LETTER TO EDITOR

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## Letter to the Editor: Time to update the language of genetics from the nineteenth to the twenty-first century: a response to Schmidtke and Cornel

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Promoting respect for the autonomy of individuals, pursuing equity in any advances by health-related genetics and being cognizant of the sensibilities of those communities impacted by either genetic diseases or those policies designed to address them must be keystones of the development of genetics in the 2020s and beyond (Schmidtke and Cornel 2020). But there is an additional, more prosaic agenda to address. We need to update the language of genetics to make it fit for the public discourses it needs to engage with.

We have been very pleased to be part of the wide ROHgen collaboration that reports the effects of autozygosity on a broad range of human phenotypes (Clark et al. 2019). Our contribution involved making data available from the birth cohort study, Born in Bradford (www.borninbradford.nhs. uk). Integral to the long-term relationship we have with the families in our cohort is a commitment to share findings that we have directly generated, or that arise from our collaborations. The findings reported in Clark et al. 2019 offer much that enriches understanding of key areas of concern in relation to autozygosity and human phenotypes. It does, like much research in this field, present challenges in reframing a complex analysis for a lay public. But additionally, and also familiar in the field, the paper generated some anxiety in our cohort research team about the reaction we might get when we share its insights with our cohort participants. We are anxious about the language of genetics and specifically those terminologies that reflect the animal models that have been important in its

Neil Small n.a.small@bradford.ac.uk evolution as a discipline, including "in-breeding", "mating" and "pedigree".

Advances in the understanding of genetics in medicine have seen a shift from a focus solely on discovery into a wider focus that now includes application. When such a shift occurs, different constituencies of interest are engaged and different questions raised. The insights of genetic science need to be translated into the language of clinical medicine and, if actions that impact on patients are to result, into the language of risk and of human costs and benefits.

Interdisciplinary interactions are challenging because of the different assumptions that underpin the dominant paradigms of practice. But the interactions between genetic scientists and clinical scientists are facilitated by a shared scientific epistemology. To fulfil the potential of genetics in terms of wider implementation, a bigger challenge exists in engaging with the general population (Table 1). The tropes of our contemporary debate on genetics centre on its potential to illuminate lifetime propensities and risks and to make possible personalised medicine. In this context, at the very least, the general public need to understand the potential and the limitations of genetic science and clinical genetics if they are to exercise informed consent as they participate in research or avail themselves of treatment. Furthermore, the public need to support the scientific endeavour by making themselves available as research subjects-agreeing to provide genetic material for example-and by supporting the political will that will ensure appropriate resource allocations for scientific and medical advance. Achieving the shift in scale that twenty-first century genetics seeks requires a language that invites the public in, not a language that invokes their fears or stigmatises them. There are many precedents that illustrate the importance and the impact of shifts in the language of medicine. It is not such a long time ago when terminology included "cripples" and "the subnormal"; we talk of seizures not fits because "fits" is not precise and because it has a connotation that is stigmatising; we have disabled people rather than "the disabled", and we

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Shifts in focus/ paradigm shifts	Disciplinary focus	Key personnel	Language needed
Discovery	Genetic science (in animals and humans)	Academic and commercial scientists/funders	Scientific precision/adding to established understandings
Utility/implementation	Clinical science	Clinicians/doctors/regulators/commissioners	Benefits (and costs)/risk
Acceptability	Behavioural science/social sci- ence	Public health/health education/voluntary sector	Inclusive/understandable/non-stigmatising

 Table 1
 Constituencies of interest engaged and language needed for wider implementation of genetics

talk of labour not delivery because we are reminded of who the most important party in the birth is!

That part of our research agenda that most pertains to these issues concerns autosomal recessive disorders in the context of a population with high levels of consanguinity (Sheridan et al. 2013.) Achieving any behaviour change that builds on an understanding of genetic risk requires our target population to accept the veracity of what we say, to recognise our benign intentions and to be clear about the actions that follow the insights of genetic and clinical science that we seek to impart. To do this, we have to invoke a language that is nonstigmatising. A service review by Salway et al. (2016) captures the challenges in accessing target communities for genetic counselling and testing, citing the need for approaches that engender trust and that are not seen as stigmatising. Conversely, when communities are approached with sensitivity, using culturally appropriate and accessible language, initiatives are responded to positively (Darr et al. 2016). In an analogous area attempts to encourage weight loss via approaches that are seen as objectifying, shaming and judgemental are counter-productive (Muenning 2008).

The scientific precision and legacy importance of terms like "pedigree" or "in-breeding" may benefit one phase of genetics evolution but do not serve well the shift into a population-based discourse. Nor does a too easy conflation of genetic risk with a social practice (a preference for marriage between blood relations in this case). While there are not easily available synonyms for legacy terms, we might consider "ancestry" or "inheritance" instead of pedigree and "related by blood" instead of in-breeding. But the development of a new terminology would benefit from the wisdom of crowds. We invite colleagues to engage in a debate about an appropriate language for the genetics of the twenty-first century—a language that is both precise and inclusive.

## References

Clark DW, Okada Y, Moore KHS, Mason D, Pirastu N, Gandin I, Mattsson H, Barnes CLK, Lin K, Zhao JH, Deelen P, Rohde R, Schurmann C, Guo X, Giulianini F, Zhang W, Medina-Gomez C, Karlsson R, Bao Y, Bartz TM, Baumbach C, Biino G, Bixley MJ, Brumat M, Chai JF, Corre T, Cousminer DL, Dekker AM, Eccles DA, van Eijk KR, Fuchsberger C, Gao H, Germain M, Gordon SD,

de Haan HG, Harris SE, Hofer E, Huerta-Chagova A, Igartua C, Jansen IE, Jia Y, Kacprowski T, Karlsson T, Kleber ME, Li SA, Li-Gao R, Mahajan A, Matsuda K, Meidtner K, Meng W, Montasser ME, van der Most PJ, Munz M, Nutile T, Palviainen T, Prasad G, Prasad RB, Priyanka TDS, Rizzi F, Salvi E, Sapkota BR, Shriner D, Skotte L, Smart MC, Smith AV, van der Spek A, Spracklen CN, Strawbridge RJ, Tajuddin SM, Trompet S, Turman C, Verweij N, Viberti C, Wang L, Warren HR, Wootton RE, Yanek LR, Yao J, Yousri NA, Zhao W, Adeyemo AA, Afaq S, Aguilar-Salinas CA, Akiyama M, Albert ML, Allison MA, Alver M, Aung T, Azizi F, Bentley AR, Boeing H, Boerwinkle E, Borja JB, de Borst GJ, Bottinger EP, Broer L, Campbell H, Chanock S, Chee ML, Chen G, Chen YDI, Chen Z, Chiu YF, Cocca M, Collins FS, Concas MP, Corley J, Cugliari G, van Dam RM, Damulina A, Daneshpour MS, Day FR, Delgado GE, Dhana K, Doney ASF, Dörr M, Doumatey AP, Dzimiri N, Ebenesersdóttir SS, Elliott J, Elliott P, Ewert R, Felix JF, Fischer K, Freedman BI, Girotto G, Goel A, Gögele M, Goodarzi MO, Graff M, Granot-Hershkovitz E, Grodstein F, Guarrera S, Gudbjartsson DF, Guity K, Gunnarsson B, Guo Y, Hagenaars SP, Haiman CA, Halevy A, Harris TB, Hedayati M, van Heel DA, Hirata M, Höfer I, Hsiung CA, Huang J, Hung YJ, Ikram MA, Jagadeesan A, Jousilahti P, Kamatani Y, Kanai M, Kerrison ND, Kessler T, Khaw KT, Khor CC, de Kleijn DPV, Koh WP, Kolcic I, Kraft P, Krämer BK, Kutalik Z, Kuusisto J, Langenberg C, Launer LJ, Lawlor DA, Lee IT, Lee WJ, Lerch MM, Li L, Liu J, Loh M, London SJ, Loomis S, Lu Y, Luan J', Mägi R, Manichaikul AW, Manunta P, Másson G, Matoba N, Mei XW, Meisinger C, Meitinger T, Mezzavilla M, Milani L, Millwood IY, Momozawa Y, Moore A, Morange PE, Moreno-Macías H, Mori TA, Morrison AC, Muka T, Murakami Y, Murrav AD, de Mutsert R, Mychaleckvi JC, Nalls MA, Nauck M, Neville MJ, Nolte IM, Ong KK, Orozco L, Padmanabhan S, Pálsson G, Pankow JS, Pattaro C, Pattie A, Polasek O, Poulter N, Pramstaller PP, Quintana-Murci L, Räikkönen K, Ralhan S, Rao DC, van Rheenen W, Rich SS, Ridker PM, Rietveld CA, Robino A, van Rooij FJA, Ruggiero D, Saba Y, Sabanayagam C, Sabater-Lleal M, Sala CF, Salomaa V, Sandow K, Schmidt H, Scott LJ, Scott WR, Sedaghati-Khayat B, Sennblad B, van Setten J, Sever PJ, Sheu WHH, Shi Y, Shrestha S, Shukla SR, Sigurdsson JK, Sikka TT, Singh JR, Smith BH, Stančáková A, Stanton A, Starr JM, Stefansdottir L, Straker L, Sulem P, Sveinbjornsson G, Swertz MA, Taylor AM, Taylor KD, Terzikhan N, Tham YC, Thorleifsson G, Thorsteinsdottir U, Tillander A, Tracy RP, Tusié-Luna T, Tzoulaki I, Vaccargiu S, Vangipurapu J, Veldink JH, Vitart V, Völker U, Vuoksimaa E, Wakil SM, Waldenberger M, Wander GS, Wang YX, Wareham NJ, Wild S, Yajnik CS, Yuan JM, Zeng L, Zhang L, Zhou J, Amin N, Asselbergs FW, Bakker SJL, Becker DM, Lehne B, Bennett DA, van den Berg LH, Berndt SI, Bharadwaj D, Bielak LF, Bochud M, Boehnke M, Bouchard C, Bradfield JP, Brody JA, Campbell A, Carmi S, Caulfield MJ, Cesarini D, Chambers JC, Chandak GR, Cheng CY, Ciullo M, Cornelis M, Cusi D, Smith GD, Deary IJ, Dorajoo R, van Duijn CM, Ellinghaus D, Erdmann J, Eriksson JG, Evangelou E, Evans MK, Faul JD, Feenstra B, Feitosa M, Foisy S,

Franke A, Friedlander Y, Gasparini P, Gieger C, Gonzalez C, Goyette P, Grant SFA, Griffiths LR, Groop L, Gudnason V, Gyllensten U, Hakonarson H, Hamsten A, van der Harst P, Heng CK, Hicks AA, Hochner H, Huikuri H, Hunt SC, Jaddoe VWV, de Jager PL, Johannesson M, Johansson Å, Jonas JB, Jukema JW, Junttila J, Kaprio J, Kardia SLR, Karpe F, Kumari M, Laakso M, van der Laan SW, Lahti J, Laudes M, Lea RA, Lieb W, Lumley T, Martin NG, März W, Matullo G, McCarthy MI, Medland SE, Merriman TR, Metspalu A, Meyer BF, Mohlke KL, Montgomery GW, Mook-Kanamori D, Munroe PB, North KE, Nyholt DR, O'connell JR, Ober C, Oldehinkel AJ, Palmas W, Palmer C, Pasterkamp GG, Patin E, Pennell CE, Perusse L, Peyser PA, Pirastu M, Polderman TJC, Porteous DJ, Posthuma D, Psaty BM, Rioux JD, Rivadeneira F, Rotimi C, Rotter JI, Rudan I, den Ruijter HM, Sanghera DK, Sattar N, Schmidt R, Schulze MB, Schunkert H, Scott RA, Shuldiner AR, Sim X, Small N, Smith JA, Sotoodehnia N, Tai ES, Teumer A, Timpson NJ, Toniolo D, Tregouet DA, Tuomi T, Vollenweider P, Wang CA, Weir DR, Whitfield JB, Wijmenga C, Wong TY, Wright J, Yang J, Yu L, Zemel BS, Zonderman AB, Perola M, Magnusson PKE, Uitterlinden AG, Kooner JS, Chasman DI, Loos RJF, Franceschini N, Franke L, Haley CS, Hayward C, Walters RG, Perry JRB, Esko T, Helgason A, Stefansson K, Joshi PK, Kubo M, Wilson JF (2019) Associations of autozygosity with a broad range of human phenotypes. Nat Commun 10:4957. https://doi.org/10.1038/s41467-019-12283-6

- Darr A, Small N, Ahmad WIU, Atkin K, Corry P, Modell B (2016) Addressing key issues in the consanguinity-related risk of autosomal recessive disorders in consanguineous communities: lessons from a qualitative study of British Pakistanis. J Community Genet 7:65–79
- Muenning P (2008) The body politic: the relationship between stigma and obesity-associated disease. BMC Public Health 8:128. https://doi. org/10.1186/1471-2458-8-128
- Salway S, Ali P, Ratcliffe G, Such E, Khan N, Kingston H, Quarrell O (2016) Responding to the increased genetic risk associated with customary consanguineous marriage among minority ethnic populations: lessons from local innovations in England. J Community Genet 7:215–228
- Sheridan E, Wright J, Small N, Corry PC, Oddie S, Whibley C, Petherick ES, Malik T, Pawson N, McKinney PA, Parslow RC (2013) Risk factors for congenital anomaly in a multi-ethnic birth cohort: an analysis of the Born in Bradford study. Lancet 382(9901):1350– 1359
- Schmidtke J, Cornel MC (2020) Editorial: contentious ethical issues in community genetics: let's talk about them. J Community Genet 11: 5–6

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