ARC Journal of Cancer Science
Volume 2, Issue 2, 2016, PP 1-11
ISSN No. (Online) 2455-6009
http://dx.doi.org/10.20431/2455-6009.0202001
www.arcjournals.org

The Chronology of Cancer Descent from Earliest Hominin to Homo Sapiens

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Abstract: *The article estimates the chances of the emergence of human cancer from its pre-sapiens predecessors. The approach of current investigation was based on the integration of recent achievements in evolutionary immunology, epidemiology, and paleo-anthropology with the development of initial results of recent investigation of the population differences in human susceptibility to cancer. The focus was on the descent of differences in hereditary immunity against cancer resulted in different population indexes of mortality among 123 human populations from across the globe. The populations were united in four groups according to their differences in susceptibility to cancer: a group of the 43 most susceptible populations, a group of Indigenous Australians, a group of 32 most resistant populations, and a group of 47 less resistant populations. Revealed differences in geographic disposition of the groups were discovered and interpreted. Causative agent of cancer disease emerged as a result of interbreeding between Homo sapiens (Cro-Magnons) and Homo neanderthlensis. These were performed on the territories of Europe and Western Asia between 45,000 ya and 24,000 ya. These new notions provide framework and landmarks for the location of bio-ecological roots of cancer and encourage the search of new ways for the restriction and elimination of human cancer.*

Keywords: *Hereditary cancer, Hereditary immunity, Herd immunity, Paleo-anthropology, Paleo-epidemiology, Selfish Genes, Sexual Transmission, Traces of foregoing epidemics Xenogamy /*

1. INTRODUCTION

The over 40 years long War on cancer forced by the U.S. National Cancer Act of 1971 and performed by National Cancer Institute (1971-2012) was recently proclaimed as a dismal failure [1;2] because the bankruptcy of its theoretical bases. The disease continues to spread throughout the nation (and the world) with growing intensity. The existed poverty of oncologic knowledge became obvious. Oncology could not find its place among the leaders of medical research and practice.

A need has emerged to develop far more enlightening knowledge that captures the essentials of cancer, especially its initial biological issues. To understudy the bankrupted paradigm of cancer, only one, the entirely new hypothesis has been proposed and developed, that is, the hypothesis of cancer xenogamous origin, parasitic subsistence, and epidemic transmission [3-5]. In contrast to traditional views these discoveries discredited the modern supposition that cancer is caused by modern lifestyles and physical-chemical environments. The studies show the origins of this disease lay in the biology of humankind including its evolution, physiology, immunology, bioecology, genetics and self-reproduction.

According to the hypothesis, cancerous disease is a type of invasive disease that is caused by a specialized cancerous parasite, a bio-ecological entity that invades the genome of attacked human body. The multiplicity of traits that belong to cancer are performed by a causative agent of the disease, an unique biological entity that evolved to invade the human body and to subsist in it at the expense of the materials, energy and functions of the invaded organism over consecutive stages of cancer subsistence, beginning from the invasion of victim's with cancerous gamete and finishing with the sexual transmission of cancer among people.

These articles continued the development of the new hypothesis and present the initial results of the first attempt to date the terms and places of the first emergence of cancer epidemics whose traits

could have been acquired by humans over their evolution. The attempt has been inspired and supported by the positive results of analogous investigations of epidemics [6-11] that emerged over the ancient wanderings of humankind in varied parts of the World. For instance, Eurasia gave the birth to Influenza (between 50.000 ya and 15.000 ya), HIV (30.000 ya – 15.000 ya), and smallpox (14.000 ya– 10.000 ya) [12].

This article develops the results of a recently pioneered investigation discovered the population differences in human susceptibility to cancer [13]. The investigation was based on the integration of recent achievements in evolutionary immunology, epidemiology, and anthropology of cancerous diseases. The focus of current investigation was on the emergence of differences in hereditary immunity against the disease which has resulted in different population indexes of mortality among 123 populations from across the globe united in four groups of population according to their differences in susceptibility to cancer: a group of the 43 most susceptible populations, a group of Indigenous Australians, a group of the 32 most resistant populations, and a group of 47 less resistant populations. Intriguing differences in the geographic disposition of the groups have been revealed and interpreted. The issues of origin, evolution, geographic disposition and dating of discovered differences are interpreted and discussed.

2. MATERIALS AND METHODS

The investigation was based on the integration of recent achievements in evolutionary immunology, epidemiology, and anthropology of cancerous diseases. It was supported by the positive results of analogous investigations of epidemics [6-11] The focus was on the emergence of differences in hereditary immunity against the disease which has resulted in different population indexes of mortality among 123 populations from across the globe, united in four groups of the populations according to their differences in susceptibility to cancer. Population immunity was considered as a kind of herd immunity to cancer in a population based on the hereditary immunity to it by a proportion of died members over time. The analysis of relevant characteristics of all cancers, excluding non-melanoma skin cancers revealed among both sexes of world populations was performed according to GLOBOCAN 2012 (IARC) [14].

Relevant data of 123 populations from across the globe have been analyzed and systematized. The results of performed systematization of relevant data allowed to conclude [13] that according to population differences in susceptibility to cancer, the observed 123 populations can be divided into four groups. The first group **(**Index of Mortality from 201 to >400) united 43 of the most susceptible populations (Supplements, Table 1). The second group (the population of Indigenous Australians) became to be recognizable only recently, just after the Australian Institute of Health and Welfare published the first comprehensive summary of cancer statistics for Indigenous Australians [15;16]. The third group (Index of Mortality between 0 - 101) united 32 populations characterized by having the highest resistance to cancer (Supplements, Table 2). The fourth group **(**Index of Mortality from 102 to 200). was formed by 48 of the least resistant populations (Supplements, Table 3).

The investigation was based on the integrations of revealed data with of the recent achievements of evolutionary immunology, epidemiology, and anthropology. The focus was on the launch of differences in the world's population's hereditary immunity against the disease. The main focus was on the differences in susceptibility to cancer among the populations. The evaluation of the differences was based on population indexes of mortality as integral evidence of either susceptibility or resistance.

3. RESULTS AND DISCUSSION

The origin of the above-noted differences has never been explored and explained before. The recently achieved knowledge of hereditary immunity allows–the first presentation of some preliminary explanations. It became obvious that discovered differences between various populations have been achieved over their evolution in various bio-ecological environments.

3.1. Estimated Date and Place for the Emergence of Human Cancer

The modern hypothesis of cancer's way of life accentuates its xenogamous origin, parasitic subsistence, and sexual epidemic transmission [3-5].The descent of human cancer has been predetermined by xenogamous genome mutations which have created, in evolution, inter-subspecies' differences in molecular constitution of intrinsic physiological systems responsible for the regulation

of cell dividing and tissue growth. Consequent xenogamous mating between gametes of such xenogamous subspecies could lead to the intrusion of genome the descendant's zygotes with components of deviant genetic information that induce carcinogenesis.

Now the cancer causative agent is considered as a part of a cancer carrior gamete whose genome contains carcinogenic component formed over many millenia interbeeding between Homo sapiens and Homo neanderthalensis. In contrast to traditional views, the modern paradigm considers the emergence of cancer diseases as a result of intrusion into human genome of a set of alien genes that can be considered as a kind of selfish genes [3]. Ever since the intruded set of alien genes became specialized cancerous parasite that evolved to invade human body with cancerous gamete and to subsist in it at the expense of its materials, energy and functions during consecutive stages of cancer subsistence, finishing with sexual transmission of cancer among people.

As a sexually-transmitted parasite, human cancer possesses a set of constitutional, adaptive, inherently immune traits that could be the result of evolution over many millennia [17]. The date of its initiation could be referred, for instance, to the epoch of xenogamous intercourse of Homo sapiens with Homo neanderthalensis [3;17]. Recently, this pioneer theory has been supported marginally by the results of paleo-archeological discoveries of 1,7-million-year-old cancer among earliest hominids [18] and 120,000+ year old Neandertal from Croatia [19;20].

Neanderthals, the closest evolutionary relatives of present-day humans, lived in large parts of Europe and western Asia before disappearing nearly 30,000 years ago. Neanderthals lived in Europe far before the expansion of modern (Cro-Magnons) human population that is thought to have begun 45,000 years ago, and may have taken 15,000-20,000 years for Europe to be colonized. During this time, the Neanderthals were slowly being displaced by the anatomically modern humans known as the Cro-Magnons. After about 25,000 years ago the fossil record of the Neanderthals ends, indicating that they had become extinct in Europe, as the last known population lived around a cave system on the remote south-facing coast of Gibraltar from 24,000 to 30,000 years ago [21].

The carcinogenic xenogamous coexistence of Homo sapiens with Homo neanderthalensis took place on the territories of Europe and western Asia. It resulted in the emergence of cancer causative agents between 45,000 years ago and 24,000 years ago. Another study of Neanderthal genes and modern human genes concluded that interbreeding took place between Neanderthals and *Homo sapiens* between roughly 80,000 to 50,000 years ago in the Middle East, resulting in Europeans and Asians having between 1% and 4% Neanderthal DNA, while sub-Saharan Africans do not have Neanderthal DNA.[22] This means that cancer causative agents could not emerge in sub-Saharan Africa.

It should be noted that *Homo sapiens* didn't only have sex with Neanderthals. Several hominids — human relatives — interbred more than 30,000 years ago. First of them is the line of early humans called Denisovans that lived in Siberia. A fourth, mystery lineage of humans was in the mix, too. It could be something like *Homo erectus*, an extinct species of human that originated in India and spread into East Asia.[23] This means that cancer causative agents could not emerge in Siberia, India and other parts of East Asia.

Comparison of remnant Neanderthal DNA has shown that this 4% is not consistent, suggesting that there was not one, but several cases of interbreeding between the two kindred species, with Caucasian and Balkan DNA contributing more to the Eurasian human lineage than the Altaic groups [24]. Neanderthals shared more genetic variants with present-day humans in Eurasia than with present-day humans in sub-Saharan Africa, suggesting that gene flow from Neanderthals into the ancestors of non-Africans occurred before the divergence of Eurasian groups from each other. Cancer could not emerge in indigenous Africa and neither in Australia as well. The continents' populations could pose only some indigenous traits characteristic of the out of Africa dispersals. The discovered feature of the current indigenous Australians (highest susceptibility to cancer) should be interpreted as an indigenous trait inherited from their out of Indigenous Africa predecessors.

3.2. Estimated Dates of the Emergence of Most Susceptible Population

3.2.1. Initial Population of Indigenous Australians

Of particular note is the intriguing disparity between Indigenous Australians belonging to the most susceptible group and non-indigenous Australians, the migrants either from Papua New Guinea or Melanesia belonging to less resistant group. Mortality differences between the two population groups

are far more striking, with indigenous Australians being approximately 50% more likely to die from cancer than for non-indigenous Australians. The cancer risk is greater for indigenous Australians than for their current non-indigenous cohabiters [15;16]. The indigenous Australians should probably be disposed among the first group of most susceptible populations (Supplements, Table 1[13]. The higher susceptibility to cancer among indigenous Australian Aboriginals can find its explanation in the history of the settling down on- this continent by human (Figure 1).

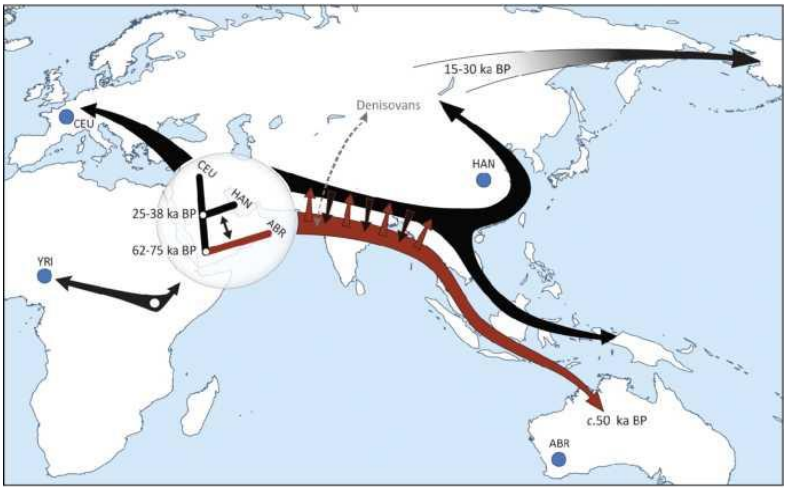

Figure1. *Reconstruction of the early spread of modern humans outside Africa [25].*

Around 100,000-80,000 years ago, three main lines of the earliest *Homo sapiens* diverged forming the colonizers of Southern Africa (the ancestors of the Khoisan (peoples), the settlers of Central and West Africa (the ancestors of western pygmies), and the inhabitants of East Africa (the ancestors of Niger–Congo- and Nilo-Saharan-speaking peoples). At the end of the Pleistocene, there were considerable changes in the climate-induced intensive processes of the earliest human migrations toward either of within or out of Africa.

Some groups of migrants moved out of the former savannahs or "Edens", and back into the remnants of the tropical forest (Figure 1 YRI) that were the homeland of their faraway ape predecessors. For over dozens of millennia, this branch of Homo sapiens has been almost totally isolated from other branches of humankind, the settlers of Eurasian with their extraordinary rich complex of bio-ecological movers for human evolution [12;26] Within Africa, this expansion did not replace but mixed with older lineages detectable today only in Africa.

Nearly 75,000–62,000 ya, some small (20-60 persons) groups of early Homo sapiens began to cross of Red sea (Figure 2) and to move out of the African Savannah territory where their descent and initial establishment had been accomplished. This initiated the dispersion of humankind around the world [25] and its further evolution at new bio-ecological zones (Figure 2). The groups moved east out of Africa along either the North Eurasian or South Asian directions. The first detectable expansion occurred around 59,000-69,000 years ago from Africa, independently colonizing western Asia and India and, following this southern route, swiftly reaching East Asia.

Figure2. *The crossing of Red sea by early Homo sapiens (around 59,000-69,000 years ago)*

Around 39,000-52,000 years ago, the western Asian branch of humankind migration (Figure 1) spread radially, bringing Caucasians to North Africa and Europe, also reaching India, and expanding to North and East Asia. More recent migrations have entangled but not completely erased these primitive footprints of modern human expansions.[21]The North Eurasian dispersal divided (38,000–25,000 ya) into European and Asian directions. The last one continued (30,000 – 15,000 ya) its way toward the American continent (30,000 - 15.000 ya) and reached nearly 14,000 ya. Since then, the native subpopulation of the American continent has been in almost total isolation from the Eurasian branches of humankind and from the relevant evolutionary processes performed among it.

The South Asian branch of human migration continued its own way toward Australia, eventually reaching this continent ~50,000 ya. Since then, the Australian branch lost all its interrelations with other branches of humankind. The great geographical discoveries and consequent intensive colonization of the American, African and Australian continents disrupted isolation of these continents. Since the beginning of the 16th century, the new settlers of opened territories brought many infections to indigenous peoples that had not been encountered before.

Many historians argue that these invasions did more to decimate isolated native populations than did warfare or enslavement, especially through epidemics of new diseases such as smallpox, influenza, measles [27-29], and probably cancer. The diseases had a devastating impact on many aboriginal populations that appeared to be originally highly susceptible. They did not have the traits of foregoing selection for hereditary immunity against these infections in their remote past. Nevertheless, the after effects of the foregoing history are seen in today's events. Thus, the paleo-epidemic story highlighted and explained the extraordinarily significant impact that cancer had on the indigenous Australian population [15;16]. In contrast, the current populations of the Earth elaborated hereditary immunity against influenza (between 50.000 and 15.000 ya), HIV (30.000 – 15.000), smallpox (14.000 – 10.000 ya) [12] and most of the others [30].

All non-African populations currently living in the world probably derived the most of their traits from the single dispersal of early humans out of Africa [25]. Over the subsequent evolution, some indigenous traits have been saved whereas other traits have been replaced, provided by new natural selection. In contrast to most resistant populations, the most susceptible populations (Supplements, Table 1) did not perform by natural selection for genetic resistance against cancerous invasion because over foregoing millenniums they subsisted in environments free of cancer i.e. in the Australia (Initial Population of Indigenous Australians) or in the isolated unknown territory (Initial Population of West European Origin).

3.2.2. Initial Population of West European Origin

The core of this group of most susceptible population is composed of representatives of Scandinavian nations (Supplements, Table 1a) and their genetic descendants. It is unknown where the aggressive seafarers came from. Undoubtedly, their initial Homeland was free of cancer and of natural selection for genetic immunity to it. However, just over the first millennium, they colonized the entirety of Western Europe (Supplements, Table 1a), but by the 9th century they had already visited the East Coast of North America. A new, improved comparative sequencing of the genomes of ancient human populations (Egyptians, Schumers, Romans, Hellas, Scandinavians, Armenians) could help to reveal its relation to cancer and where the populations came from.

Over the great geographical discoveries and consequent intensive colonization of the American and Australian continents, their descendants formed very bright zones of migrated susceptible populations on the territories of Australia, USA, Canada, New Zealand, Argentina, Brazil, Armenia and Russia (Supplements, Table 1b). The recent appearance of susceptible populations in Middle Asia (Kazakhstan) was formed by compulsory migration forced by the despotic Soviet politics. The susceptibility of the citizens of Japan and the Korean Republic could have arisen after the sojourn of American militants in the countries. (Supplements, Table 1b).

The considered feature of the most susceptible populations could have arisen between 50.000 – 10.000 ya. Now, the feature continues to subsist as an indigenous trait inherited from their ancient European predecessors. Only migration hypothesis can be proposed about the origin of the high susceptibility of the Armenian population (Supplements, Table 1b) disposed at the center of the Near East. Which events or processes could create the same properties among Scandinavians, Armenians,

and indigenous Australians if they are located so far from each other? The current volume of scientific knowledge is not enough to answer this question.

In contrast to resistant populations (section 3.3), the subsistence of most susceptible populations could emerge without interaction with a causative agent of cancer [3;31]. Such state could be achieved by physical segregation between the invader and its victim. In the case of indigenous Australians, such segregation was performed by strong geographical isolation of the Australian continent. For 50 millennia, the Australian branch of Homo sapiens has been in almost total isolation from other populations of the species [25], as well as from the epidemic processes that performed the intensive evolution of the Eurasian branches [26]. That is why the Australian branch did not develop a genetic resistance against Eurasian infections and cancer as well. This can mean that cancer could not have emerged before the Exodus out of Africa.

3.3. Dates and Places of the First Emergence of Most Resistant Population

The most resistant populations exist exclusively in the tropical and subtropical territories of Africa and South West Asia (Supplements, Table 2). The current contours of the group's disposition allow a hypothesis to be made regarding the migrations of such populations from the maternal Asian tropical core toward the Africa and the territories of Yemen, Oman, Saudi Arabia, India, Nepal, and Uzbekistan.

The emerged epidemics of cancer should lead initially to cruel natural selection and the formation of most resistant populations. This is the usual way for the evolution of any invasive epidemics [30]. The appearance of the most resistant populations could be associated with their more ancient confrontation with cancer, which resulted in intensive natural selection for the genetically predetermined ability to withstand cancerous invasion. This scenario allows the emergence of the resistance to cancer on the tropical territories of Africa and Asia fare after the exodus of a couple of humans out of Africa (70.000 ya), but over their subsequent 50.000 years wandering around the east hemisphere, except Australia (Figure 2). The considered feature of the most resistant populations could arise over 50.000 – 10.000 ya [13]. Now, the feature continues to subsist as an indigenous trait inherited from their ancient predecessors.

4. Ancient Geographic Dispositions of Discovered Groups

4.1. Dispositions of Populations after the Emergence of Cancer

According to geographic dispositions of current human populations differing in susceptibility to cancer (Figure 3) and it retro-interpretations, various geographic and bio-ecological dispositions of human populations differing in susceptibility to cancer could arise on the same different territories of West Hemisphere (Figure 4). Relevant bio-ecological conditions could arise differently for most resistant populations either in Central West Africa or in the South West Asia.

Highly susceptible populations also should be subsisted among ancient dispositions, but in any case the territories should be lesser. This group of populations can be present only on Scandinavian territories and in the Australian continent, thanks to it settling by indigenous Australians.

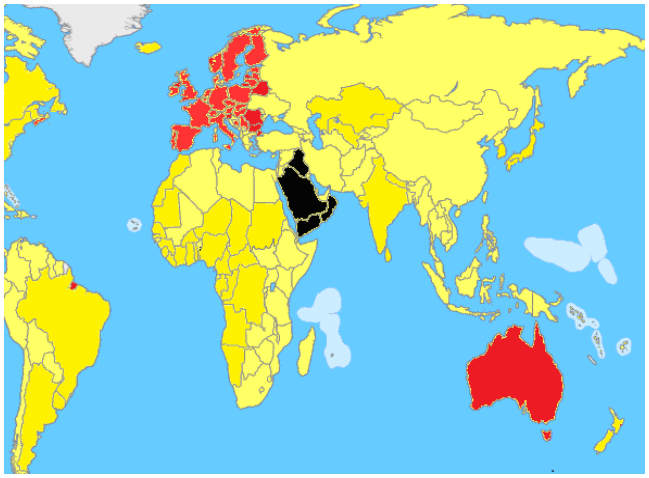

Figure3. *Earliest Dispositions of susceptible and resistant populations after the emergence of cancer (between 45,000 years ago and 24,000 years ago).*

Most susceptible populations **(**Index of Mortality from 201 to >400).

Most resistant populations (Index of Mortality between 0 - 101).

Less resistant populations **(**Index of Mortality from 102 to 200).

4.2. Dispositions of Populations before the Grate Geographic Discoveries

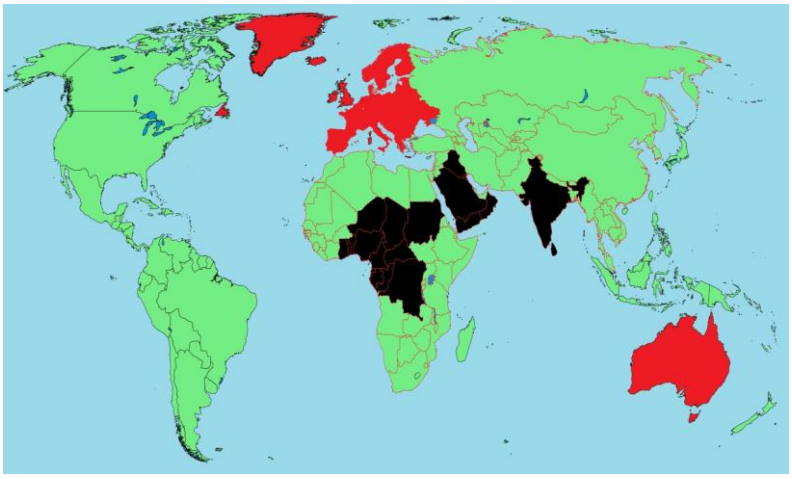

Figure4. *Ancient Geographic dispositions of human populations differing in susceptibility to cancer before the Grate Geographic Discoveries (1600 years ago).*

Most susceptible populations **(**Index of Mortality from 201 to >400).

Most resistant populations (Index of Mortality between 0 - 101).

Less resistant populations **(**Index of Mortality from 102 to 200).

The strongly stated data about the emergence of most susceptible populations after the Grate Geographic Discoveries on the territories of Australia, Canada, United States, Brasilla, Argentina, Middle Asia and so all (Figure 4) can not be used in the ancient times.

5. Current Geographic Dispositions of Discovered Groups

The current geographic dispositions of the revealed groups, except indigenous Australians are illustrated by the map (Figure 5). The illustration allows accentuation of the most noteworthy, but intriguing differences in the geographic disposition of the above presented groups of populations. The groups are found to be very different in their current geographic dispositions.

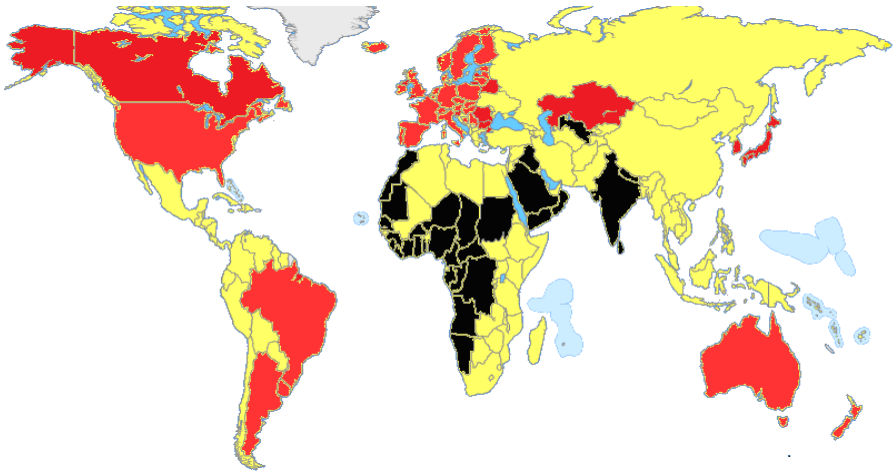

Figure5. *Geographic dispositions of current human populations differing in susceptibility to cancer after the Grate Geographic Discoveries (according to [13].*

Most susceptible populations **(**Index of Mortality from 201 to >400).

Most resistant populations (Index of Mortality between 0 - 101).

Less resistant populations **(**Index of Mortality from 102 to 200).

5. Supplements: The Limits of Population Differences in Susceptibility to Cancer

Table1. *Most susceptible populations*

a. Populations of West European Origin

1. Belarus	218.6	16. United Kingdom	272.90
2. Romania	224.20	17. Slovakia	276.95
3. Poland	229.59	18. Italy	278.61
4. Bulgaria	234.80	19. Germany	283.84
5. Montenegro	238.25	20. Iceland	284.35
6. Macedonia	239.27	21. Hungary	285.39
7. Estonia	242.84	22. Lichtenstein	286.97
8. Portugal	246.21	23. Switzerland	286.97
9. Latvia	246.77	24. Czech Republic	293.83
10. Spain	249.45	25. France	303.54
11. Lithuania	251.87	26. The Netherlands	304.80
12. Austria	254.09	27. Ireland	307.91
13. Croatia	266.86	28. Norway	318.29
14. Serbia	269.74	29. Belgium	321.05
15. Sweden	269.995	30. Denmark	338.09

b. Migrated populations

31. Russia	204.30	37. Armenia	257.02
32. Turkey	205.08	38. New Zealand	295.02
33. Brazil	205.48	39. Canada	295.72
34. Argentina	216.68	40. New Caledonia	297.91
35. Japan	217.11	41. Korean Republic	307.77
36. Kazakhstan	236.48	42. USA	317.97
		43. Current Australi	322.98

Table2. *Most resistant populations (Index of Mortality < 102*

African Populations
1. Niger 63.42 2. Benin 64.30
3. The Gambia 68.24
4. Cape Verde 74.88
5. Namibia 82.66
6. Guinea Bissau 83.05
7. Mauritania 85.66
8. Chad 88.11
9. Congo 88.18
10. Burkina Faso 88.2
11. Maldives 88.93
12. Cote d Ivoire 88.96
13. Liberia 89.21
14. Guinea 90.02
15. Gabon 90.15
16. Sudan 91.10
17. Togo 91.14
18. Ghana 91.66
19. Sierra Leone 92.27
20. Central African Republic 92.86
21. Western Sahara 97.22
22. Cameroon 97.56
23. Nigeria 100.13
24. Angola 100.81
25. Senegal 101.21

West Asian Populations
26. Yemen 80.36
27. Oman 82.05
28. Saudy Arabia 91.06

Table3. *Less resistant populations*

The existence of less resistant populations (Table 3) was revealed on Asian, African, European, and American continents, as well as on the archipelagic islands of South East Asia (Indonesia, Malaysia, Philippines, and Papua New Guinea neighbored to Australia.)

Table 3.

Less resistant populations (Index of Mortality from 100 to 200)

West Asian Populations
1. Erithrea 101.7
2. Kuwait 102.12
3. Ethiopia 108.03

Melanesian populations

South East Asian Populations
23. Thailand 137.48
24. Indonesia 133.52
25. Philippines 139.98
26. Vietnam 140.41

4. Vanuatu 107.76
5. Solomon Islands 116.34

North African populations

6. Tunisia 110.57
7. Mali 111.42
8. Morocco 117.84
9. Algeria 123.49
10. Libya 124.12
11. Egypt 152.04

Central Asian Populations

12. Bangladesh 104.45
13. Pakistan 111.82
14. Afghanistan 115.23
15. Iran 127.69
16. Kyrgyzstan 137.65

Near East Populations

17. Azerbaijan 141.94
18. Syrian Arab Republic 145.91
19. Jordan 155.40
21. Greece 163.00
22. Georgia 181.04
27. Lao PDR 143.83
28. Papua New Guinea 165.23
29. China 173.97
30. Korean Dem Republic 181.19

Central American Populations

31. Nicaragua 114.42
32. Mexico 131.54
33. Honduras 131.25
34. Guatemala 130.39.
35. Panama 148.44
36. Costa Rica 149.73
37. Dominican Republic 153.41
38. Belize 160.69

South American Populations

39. Bolivia 143.39
40. Paraguay 147.77
41. Venezuela 150.03
42. Peru 154.52
43. Suriname 159.64
44. Colombia 160.63
45. French Guyana 160.88
46. Ecuador 164.45
47. Guyana 165.93 4
48. Chile 175.69

6. CONCLUSION

This article aimed to contribute to the further development of the entirely new hypothesis of cancer xenogamous origin, parasitic subsistence, and epidemic transmission as an innovative understudy of the bankrupted paradigm of cancer. The article develops the initial results of a recently pioneered investigation of the population differences in human susceptibility to cancer. The focus of the current investigation was based on the integration of recent achievements in evolutionary immunology, epidemiology, and anthropology of cancerous diseases.

The focus was on the origin of differences in hereditary immunity against the disease which has resulted in different population indexes of mortality among 123 populations from across the globe, united in four groups of population according to their differences in susceptibility to cancer: 1) a group of very susceptible indigenous Australians, 2) a group of 43 most susceptible West European aborigines and their genetic descendants, 3) a group of the 32 most resistant populations and 4) a group of the 47 least resistant populations. Intriguing differences in the geographic disposition of the groups have been discovered and interpreted.

Human cancer emerged after the exodus of first human out of Africa. This happened between 45,000 years ago and 24,000 years ago as a result of xenogamous interbreeding between modern Homo sapiens (Cro-Magnons) and Homo neanderthalensis on the territories of Europe and Western Asia. Its spread around the world was after the Grate Geographic Discoveries.

Before this article, intriguing but not explainable was the origin of higher susceptibility of the current descendants of ancient Western European seafarers. Two groups, indigenous Australians and West European aborigines, pose their own features of high susceptibility inherited from their African predecessors. The features of resistant groups arise over their confrontation with cancer's causative agents after the exodus of humankind out of Africa i.e. on the territories out of indigenous Africa. These new notions provide framework and landmarks for the location of bio-ecological roots of cancer and encourage the search of new ways for the restriction and elimination of human cancer.

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