Original Paper

Community Genetics

Community Genet 2005;8:152–160
DOI: 10.1159/000086758

Demogenetic Study of Three Populations within a Region with Strong Founder Effects

Ève-Marie Lavoie Marc Tremblay Louis Houde Hélène Vézina

Interdisciplinary Research Group on Demography and Genetic Epidemiology (GRIG), University of Quebec, Chicoutimi, Canada

Key Words
Founder effect · Hereditary disorders · Inbreeding · Population genetics · Population history

Abstract
Objectives: The population of the Saguenay-Lac-St-Jean (SLSJ) region (Quebec, Canada) is known to have a relatively high prevalence of certain hereditary disorders, which can be explained by the consequences of founder effects. This study aims at providing new insights on the origins and subregional stratification of these founder effects. ***Methods:*** The genealogies of 300 individuals were reconstructed and analyzed using the BALSAC population register. ***Results:*** Inbreeding and kinship levels are higher in Lower Saguenay than in Upper Saguenay and Lac-St-Jean. The population of Lower Saguenay also distinguishes itself because of a fewer number of distinct ancestors. ***Conclusion:*** Beyond the genetic features that characterize the whole region, SLSJ also displays intraregional variability. Thus it is important to take into account the settlement patterns and the demographic history of this population for a better appraisal of its contemporary genetic structure.

Introduction

Settlement of Saguenay-Lac-St-Jean

The Saguenay-Lac-St-Jean (SLSJ) region (a population of 282,000) is located 200 km north of Quebec City (fig. 1). Settlement in this region followed a population expansion which occurred in the St-Lawrence Valley at the beginning of the 19th century. The inhabitants of the Charlevoix region (east of Quebec City) turned to the nearby SLSJ region and a current of emigration started in 1838 which continued until the early 20th century [1]. It is estimated that between 1838 and 1871, 80% of the SLSJ immigrants came from Charlevoix. Afterwards, industrialization and urbanization contributed to diversify the origins of the migrants [1]. In addition to the high proportion of migrants from Charlevoix, the close family ties of these migrants gave them an advantage by facilitating their settlement. For these reasons, Charlevoix and SLSJ inhabitants are often considered as belonging to the same genetic pool [2].

Genetic Characteristics of the SLSJ Population

As a consequence of the high prevalence of certain hereditary diseases, numerous studies on the population genetics of SLSJ have been conducted. The SLSJ population is characterized by a founder effect [3, 4]: it has been

KARGER

Fax +41 61 306 12 34
E-Mail karger@karger.ch
www.karger.com

1422–2795/05/0083–0152$22.00/0

Accessible online at:
www.karger.com/cmg

Hélène Vézina, PhD
555, boulevard de l'Université
Chicoutimi, Quebec G7H 2B1 (Canada)
Tel. +1 418 545 5517, Fax +1 418 545 5518
E-Mail helene_vezina@uqac.ca

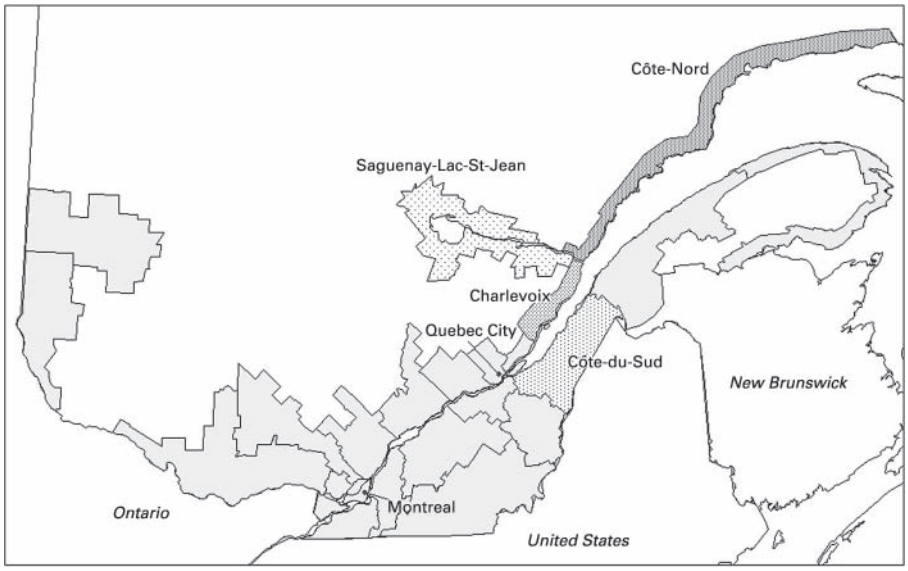

Fig. 1. Geographic situation of Saguenay-Lac-St-Jean.

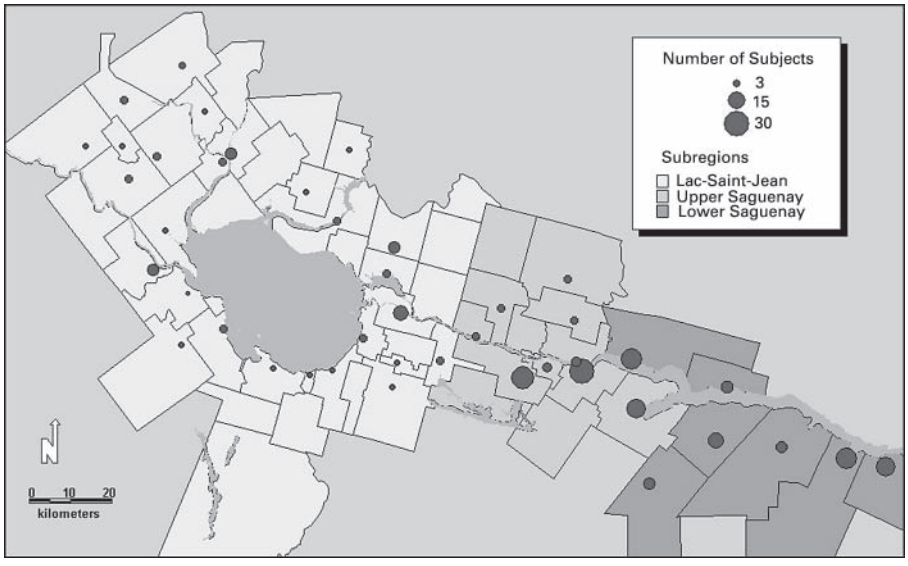

Fig. 2. Distribution of subjects in the three SLSJ subregions.

shown that 82% of the region's gene pool originated from nearly 2,600 founders who settled in New France during the 17th century [5]. Some of these founders are believed to have introduced rare deleterious genes in the Quebec population [6]. The demographic behaviour of these founders' descendants is at the heart of the process by which some of these rare alleles, such as those associated with Charlevoix-Saguenay spastic ataxia and human cytochrome oxidase deficiency, were transmitted and are now found at an elevated frequency in the contemporary SLSJ population [7, 8]. Other diseases, such as myotonic dystrophy or cystic fibrosis, without being specific to the region, also have a relatively high impact in the SLSJ population [9, 10]. In contrast, some diseases present elsewhere are practically non-existent in the SLSJ region, such as haemophilia or Friedreich ataxia [11]. It has been shown that some mutations are specific, until proven otherwise, to the French Canadian population and spread into the Quebec's gene pool by founder effect [4].

Using extensive genealogical data and various demogenetic measures, this study aims at a better understanding of the origins and stratification of the SLSJ gene pool. Specifically, we wanted to verify to what extent the founder effect and its consequences showed variability within the region.

The Saguenay-Lac-St-Jean Subregions

In order to achieve our goals, the region was divided into three subregions (Lower Saguenay, Upper Saguenay and Lac-St-Jean), based on geographical and historical criteria. The first settlers in SLSJ were established in the 1840's on the south shore of the Saguenay River, in the Upper and Lower Saguenay subregions. Settlement in the Lac-St-Jean subregion came a few years later. Nowadays, Upper Saguenay has the largest population (more than half of the region's) and is more industrialized than the other subregions [1]. Three hundred genealogies (100 for each subregion) were reconstructed using the BALSAC population register [12]. The geographical origins of the subjects (the starting points of the genealogies) reflect the distribution of the current population within each subregion (fig. 2). Inbreeding and kinship coefficients were measured, as well as the ancestors' frequencies and distributions in the genealogies. The geographical origins and the genetic contribution of the regional founders were also examined.

Methods

The BALSAC Population Register and the BALSAC-RETRO Genealogical Database

Data used in this study were retrieved from the BALSAC population register and the BALSAC-RETRO database. The BALSAC register contains information on 2.1 million marriages, births and deaths that occurred during the last two centuries in the Province of Quebec [12, 13]. The SLSJ region has been entirely covered from the beginning of settlement in the 1830's to 1971. The BALSAC-RETRO database contains genealogical information on 340,000 individuals who married in Quebec, from the 17th to the 20th century [13].

Selection of Subjects and Genealogical Reconstruction

For each of the three Saguenay subregions, 100 marriages celebrated between 1945 and 1965 were randomly selected in the BALSAC register. One spouse per marriage was chosen (50 males and 50 females in each subregion) and the genealogies of the 300 subjects were reconstructed using the BALSAC register and the BALSAC-RETRO database. Other sources were used to complete the genealogies, such as the Population Register of Early Quebec [14], genealogical dictionaries, marriage repertories or microfilms of parish registers. The genealogical reconstruction was performed as far back as sources would allow, up to the first European pioneers of the St. Laurence Valley (16 generations in some cases). All genealogies were submitted to various validation procedures in order to minimize the presence of false links [15].

Demogenetic Analyses

Demogenetic analyses were performed on each genealogical corpus, using various procedures developed by the BALSAC Project team and by the Interdisciplinary Research Group in Demography and Genetic Epidemiology (GRIG) [16]. These analyses include the count of all ancestors appearing in the genealogies, calculation of the average genealogical depth, of inbreeding and kinship coefficients and of genetic contribution of ancestors, including the SLSJ founders.

Count of Ancestors. For each subgroup, the total number of genealogical links that we identified was established. As many ancestors are mentioned more than once, the number of distinct ancestors was also calculated [16]. For each ancestor, the number of subjects to which they were related and the number of times they appeared in the genealogies were computed.

Completeness of Genealogies. The completeness of genealogies (C_x) was calculated as the proportion of known ascendants among all expected ascendants at each generation [17].

$$C_x = \frac{\text{number of known ancestors at generation x}}{\text{number of expected ancestors at generation x}}$$

Genealogical Depth. The genealogical depth (D) can be interpreted as the mean value of the generation of the founders in a genealogical corpus. The genealogical depth (D) was calculated as follows:

$$D = \sum_{x=0}^{n} x \frac{F_x}{T_x}$$

where F_x is the number of founders for generation x and T_x, the number of expected ancestors for generation x [18].

Kinship Coefficient. The kinship coefficient (Φ) is the probability that one allele chosen at random in a given person is identical by descent to another allele, at the same locus, in another person [19]. The kinship coefficient between two individuals (B_1 and B_2) was calculated as follows:

$$\Phi(B_1, B_2) = \sum_{A}\sum_{L}(1/2)^{n(A,L)+m(A,L)+1}(1+F(A))$$

where A is the common ancestor to B_1 and B_2, L is the genealogical link between B_1 and B_2 from A, m(A,L) is the number of generations between individual B_1 and common ancestor A by the genealogical link L, n(A,L), the number of generations between individual B_2 and common ancestor A by the genealogical link L and F(A), the value of the inbreeding coefficient for ancestor A. The mean kinship coefficient of a group of individuals was calculated by identifying, for each pair of individuals, all known common ancestors over all known genealogical links and dividing the sum of these coefficients by the total number of possible pairs. For a group of 100 subjects, this number is 4,950.

Inbreeding Coefficient. The inbreeding coefficient is the probability that an individual has inherited, at a given locus, two identical alleles originating from a common ancestor, one from the father and the other from the mother [20]. The inbreeding coefficient of an individual corresponds to the kinship coefficient of his parents. This coefficient was calculated as follows [19]:

$$F(I) = \Phi(P, M) = \sum_{A}\sum_{C}(1/2)^{n(A,C)+m(A,C)+1}(1+F(A))$$

where A is the common ancestor to P and M, C is the genealogical path between P and M from A, m(A,C) is the number of generations between father P and common ancestor A by the genealogical path C, n(A,C), the number of generations between mother M and common ancestor A by the genealogical path C and F(A), the value of

inbreeding coefficient for ancestor A. For each subregion, the mean of the 100 inbreeding coefficients was calculated.

Statistical Analysis of Kinship and Inbreeding Coefficients

As the classic t test for comparing two mean kinship values is not valid due to the dependence between coefficients, the comparison was carried out by a permutation test. The test statistic is the mean kinship difference and the p value for the null hypothesis was obtained by performing 5,000 permutations. The dependence is controlled by first permuting the two groups of individuals and then computing all the kinship coefficients. This procedure gives an estimated p value with a precision of

$$\pm 2\sqrt{p(1-p)/5000}$$

so all the p values near the significance level should be interpreted as a 'possible' rejection of the null hypothesis. As each subject has its own inbreeding coefficient, dependence is not an issue and the classical t test was used to compare the mean values obtained for each group.

Genetic Contribution of Regional Founder. Regional founders were defined as the first ancestors who married in the Saguenay region. Their geographical origins were determined using the place of marriage of their parents. Genetic contribution of every regional founder to each subregional group was calculated based on the frequency and generation level of its appearances in the genealogies. For each subregion, this contribution represents the proportion of the gene pool that comes from this founder. For a given founder, the genetic contribution was calculated as follows:

$$CG = \sum_{i=1}^{S} \sum_{j=1}^{L} (1/2)^{g_{i,j}}$$

where S is the number of subjects linked to the founder, L the number of genealogical links between a subject and the founder and $g_{i,j}$ the number of generations between the founder and the subject i at the genealogical link j [16].

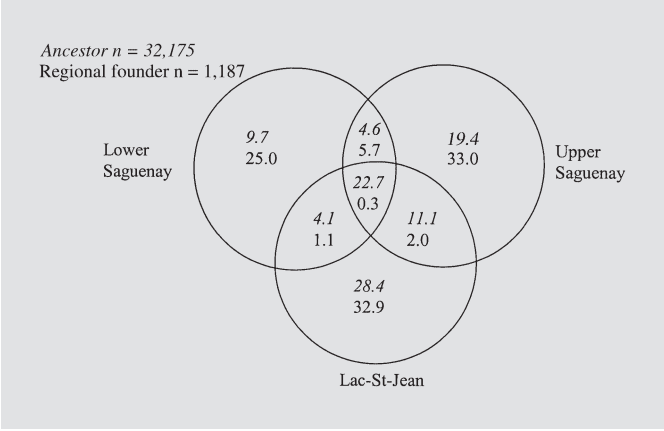

Fig. 3. Distribution (%) of ancestors and regional founders among the three subregions.

Table 1. General characteristics of the 300 genealogies

	Lower Saguenay	Upper Saguenay	Lac-St-Jean
Number of genealogies	100	100	100
Total ancestral links	320,918	290,252	289,868
Distinct ancestors	13,224	18,593	21,319
Mean number of occurrences	24.3	15.6	13.6
Mean genealogical depth (s.d.)	10.1 (1.6)	9.6 (1.6)	9.8 (1.8)
Maximum genealogical depth	15	16	15

Results

General Characteristics of the Genealogies

About 300,000 ancestors were identified in each group of genealogies (table 1). As many ancestors appear on several occasions in these genealogies (from 13 to 24 times on average, according to the different subregions), the number of distinct ancestors is much lower (between 13,224 and 21,319). For each subregion, genealogical paths have an average depth of 10 generations and some reach 16 generations.

Of the 32,175 distinct ancestors identified in the 300 genealogies, 22.7% are common to the three subregions and 19.8% were identified in two of the three subregions (fig. 3). Ten percent of the ancestors are specific to Lower Saguenay, compared to 19% for Upper Saguenay and 28% for Lac-St-Jean. Most of the 1,187 ancestors who were identified as regional founders (91%) are specific to one subregion. Very few founders (0.3%) are found in the genealogies of the three subregions and less then 10% are common to two subregions.

The distribution of ancestors according to their specificity and to the number of genealogies where they appear is given in table 2. Among ancestors specific to one subregion, the number of genealogies where they appear does not exceed 20, while less than 0.5% of the ancestors common to two subregions are found in 21–50 genealogies. The distribution of the ancestors common to all three subregions is much wider, with 302 ancestors appearing in more than 200 genealogies. In total, nearly 25% of all ancestors were found in more than 5 genealogies.

The completeness of every subregion's genealogies is similar at each generation and follows the same tendency (fig. 4). Completeness slowly decreases from the 3rd to the 10th generation and more rapidly afterwards. At the10th generation, completeness is still relatively high: 78% in Lower Saguenay against 70% in Upper Saguenay and 71% in Lac-St-Jean.

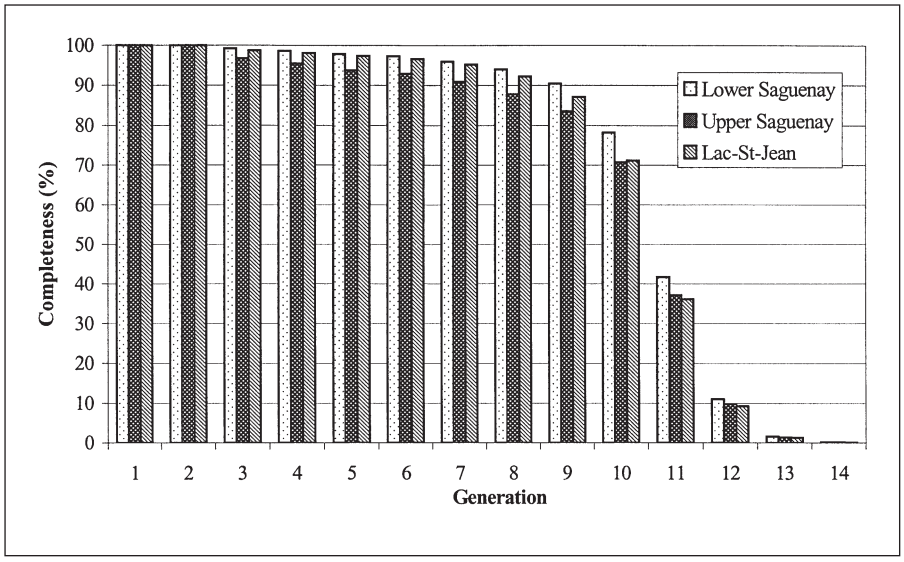

Fig. 4. Completeness of the genealogies.

Table 2. Distribution of ancestors according to their subregional specificity and to the number of genealogies in which they appeared

Number of genealogies	Specific to			Common to 2 subregions	Common to 3 subregions	Total (%)
	Lower Saguenay	Upper Saguenay	Lac-St-Jean			
1	2,728	5,450	6,989	–	–	15,167 (47.1)
2	195	648	1,370	2,124	–	4,337 (13.5)
3–5	141	151	730	3,044	965	5,031 (15.6)
6–20	52	3	48	1,183	3,168	4,454 (13.8)
21–50	0	0	0	28	1,514	1,542 (4.8)
51–100	0	0	0	0	696	696 (2.2)
101–200	–	–	–	0	646	646 (2.0)
201–300	–	–	–	–	302	302 (0.9)
Total	3,116	6,252	9,137	6,379	7,291	32,175 (100.0)

Kinship

Mean kinship coefficients in each subregion and between subregions are shown in figure 5. For the first generations (3rd–5th), kinship levels are low. Kinship coefficients in each subregion increase rapidly between the 6th and the 10th generation. After the 11th generation, they stabilize due to the interruption of genealogical branches. Kinship coefficients are significantly higher ($p < 0.05$) in the Lower Saguenay, regardless of the generation level. The lowest kinship coefficients are observed in Lac-St-Jean, however the differences between Lac-St-Jean and Upper Saguenay do not reach significance.

At each generation, the highest interregional kinship coefficients are observed between the individuals of Lower and Upper Saguenay. As a group, subjects from Upper Saguenay are in fact more closely related to subjects from Lower Saguenay than they are to each other. Interestingly, kinship coefficients between Lower Saguenay and Lac-St-Jean are higher than those between the neighbouring subregions of Upper Saguenay and Lac-St-Jean. However, the differences between the two series of coefficients are not highly significant ($0.056 < p < 0.242$). Also, the kinship coefficient in the subregion of Lac-St-Jean is lower at each generation than interregional kinship coefficients involving this subregion.

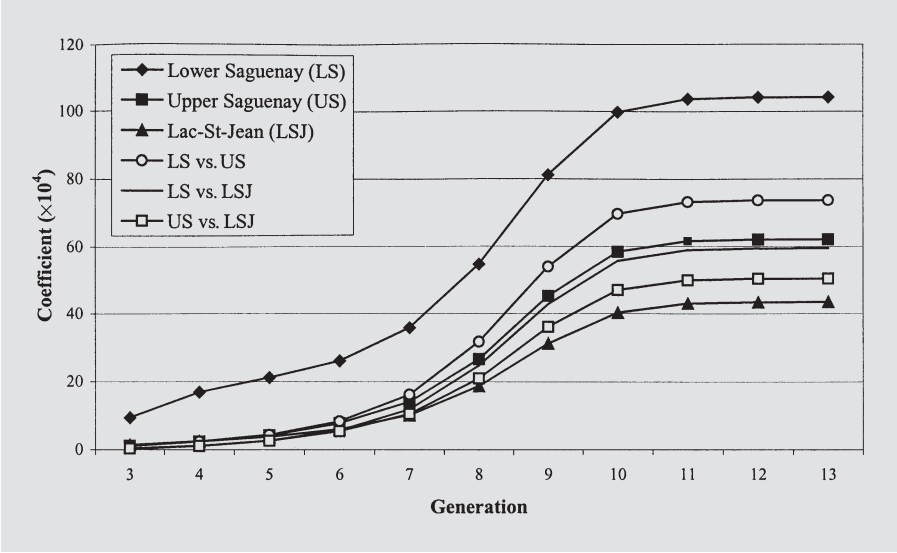

Fig. 5. Mean kinship coefficients within and between the three subregions.

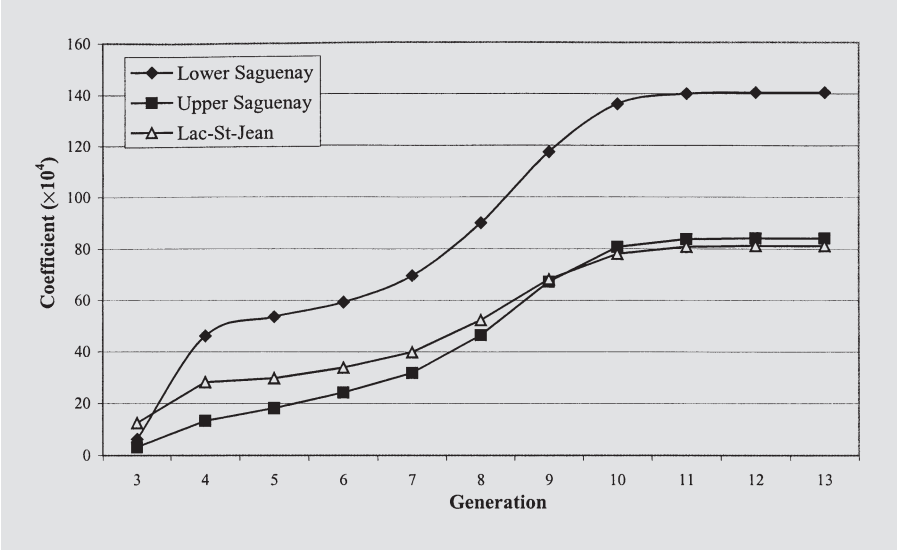

Fig. 6. Mean inbreeding coefficients within the three subregions.

Inbreeding

At the 3rd generation, the inbreeding coefficient is low in all groups, indicating the absence of marriages between closely related ancestors in the genealogies (fig. 6). From the 4th generation, Lower Saguenay's coefficients increase rapidly and they become significantly higher than the inbreeding coefficients of the two other subregions. At maximum depth, consanguinity is almost twice as high in Lower Saguenay than in Upper Saguenay and Lac-St-Jean ($p < 0.001$). From the 3rd to the 9th generation, Upper Saguenay's coefficients are lower than those of Lac-St-Jean but the differences are not significant ($p > 0.10$). Mean coefficients stop increasing after the 11th generation at 0.014 for Lower Saguenay and 0.008 for Upper Saguenay and Lac-St-Jean.

Genetic Contribution of Regional Founders

Figure 7 shows that founders originating from the Charlevoix region represent nearly 74% of the Lower Saguenay's gene pool. The Charlevoix contribution is lower in the two other subregions (61% in Upper Saguenay and 48% in Lac-St-Jean). The remainder of the genetic contribution comes from founders originating from all other regions of the Province of Quebec (see figure 1 for localisation of regions), especially from the Côte-du-Sud region (up to 15% of the Lac-St-Jean's gene pool). Together,

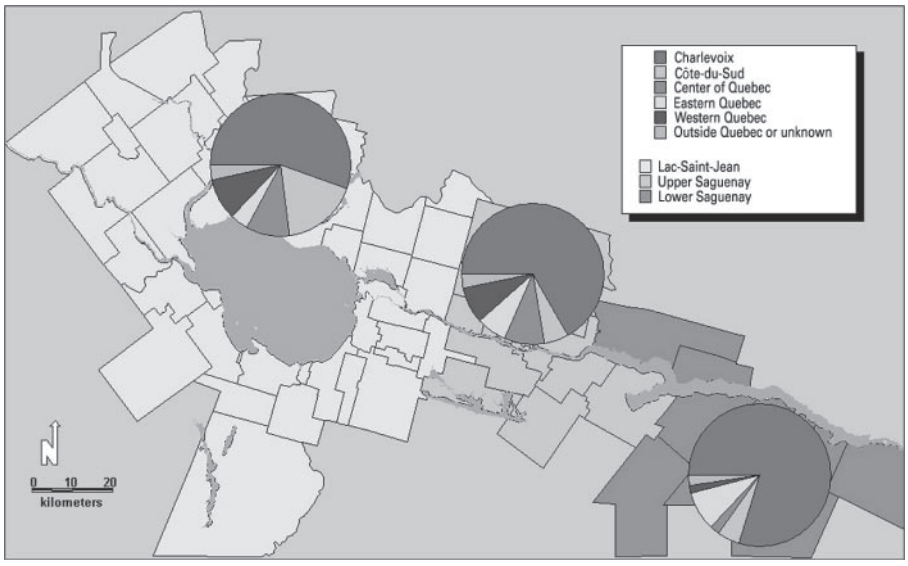

Fig. 7. Genetic contribution of regional founders by place of origin in each subregion.

Table 3. Distribution of sibships among regional founders according to sibship size

Sibship size	Number of sibships	Number of founders
2	127	254
3	48	144
4	15	60
5	4	20
6	3	18
Total	197	494

Charlevoix, the Côte-du-Sud and Côte-Nord regions account for more than 83% of Lower Saguenay's gene pool, 69% of Upper Saguenay's and 65% of Lac-St-Jean's gene pool.

Genealogical links show that 42% of these regional founders have at least one other member of their sibship who also migrated to SLSJ (table 3). More than 60% of these sibships are composed of 2 founders while up to 6 regional founders were found from a single sibship.

Discussion

The SLSJ population is often referred to as a highly 'homogeneous' population. In some respects, that may be true, but our findings clearly show that some degree of heterogeneity can be observed at the subregional level. Indeed, for each demogenetic parameter, the Lower Saguenay subregion shows a different picture than that of the two other SLSJ's subregions. For instance, kinship coefficients are significantly higher in Lower Saguenay, suggesting lower genetic heterogeneity in this subregion. Values of kinship coefficients between the three subregions suggest the possibility of preferential migratory movements from Lower Saguenay towards Lac-St-Jean, which could explain why the two adjacent regions of Upper Saguenay and Lac-St-Jean have a lower between-group kinship than that of the two relatively distanced regions of Lower Saguenay and Lac-St-Jean. These results show that internal migration is an important factor to consider when studying the genetic structure of a population. A so-called 'isolate' with a strong initial founder effect may display significant internal variations due to differential migratory behaviour across generations.

Another interesting finding of this study is the higher kinship between the Lac-St-Jean subjects and the subjects of the two other subregions than among the subjects of Lac-St-Jean themselves. In Upper Saguenay, within-group kinship is also lower than the kinship between subjects of Lower and Upper Saguenay. Despite the observed variability, these results point toward the absence of stratification in the SLSJ region, at least based on our division of the territory.

The maximum value for inbreeding is significantly higher in Lower Saguenay than in the two other subregions. Contrary to Upper Saguenay and Lac-St-Jean,

Lower Saguenay did not benefit from the diversification caused by migration from other regions [1]. Upper Saguenay and Lac-St-Jean have similar inbreeding coefficients. The coefficients of each subregion stabilize after the 11th generation, corresponding to the arrival of the European founders. The first significant increase of the inbreeding coefficients happens at the 4th generation (great-great-grandparents), that of the first SLSJ settlers [21, 22]. These results confirm once again that, contrary to popular belief, close inbreeding is not important in SLSJ and hence cannot explain the observed frequencies of hereditary diseases in the region [8].

Results also indicate that the vast majority of regional founders are specific to a single subregion and that many of these founders came from the Charlevoix region. The importance of Charlevoix in terms of genetic contribution of the founders has been shown in other studies [1, 2, 23]. Among the three subregions of SLSJ, Lower Saguenay is the most similar to the Charlevoix region. More heterogeneity is observed in the places of origin of Upper Saguenay and Lac-St-Jean founders, which can be explained by the characteristics of the settlement [23, 24]. The presence of sibships among regional founders also confirms the family-type migration.

The relationship between kinship and inbreeding levels and hereditary diseases depends on several factors associated with the formation and structuration of the genetic pool in the concerned populations [25, 26]. Close kinship and inbreeding are low in all SLSJ subregions but are more frequent in Lower Saguenay because of smaller population size and immigration input. Based on the genetic contribution of the founders, one could think that Lower Saguenay is particularly representative of Charlevoix's situation in terms of hereditary diseases. However, the current population of Lower Saguenay represents less than 2.5% of the regional population and typical Charlevoix diseases appear everywhere in SLSJ.

Conclusion

The results of this demogenetic study indicate that, beyond the genetic and genealogical features that characterize the whole region and which provide evidence of a strong founder effect, the SLSJ population also displays intraregional variability. The neighbouring region of Charlevoix accounts for the greatest part of the genetic contribution of the settlers of the three subregions but its importance is higher in Lower Saguenay. In Lac-St-Jean and in Upper Saguenay, the founders' genetic contribution is more diversified in terms of places of origins, leading to lower kinship levels.

Could this intraregional variability have an influence on the current distribution of hereditary disorders that are found at an elevated frequency in the area? Despite the observed variability among subregions, our results on kinship coefficients do not support the existence of stratification in the SLSJ gene pool, at least not at this geographical level. Further investigation of this matter could prove of importance at a time where discussions are taking place as to whether population screening should be offered in the region for the identification of carriers of the most common recessive disorders (those with a regional carrier frequency between 4 and 5%) [27].

For instance, studies conducted on a smaller geographical scale, such as the community level, might reveal more specific results which could be used to improve the efficiency of a large-scale screening in the population. Additional work is also needed to understand why some genes reached the observed frequencies in SLSJ and are not uniformly distributed among Quebec's other regional populations. Like SLSJ, each region has its own settlement history, and interregional comparisons may shed some light on the geographical expansion and concentration of genes in the population of Quebec.

From a population genetics perspective, the results of this study point toward the importance of taking into account the settlement patterns and the demographic history of a population for a better understanding of its contemporary genetic structure. From a community genetics point of view, our findings may help practitioners or clinicians to improve their awareness of the possible effects of differential demographic behaviour and to be careful in their interpretation of the broad 'regional' characteristics when working with a subregional population.

Acknowledgements

The authors wish to thank Michèle Jomphe and France Néron from the BALSAC Project and Laurent Richard from the Historical Geography Laboratory at Laval University for technical assistance. This research was supported by grants from the Canadian Institutes for Health Research (ECOGENE-21 Research Alliance), the Social Sciences and Humanities Research Council of Canada, the 'Fondation de l'Université du Québec à Chicoutimi' and the 'Fonds pour la formation des chercheurs et l'aide à la recherche' (Quebec).

References

1 Pouyez C, Lavoie Y: Les Saguenayens, introduction à l'histoire des populations du Saguenay XVIe–XXe siècles. Québec, Presses de l'Université du Québec, 1983.

2 Gauvreau D, Guerin M, Hamel M: De Charlevoix au Saguenay: mesures et caractéristiques du mouvement migratoire avant 1911; in Bouchard G, DeBraekeleer M (eds): Histoire d'un génome. Québec, Presses de l'Université du Québec, pp 145–161.

3 Vézina H: Démographie génétique et maladies héréditaires au Québec: l'état des recherches. Cah Que Demogr 1996;25:293–322.

4 Scriver C: Human genetics: Lessons from Quebec populations. Annu Rev Genomics Hum Genet 2001;2:96–101.

5 Heyer E, Tremblay M: Variability of the genetic contribution of Quebec population founders associated to some deleterious genes. Am J Hum Genet 1995;56:970–978.

6 Heyer E, Tremblay M, Desjardins B: Seventeenth-century European origins of hereditary diseases in the Saguenay population. Hum Biol 1997;69:209–224.

7 Mootha VK, Lepage P, Miller K, Bunkerborg J, Reich M, Hjerrild M, Delmonte T, Villeneuve A, Sladek R, Xu F, Mitchell G, Morin C, Mann M, Hudson TJ, Robinson B, Rioux JD, Lander ES: Identification of a gene causing human cytochrome c oxidase deficiency by integrative genomics. Proc Natl Acad Sci USA 2003;100:605–610.

8 Bouchard G, DeBraekeleer M: Pourquoi des maladies héréditaires? Population et génétique au Saguenay-Lac-St-Jean. Sillery, Septentrion, 1992.

9 Mathieu J, DeBraekeleer M, Prevost C: Genealogical reconstruction of myotonic dystrophy in the Saguenay-Lac-Saint-Jean area (Quebec, Canada). Neurology 1990;40:839–842.

10 Daigneault J, Aubin G, Simard F, DeBraekeleer M: Incidence of cystic fibrosis in Saguenay-Lac-St.-Jean (Quebec, Canada). Hum Biol 1992;64:115–119.

11 Corporation de recherche et d'action sur les maladies héréditaires, Chicoutimi. http://www.coramh.org/coramh. Consulted on 4 Feb 2004.

12 Bouchard G, Roy R, Casgrain B, Hubert M: Computer in human sciences: From family reconstitution to population reconstruction; in Nissan E, Schmidt KM (eds): From Information to Knowledge: Conceptual and Content Analysis by Computer. Oxford, Intellect, 1995, pp 201–227.

13 Bouchard G: Projet BALSAC. Rapport annuel 2002–2003. Chicoutimi, Document de l'IREP, 2003. http://www.uqac.uquebec.ca/balsac/.

14 Légaré J: A population register for Canada under the French Regime: Context, scope, content, and applications. Can Stud Popul 1988; 15:1–16.

15 Bouchard G: The processing of ambiguous links in computerized family reconstruction. Hist Methods 1986;19:9–19.

16 Jomphe M, Tremblay M, Vézina H: Analyses généalogiques à partir du fichier RETRO. Document du Projet BALSAC No. I-C-215, 2002.

17 Jetté R: Traité de généalogie. Montréal, Les Presses de l'Université de Montréal, 1991.

18 Cazes MH, Cazes P: Comment mesurer la profondeur généalogique d'une ascendance? Population 1996;51:117–140.

19 Wright S: Coefficient of inbreeding and relationship. Am Nat 1922;56:330–338.

20 Malecot G: Les mathématiques de l'hérédité. Paris, Masson, 1948.

21 DeBraekeleer M, Bouchard G, Gradie M: Consanguinité et parenté au Saguenay; in Bouchard G, Debraekeleer M (eds): Histoire d'un génome. Québec, Presses de l'Université du Québec, 1991, pp 323–342.

22 Tremblay M, Jomphe M, Vézina H: Comparaison de structures patronymiques et génétiques dans la population québécoise; in Brunet G, Darlu P, Zei G: Le patronyme: histoire, anthropologie, société. Paris, CNRS Editions, Paris, 2001, pp 367–389.

23 Lambert JF: Effet fondateur et origine de la mutation D9N du gène de la lipase lipoprotéique au sein de la population du Saguenay-Lac-St-Jean. MSc Thesis, Université du Québec à Chicoutimi/Université Laval, 2002.

24 Roy R, Bouchard G, Declos M: La première génération de Saguenayens: provenance, apparentement, enracinement. Cah Que Demogr 1988;17:113–134.

25 Gradie M, Jorde L, Bouchard G: Genetic structure of the Saguenay, 1852–1911: Evidence from migration and isonymy matrices. Am J Phys Anthropol 1988;77:321–333.

26 Morissette J: La consanguinité dans la population de Charlevoix (1680–1852); in Bouchard G, DeBraekeleer M (eds): Histoire d'un génome. Québec, Presses de l'Université du Québec, 1991, pp 107–120.

27 Vigneault A, Brisson D, Bélanger C, Gaudet D: Community genetics in Eastern Quebec: The experience of the Corporation for research and action on hereditary diseases. Community Genet 2000;3:151–155.