

## **The measurement of ancestral roots with genealogical data**

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## **Abstract**

This study presents a new method to measure the depth of ancestral roots in a population. This method sheds light on the migratory movements which led to present-day population distribution across space. The method was applied to a dataset of 5,100 ascending genealogies from seventeen regions of the province of Quebec (Canada). Dates of marriage of the earliest ancestors married in the same region as their descendants were used to measure the age of individual ancestral roots. The average regional ages vary between 16 and 157 years, while some individual roots reach as far back as 300 years in the same region. The proposed method can be useful for assessing how deeply rooted a contemporary population is at a local, regional or other geographical level.

**Keywords:** ancestral roots, genealogies, regional founders, population database.

## Introduction

“Our family has been here for generations”. Such a statement on multi-generation presence characterizes individuals or families who consider themselves to be deeply rooted in their territory. Transmission and presence of family names are often used to measure this type of territorial ancestry, or the homogeneity or heterogeneity of a population (see, for example, Colantonio et al. 2003; King et al. 2006; Longley, Webber and Lloyd 2007; Lucchetti et al. 2011; Darlu et al. 2012; Parkin 2015; Roman-Busto 2015). However, the family name represents, at the individual level, but one branch (usually the paternal line) of a complete genealogical tree. As such, it may not be a precise indicator of a person’s ancestral roots. A more accurate picture of ancestral roots should be based on all branches of the genealogy.

Following a previous study which presented a method to measure ancestral roots in terms of the number of generations (Tremblay 2014), here we propose a new method to express these roots in terms of years. This method uses deep-rooted ascending genealogies, containing information on places and dates of marriage of all ancestors identified in the population. The measure is calculated from the point of view of the contemporary population, and reflects the extent of historic migratory movements which led to present-day settlement patterns.

### *Genealogies and the Quebec population*

For centuries, people have searched for their ancestors and worked at reconstituting family trees (Gauthier 2008). With the proliferation of easy-access websites such as Ancestry and FamilySearch, genealogical research has become increasingly popular (Bishop 2008; Kramer 2011; de Groot 2015). But genealogies are much more than a popular pastime. The usefulness of genealogical data has indeed long been recognized in several areas of scientific research, from the historical sciences to demography (Lynch et al. 1985; Brunet and Bideau 2000), genetic epidemiology (Newman et al. 2001; Zaitlen et al. 2013; Tremblay et al. 2014) and population genetics (Helgason et al. 2005; Larmuseau et al. 2012; Gauvin et al. 2014). When carefully reconstructed with reliable data, genealogies can reveal a lot about the history, evolution and structure of a population (Heyer 1999; Gagnon and Heyer 2001; Tremblay et al. 2009; Moreau et al. 2011).

The population of Quebec represents an excellent laboratory for this type of investigation, because of the high quality of existing data. Baptism, marriage and burial records covering nearly the entire Quebec population since the early 17<sup>th</sup> century have been particularly well preserved over the years (Charbonneau et al. 2000). The digitizing and linkage of these records led to the creation of exceptional population databases that have been used by many scholars in recent decades (BALSAC 2016; Dillon et al. 2017).

The province of Quebec is located in the eastern part of Canada. Its territory is divided into 17 regions covering approximately 1.5 million square kilometres (Figure 1). Most of the population of 8.3 million lives in the southern part of the province, in regions located along the St-Lawrence river (Girard et al. 2016). The first settlers of European descent (mostly from France), who arrived in Quebec during the 17<sup>th</sup> and 18<sup>th</sup> centuries, were established in these regions (Charbonneau et al. 2000). After the takeover of the colony by British authorities in 1760, immigrants from Great-Britain and Ireland started to settle in Quebec, mainly in or near the Montreal region (McInnis

2000a). Regions located further north and east, such as Saguenay-Lac-St-Jean, Côte-Nord, Abitibi-Témiscamingue and Nord-du-Québec, were developed during the 19<sup>th</sup> and early 20<sup>th</sup> centuries.

## Data and methods

Data was retrieved from the BALSAC and PRDH population registers. These databases contain demographic and genealogical data on the population of Quebec from the 17<sup>th</sup> to the 20<sup>th</sup> century (BALSAC 2016; Dillon et al. 2017). For the purpose of this study, a dataset composed of 5,100 ascending genealogies was constructed. The starting points of the genealogies (the subjects) are individuals who were married between 1966 and 1985 in one of the seventeen Quebec regions (300 genealogies per region). These subjects were chosen at random among the available marriage records (one subject per married couple)<sup>1</sup>. Dates and places of marriage of all ancestors identified in the genealogies were used to calculate the age of ancestral roots in each region.

The genealogical branches go back to the first immigrants who came to the province of Quebec<sup>2</sup>. In many cases, this goes back as far as 16 or 17 generations (early 17<sup>th</sup> century). But not all branches reach this depth. In order to give an idea of the length of these genealogical branches, the mean genealogical depth was calculated for each region. This measure illustrates the richness of the data collected (Cazes and Cazes 1996). It is based on the genealogical completeness ( $C_g$ ) which shows the proportion of ancestors identified at each generation, for an expected value of  $2^g$  ancestors (where  $g$  is the generation) per genealogy:

$$C_g = A_g / (N \cdot 2^g)$$

where:

$g$  = generation (generation of subjects' parents = 1)

$A_g$  = number of known ancestors at generation  $g$

$N$  = number of genealogies

Summing completeness over all generations gives the mean genealogical depth.

All regional founders were identified in each genealogy, and their genetic contribution to the subjects was calculated<sup>3</sup>. The regional founders are the first ancestors, going up every genealogical branch, whose parents were married outside of the subject's region (see Figure 2). The genetic contribution allows us to specify the relative contribution of each founder to the subject's gene pool (O'Brien et al. 1994). This measure takes into account the number of occurrences of the founder in the genealogy and the distance, in number of generations, between the founder and the subject (Heyer 1995)<sup>4</sup>.

The age of the subject's ancestral roots was calculated by weighting regional founders with their genetic contribution to the subject and the number of years between them. Since the exact date of arrival of each founder in the region is not known, the mid-point between the founders' year of marriage and that of their parents (who, by definition, were married outside of the region) was used as a proxy. The calculation is as follows:

$$\sum_{i=1}^f ([M_s - 0.5(M_i + M_{Pi})] \sum_{j=1}^c 0.5^{g_{ij}})$$

where:

$f$  = number of regional founders linked to the subject

$c$  = number of genealogical paths between founder and subject

$g_{ij}$  = number of generations, in each genealogical path, between founder and subject

$M_s$  = subject's year of marriage

$M_i$  = founder's year of marriage (latest possible year of arrival of the founder in the region)

$M_{Pi}$  = founder's parents' year of marriage (earliest possible year of arrival of the founder in the region)

The result is expressed in years and provides an estimate of the length of the subject's ancestral roots in his/her region (see example in Figure 2)<sup>5</sup>.

For comparison purposes, age of individual *paternal* and *maternal* roots were also calculated, based on the paternal or maternal lines in each genealogy. The paternal line contains the father of the subject, his paternal grandfather, the father of his paternal grandfather, and so on. Similarly, the maternal line is formed by the subject's mother, his maternal grandmother, etc. In both cases, only one regional founder appears for each subject (the paternal or maternal founder) and his/her genetic contribution is equal to 1. In the example provided in Figure 2, the paternal founder is labelled as F<sub>2</sub>, while F<sub>8</sub> represents the maternal founder.

Analyses of genealogical data was done with the help of the GENLIB software (Gauvin et al., 2015).

## Results and discussion

Approximately one million ancestors were identified in the genealogies of each region, but several ancestors appear in more than one region and in more than one genealogy. On average, the genealogies contain between 2,904 and 4,918 ancestors (Table 1). The lowest value is that of the Gaspésie-IDLM region, which is in accordance with its lower genealogical depth of 9.2 generations. Conversely, the Saguenay-Lac-St-Jean region shows the highest mean number of ancestors and the highest genealogical depth (10.6 generations). Maximal genealogical depth varies between 16 and 18 generations. These results give a good idea of the overall completeness (the proportion of ancestors identified) of the Quebec genealogies. In all regions, completeness is above 80% from the 1<sup>st</sup> to the 7<sup>th</sup> generation, which means that at least 80% of the ancestors were identified up to the 7<sup>th</sup> generation. After the 10<sup>th</sup> generation, completeness decreases more rapidly, as the genealogical branches reach the immigrant ancestors.

The mean values of the age of individual ancestral roots vary from 16 years (Nord-du-Québec region) to 157 years (Chaudière-Appalaches region). Regions located in the central and eastern parts of the province tend to show the highest values (above 100 years), while the northern and western regions have lower values. Results show that the mean ages of paternal and maternal roots

are very similar to the mean ages of all ancestral roots. Differences tend to be more important in the regions where these ages are the highest, which can be explained by longer genealogical paths leading to the regional founders in these regions.

Age of individual ancestral roots also show significant differences from one region to another, but also within each region (Figure 3). Among the western regions (Figure 3a), Montreal and Montérégie have the highest values, but the proportion of roots with an age above 150 years (2% and 24%, respectively) remains relatively low in these two regions, in comparison with most of the central regions (Figure 3b). Laval has a number of subjects with ages of ancestral roots above 150 years, although 87% of the subjects from this region have roots with ages lower than 20 years. Outaouais has relatively few subjects with roots over 120 years, but has the highest median value among the western regions, with 50% of the subjects over 86 years. Laurentides has a small median value of 23 years, but 25% of its subjects reach 120 years or more. None of the Abitibi-Témiscamingue subjects have roots above 85 years.

Subjects from Capitale-Nationale (central regions, Figure 3b) have the most ancient ancestral roots, 21% of which exceed 240 years (the highest value reaches 308 years). In Chaudière-Appalaches, 73% of the subjects have roots above 120 years, and 50% are over 197 years. Mauricie (127 years), Lanaudière (124 years) and Centre-du-Québec (111 years) also have a relatively high median value. The Estrie region show the lowest values among the central regions.

Bas-St-Laurent and Gaspésie-IDLM show similar distributions of their subjects' ancestral age, although the values are a little higher in Bas-St-Laurent (Figure 3c). Half the subjects in Bas-St-Laurent have roots over 170 years, in comparison with 25% of the subjects in Gaspésie-IDLM. The distribution of the subjects' ancestral ages in Saguenay-Lac-St-Jean is somewhat similar to that of the Outaouais region (Figure 3a), but with a higher median value of 103 years. Along with Laval (Figure 3a), Nord-du-Québec has the smallest median value (14 years). Côte-Nord also has one of the smallest median value (26 years), but 40% of its subjects' ancestral ages are over 67 years, while Nord-du-Québec show no individual ancestral age above 54 years.

These results reflect both the age of initial settlements in the Quebec regions and the migration movements that occurred during their history.<sup>6</sup> Montreal, which is the most populated region of Quebec (2 million inhabitants in 2015), was founded in 1642. During the industrialisation period (19<sup>th</sup> century), it received thousands of migrants coming from other Quebec regions (McInnis 2000a; Olson and Thornton 2011). Since the end of the 19<sup>th</sup> century, Montreal has also received the highest proportion of international immigrants coming to Quebec (McInnis 2000b). It still experiences many interregional movements each year (Girard et al. 2016; St-Amour 2016). Located nearby Montreal, Laval was also founded relatively early (around 1675), but most settlements in this region occurred much later (Fortin et al. 2008). Laval is also the smallest region of Quebec in terms of area, which, all things being equal, makes it less suitable for the retention of descendants over a long period.

Capitale-Nationale is where the very first European settlements in Quebec occurred (Quebec City was founded in 1608). Therefore, it is not surprising that the oldest ancestral roots are found in this region. But, in comparison with regions such as Chaudière-Appalaches, Bas-St-Laurent and Gaspésie, Capitale-Nationale had a good share of interprovincial migrants during the 20<sup>th</sup> century (André 2008). Apart from this latter region, Central and Eastern regions have historically

experienced lower in-migration levels than most of the Western regions. Abitibi-Témiscamingue and Nord-du-Québec were colonized much later than the other regions (Vincent et al. 2005; Girard et al. 2012), which explains their low mean and maximum ancestral ages.

Figure 4 compares the ages of individual regional roots with those obtained when only the paternal lines (Figure 4a) or only the maternal lines (Figure 4b) in each genealogy are taken into account (for practical reasons, results for the seventeen regions are pooled in the same graph). Results for maternal and paternal lines are also compared (Figure 4c). Since the three methods yield the same results when the regional founder is the subject himself, these cases are not included in the figures (for the most part, these are cases for which the ages of ancestral roots are below 30 years). Although both figures 4a and 4b show a relatively high correlation between the two values ( $r = 0.781$  for paternal roots and  $r = 0.779$  for maternal roots), there are many instances where the differences are fairly high (in both directions). Figure 4c shows that the correlation between ages of maternal and paternal roots is even much lower ( $r = 0.424$ ). This means that paternal or maternal lines cannot be taken as precise indicators of individual ancestral roots in the Quebec regions.

## Conclusion

This study presented a method to measure ancestral roots in a given territory. Taking into account detailed information about dates and places of marriage of ancestors identified in deep-rooted ascending genealogies of Quebec residents, results showed that the age of regional ancestral roots vary greatly. This is explained by differences in settlement and migration histories. Regions which were settled earlier or with low in-migration have the oldest roots. Younger roots characterise regions which were populated more recently or have experienced many migrations. At the individual level, these results reflect the magnitude of regional persistence among the ancestors of contemporary Quebec residents.

Results also showed that paternal and maternal lines are, on average, about the same age as all ancestral lines. However, on the individual level they are often not representative of the whole genealogical tree. Assessments of multi-generational presence in a territory should thus be based, preferably, on all ancestors and not only those from either the paternal or maternal lines. Given data availability, the method used here could be applied to other populations with similar or different geographical subdivisions. Results derived from using this method could provide useful knowledge about the regional diversity of settlement history in a given territory, by differentiating regions in which the population is deeply rooted from those where the ancestral roots are shorter. Such knowledge may help researchers better understand the social and genetic structure of a population by depicting the relative genealogical homogeneity or heterogeneity of communities across space.

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## Notes

1. These marriages are essentially Catholic. Marriages of other faiths or unions which have not been the subject of a marriage certificate were thus excluded from the samples. A total of 919,507 marriages were recorded in Quebec between 1966 and 1985 (Girard et al. 2016), of which approximately 87% were Catholic (the exact proportion is not known). For each region, the distribution of subjects according to their place of marriage is proportional to the population of the municipalities of the region according to the 1976 census (mid-point of the subjects' marriage period).

2. In some cases, due to missing data, information about the first immigrant was unknown. Overall, 97% of the total genetic contribution to the 5100 subjects was traced to known immigrants.

3. Regional founders must not be confused with immigrant founders. Immigrant founders refer to the territory of Quebec as a whole, whereas regional founders refer to specific regions of Quebec. Hence, the genealogical branches do not necessarily end with regional founders (in fact, most branches don't). Since all regional founders are known, their genetic contribution to the subjects is totally (100%) explained (there is no missing data).

4. Some founders can appear several times in a single genealogy, through different branches of various lengths. The probability of multiple appearances increases with the number of generations separating the founder and the subject. For example, in the Capitale-Nationale genealogies, one couple of regional founders who were married in 1657 (from 8 to 13 generations back) appears 1668 times in the 300 genealogies, for an average of 5.6 appearances per genealogy; this couple explains 0.97% of the region's gene pool. Most founders, however, appear only a few times. In the Capitale-Nationale genealogies, 53% of the regional founders appear less than 4 times in the 300 genealogies; the average among all regional founders is 25 appearances in the 300 genealogies, for an average of 0.08 appearance per genealogy and an average genetic contribution of 0.03%.

5. As stated previously, all regional founders have been identified in the genealogies. In the case of missing data, the age of regional ancestral roots could still be calculated based on all known regional founders, assuming that the average contribution of unknown founders is similar to that of known founders. Alternatively, the contribution of the earliest ancestors (going up every genealogical branch) married in the same region as the subject could be used if the place of marriage of their parents is unknown; in such cases, the age of regional ancestral roots must be considered as a minimal value.



6. Since these results were obtained using data from ascending genealogies, they do not represent all the migration movements that occurred in the regions since the beginning of settlement. The objective of this study was to measure the ancestral roots of contemporary people in the population based on information about their ancestors. As such, results cannot reflect migrations of people who did not have descendants in the contemporary population. In fact, they may be best interpreted as a kind of “resulting intergenerational interregional migration” in Quebec since the early 17<sup>th</sup> century.

## References

André, D. 2008. Évolution historique de la population des municipalités au Québec. *Données sociodémographiques en bref* 12(2):1-4.

BALSAC. 2016. *BALSAC Population database*. Chicoutimi : Université du Québec à Chicoutimi. <http://balsac.ugac.ca/english/>

Bishop, R. 2008. In the grand scheme of things: an exploration of the meaning of genealogical research. *The Journal of Popular Culture* 41:393-412.

Brunet, G., and A. Bideau. 2000. Démographie historique et généalogie. *Annales de démographie historique* 2000-2:101-10.

Cazes, M.-H., and P. Cazes. 1996. Comment mesurer la profondeur généalogique d’une ascendance. *Population* 51:117-40.

Charbonneau H., B. Desjardins, J. Légaré, and H. Denis. 2000. The population of the St-Lawrence Valley, 1608-1760. In *A Population History of North America*, edited by M.R. Haines and R. H. Steckel, 99-142. Cambridge: Cambridge University Press.

Colantonio, S. E., G. W. Lasker, B. A. Kaplan, and V. Fuster. 2003. Use of surname models in human population biology: a review of recent developments. *Human Biology* 75:785-807.

Darlu, P., G. Bloothoof, A. Boattini, L. Brouwer, M. Brouwer, G. Brunet, P. Chareille, J. Cheshire, R. Coates, K. Dräger, B. Desjardins, P. Hanks, P. Longley, K. Mandemakers, P. Mateos, D. Pettener, A. Uselli, and F. Manni. 2012. The family name as socio-cultural feature and genetic metaphor: from concepts to methods. *Human Biology* 84:169-214.

de Groot, J. 2015. International Federation for Public History plenary address: on genealogy. *The Public Historian* 37:102-27.

Dillon, L., M. Amorevieta-Gentil, M. Caron, C. Lewis, A. Guay-Giroux, B. Desjardins, and A. Gagnon. 2017. The Programme de recherche en démographie historique: past, present and future developments in family reconstitution. *History of the Family*. <http://dx.doi.org/10.1080/1081602X.2016.1222501>

Fortin, J.-C., N. Perron, and J. Saint-Pierre. 2008. *Histoire de Laval*. Québec: Presses de

l'Université Laval.

Gagnon, A., and E. Heyer. 2001. Fragmentation of the Québec population genetic pool (Canada): evidence from the genetic contribution of founders per region in the 17<sup>th</sup> and 18<sup>th</sup> centuries. *American Journal of Physical Anthropology* 114:30–41.

Gauthier, M.-É. 2008. *Mille ans d'histoire de l'arbre généalogique en France*. Rennes: Éditions Ouest-France.

Gauvin, H., J.-F. Lefebvre, C. Moreau, È.-M. Lavoie, D. Labuda, H. Vézina, and M.-H. Roy-Gagnon. 2015. GENLIB: an R package for the analysis of genealogical data. *BMC Bioinformatics* 16:160, doi: 10.1186/s12859-015-0581-5.

Gauvin, H., C. Moreau, J.-F. Lefebvre, C. Laprise, H. Vézina, D. Labuda, and M.-H. Roy-Gagnon. 2014. Genome-wide patterns of identity-by-descent sharing in the French Canadian founder population. *European Journal of Human Genetics* 22:814–21.

Girard, C., A.-B. Charbonneau, and F. F. Payeur. 2016. *Le bilan démographique du Québec, édition 2016*. Québec: Institut de la statistique du Québec.

Girard, R., R. Auger, V. Collette, D. Denton, Y. Labrèche, and N. Perron. 2012. *Histoire du Nord-du-Québec*. Québec: Presses de l'Université Laval.

Helgason, A., B. Yngvadóttir, B. Hrafnkelsson, J. Gulcher, and K. Stefánsson. 2005. An Icelandic example of the impact of population structure on association studies. *Nature Genetics* 37:1:90-95.

Heyer, E. 1995. Genetic consequences of differential demographic behaviour in the Saguenay region, Quebec. *American Journal of Physical Anthropology* 98:1-11.

Heyer, E. 1999. One founder/one gene hypothesis in a new expanding population: Saguenay (Quebec, Canada). *Human Biology* 71:99-109.

King, T. E., S. J. Ballereau, K. E. Schürer, and M. A. Jobling. 2006. Genetic signatures of coancestry within surnames. *Current Biology* 16:384-88.

Kramer, A.-M. 2011. Kinship, affinity and connectedness: exploring the role of genealogy in personal lives. *Sociology* 45:379-95.

Larmuseau, M. H .D., C. Ottoni, J. A. M. Raeymaekers, N. Vanderheyden, H. F. M. Larmuseau, and R. Decorte. 2012. Temporal differentiation across a West-European Y-chromosomal cline: genealogy as a tool in human population genetics. *European Journal of Human Genetics* 20:434-40.

Longley, P., R. Webber, and D. Lloyd. 2007. The quantitative analysis of family names: historic migration and the present day neighborhood structure of Middlesbrough, United Kingdom. *Annals of the Association of American Geographers* 97:31-48.

Lucchetti, E., M. Tasso, I. Amoruso, and G. Caravello. 2011. The border effect in surname structure: an Italian-Slovenian case study. *Human Biology* 83:393-404.

Lynch, K. A., G. P. Mineau, and D. L. Anderton. 1985. Estimates of infant mortality on the Western frontier: the use of genealogical data. *Historical Methods* 18:155-64.

McInnis, M. 2000a. The population of Canada in the nineteenth century. In *A Population History of North America*, edited by M.R. Haines and R. H. Steckel, 371-432. Cambridge: Cambridge University Press.

McInnis, M. 2000b. Canada's population in the twentieth century. In *A Population History of North America*, edited by M.R. Haines and R. H. Steckel, 529-99. Cambridge: Cambridge University Press.

Moreau, C., C. Bhérer, H. Vézina, M. Jomphe, D. Labuda, and L. Excoffier. 2011. Deep human genealogies reveal a selective advantage to be on an expanding wave front. *Science* 334:1148-50.

Newman, D. L., M. Abney, M. S. McPeck, C. Ober, and N. J. Cox. 2001. The importance of genealogy in determining genetic associations with complex traits. *The American Journal of Human Genetics* 69:1146-48.

O'Brien, E., R. A. Kerber, L. B. Jorde, and A. R. Rogers. 1994. Founder effect: assessment of variation in genetic contributions among founders. *Human Biology* 66:185-204.

Olson, S., and P. Thornton. 2011. *Peopling the North American City: Montreal 1840-1900*. Montreal: McGill-Queen's University Press.

Parkin, H. 2015. The fourteenth-century poll tax returns and the study of English surname distribution. *Historical Methods* 48:1-12.

Roman-Busto, J. 2015. Influence of changes in political barriers and of geographic distance on kinship inferred from surnames and migration data in Olivenza, Spain, and surrounding Portuguese areas. *Human Biology* 87:122-31.

St-Amour, M. 2016. La migration interrégionale au Québec en 2014-2015: la région des Laurentides sort grande gagnante, la Côte-Nord grande perdante. *Coup d'œil sociodémographique* 46. Québec: Institut de la statistique du Québec.

Tremblay, M. 2014. Regional borders and territorial ancestry: a genealogical analysis. In *Grenzen in genealogie en heraldiek / Frontiers in genealogy and heraldry / Frontières dans la généalogie et l'héraldique*, edited by J. T. Anema, R. J. F van Drie, R. K. Vennik, and B. P. M. Kernkamp, 359-68. The Hague: Stichting De Nederlandse Leeuw.

Tremblay, M., T. Bouhali, D. Gaudet, and D. Brisson. 2014. Genealogical analysis as a new approach for the investigation of drug intolerance heritability. *European Journal of Human Genetics* 22:916-22.

Tremblay, M., M. Letendre, L. Houde, and H. Vézina. 2009. The contribution of Irish immigrants to the Quebec (Canada) gene pool: an estimation using data from deep-rooted genealogies. *European Journal of Population* 25:215-33.

Vincent, O., M. Asselin, B. B. Gourd, C. Mercier, R. Viau, M. Côté, J.-P. Marquis, M. Riopel, and C. Sabourin. 2005. *Histoire de l'Abitibi-Témiscamingue*. Québec: Presses de l'Université Laval.

Zaitlen, N., P. Kraft, N. Patterson, B. Pasaniuc, G. Bhatia, S. Pollack, and A. L. Price. 2013. Using extended genealogy to estimate components of heritability for 23 quantitative and dichotomous traits. *PLoS Genetics* 9: e1003520.

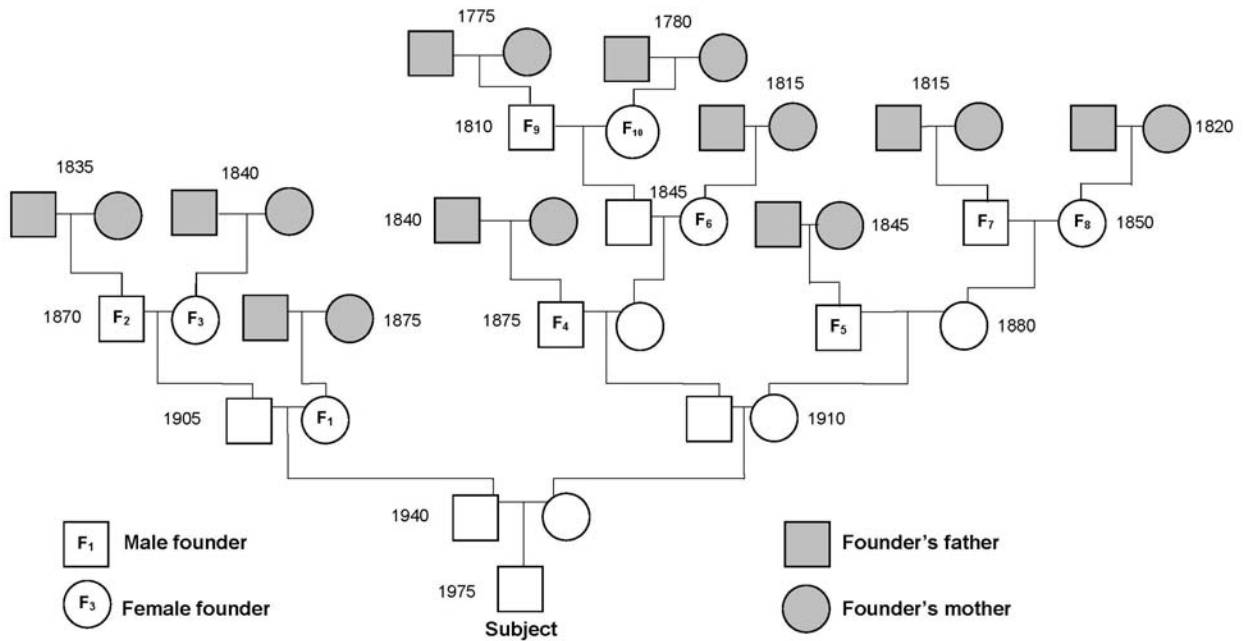
**TABLE 1.** Number of ancestors, genealogical depth and age of ancestral roots in the genealogies of the Quebec regions

no	Region	Mean number of ancestors identified per genealogy	Mean genealogical depth (generations)	Maximal genealogical depth (generations)	<i>Mean age of ancestral roots (years)</i>	<i>Mean age of paternal roots (years)</i>	<i>Mean age of maternal roots (years)</i>
01	Bas-St-Laurent	3,901	10.1	16	148	144	146
02	Saguenay-Lac-St-Jean	4,918	10.6	16	91	87	93
03	Capitale-Nationale	4,000	10.2	16	140	147	137
04	Mauricie	3,687	10.1	16	119	122	120
05	Estrie	4,148	10.2	16	60	60	60
06	Montréal	3,504	9.8	16	56	55	56
07	Outaouais	3,525	9.6	16	80	81	80
08	Abitibi-Témiscamingue	4,015	10.2	17	41	41	41
09	Côte-Nord	3,817	9.7	17	52	51	53
10	Nord-du-Québec	4,379	10.3	16	16	17	16
11	Gaspésie-IDLM	2,904	9.2	18	124	127	126
12	Chaudière-Appalaches	4,143	10.4	16	157	155	163
13	Laval	3,909	10.1	16	24	25	22
14	Lanaudière	3,683	10.1	16	109	114	109
15	Laurentides	3,892	10.2	17	67	69	67
16	Montréal	3,309	9.7	16	77	74	77
17	Centre-du-Québec	3,435	10.1	16	100	97	99

**FIGURE 1.** The Quebec regions. *Source.* Institut de la statistique du Québec.

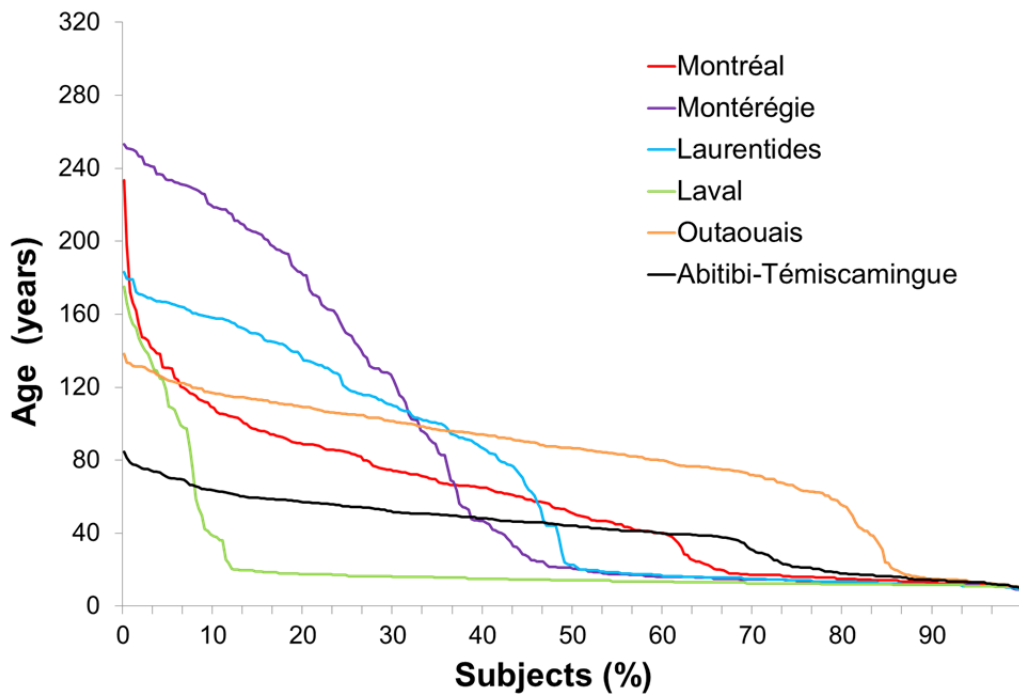


**FIGURE 2.** Calculation of the age of individual ancestral roots (example). *Note.* In this example, the subject's genealogy shows ten regional founders (F<sub>1</sub> to F<sub>10</sub>). Subject's ancestors, leading up to the founders, were married in the same region as the subject. Founders' parents were married outside the subject's region of marriage. The genetic contribution of founder F<sub>1</sub> (the subject's paternal grand-mother) is equal to 0.25. In terms of years, the contribution of F<sub>1</sub> to the age of the subject's ancestral roots is equal to  $[1975 - 0.5 \times (1905 + 1875)] \times 0.25 = 21.25$  years. Founders F<sub>2</sub>, F<sub>3</sub>, F<sub>4</sub> and F<sub>5</sub> (four of the subject's eight great-grand parents) each have a genetic contribution of 0.125. The contribution of F<sub>2</sub> to the age of the subject's ancestral roots is equal to  $[1975 - 0.5 \times (1870 + 1835)] \times 0.125 = 15.31$  years. The sum of the contributions of the ten regional founders, which corresponds to the age of the subject's ancestral roots, is equal to 118.36 years.



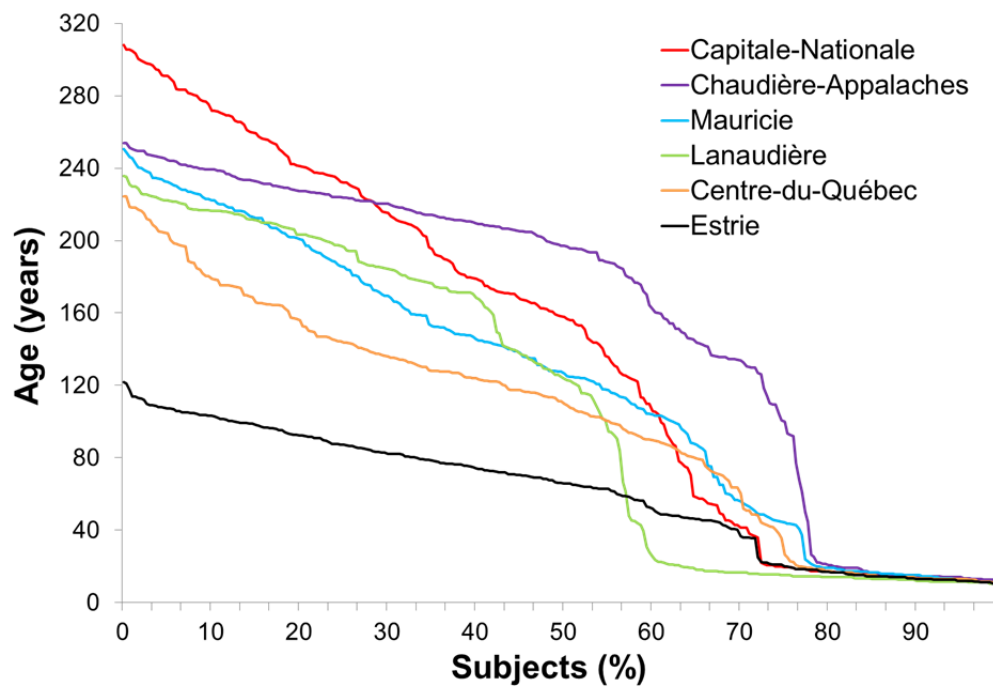
**FIGURE 3.** Age of individual ancestral roots (per decreasing order in each region). *Note.* This figure shows, for each region, the distribution of the subjects according to the age of their ancestral roots. Results are shown in decreasing order, starting with subjects having the highest ages. For better readability, the 17 regions have been regrouped into three different graphs according to their geographical location (western, central and north-eastern regions of the province).

a) Western regions

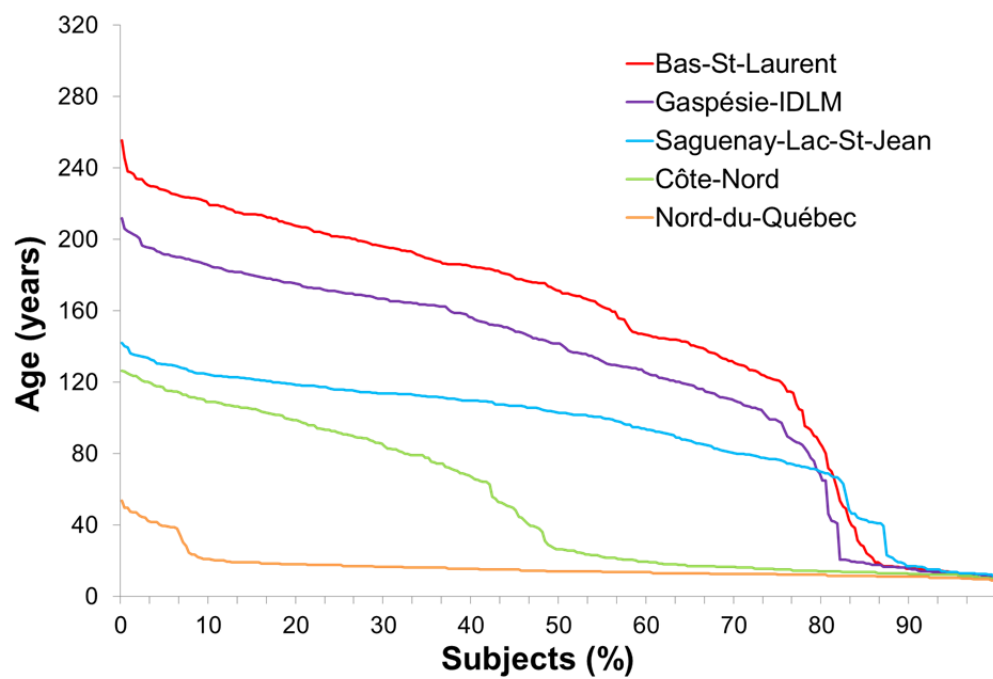




b) Central regions

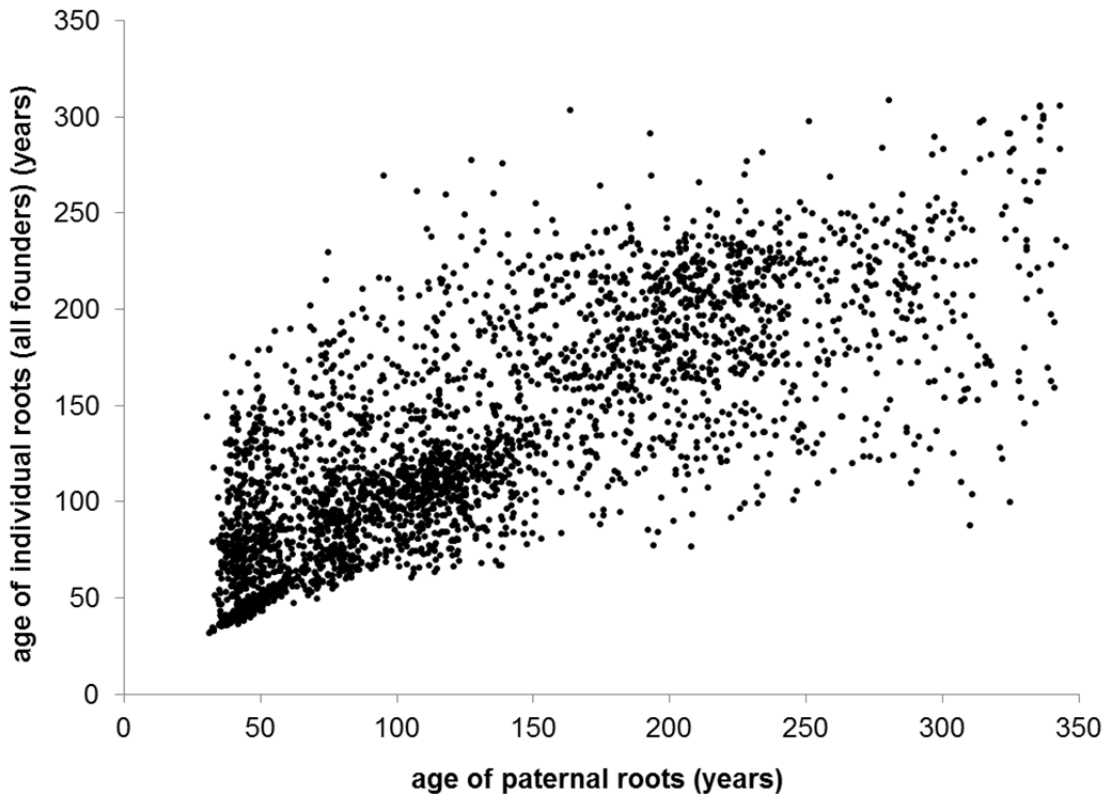


c) North-eastern regions



**FIGURE 4.** Comparison of ages of individual ancestral roots. *Note.* This figure compares different sets of ancestral roots, calculated when considering all founders, only paternal founders or only maternal founders. In each graph, each dot shows the values, for a given subject, of the ages of his/her ancestral roots according to two of the three measures.

a) All founders vs. paternal founders



b) All founders vs. maternal founders



c) Maternal vs. paternal founders

