparisons, it is impossible to determine whether these differences are due to an increase in genetic knowledge in the lay public (the possibility that we find the most likely) or other study-specific demographic differences (including geographical differences, sampling differences, sample-specific attributes differences). Nevertheless, the difference in overall genetic knowledge found in the source papers appears to be, in part, driven by item selection and the proportion of items representative of specific subcategories of genetic knowledge. It has yet to be established that the items used in the current paper are appropriate for measuring genetic knowledge in the population. With the exception of items sourced from Jallinoja and Aro [12], the current paper and source papers assessed genetic knowledge using items that have not been previously validated and that did not undergo formal validation in the present analysis. The addition of items to comprehensibly measure genetic knowledge in the areas of social group and behaviour is highly desirable in future research. Furthermore, items that assess individuals' understanding of multi-factorial disease and penetrance should be considered [2, 25, 47] to ensure that a sufficient depth of knowledge is understood by those being assessed.

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Statement of Ethics

Ethics approval for this study was granted by an institutional Human Research Ethics Committee.

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