

# Population genetics in relation to plants and animals

Smita shukla Parveen garg\*

Department of Zoology Swami Shraddhanand College University of Delhi

Department of Botany Swami Shraddhanand College University of Delhi\*

## ABSTRACT

Population genetic seeks to understand why the frequencies of alleles and genotypes change over time within and between population. Population genetics provides the genetic structure of population and how they change geographically and over time. Population genetics is the study of genetic variation within and among population and the evolutionary factors that explain this variation. Population genetics attempt to explain the genetic diversity in present population and the changes in allele in genotype frequencies over time. For testing demographic dynamics, integration of population size estimates individual behaviour of adaptation to local environment. Population genetics shows distribution and changes of allele frequency in a population, as it is subject to the four main evolutionary processes, genetics drift, natural selection, mutation and recombination. Genetics differences and creation Population structure genetic diversity can inform resources management and conservation activities affected by selection, genetics drift, and gene flow within a population. This review indicated strengths limitations future possibilities and challenges. We therefore highlight when combining population genetic data with behavioral, modelling, morphological ecological data on multiple synergistic effect

**KEY WORD** Mutation Recombination

## INTRODUCTION

Population genetics is the basic insights it provides into the mechanism of evolution, some of which are far from intuitively obvious. Population genetics structure is genetics creation in time and space. Traditionally population genetics structure assessments provide information on the dispersal of species, mating behaviour and the delimitation of species and population boundaries. Population genetics studies the genetics composition of biological populations and the changes in genetic composition that result from the operation of various factors, including natural selection. Genetic variation can be caused by mutation, random mating, random drift and recombination between homologous chromosomes during meiosis. Natural selection, mutation, random genetics drift and migration brings changes into or out of the population. Changes to the mating pattern can changes the genotype but not allele frequencies. Genetic composition of populations including distributions and changes in genotype and phenotype frequency in response to the processes of natural selection, genetic drift, mutation and gene flow. Population genetics can provide insight into ecological and evolutionary processes that is mutation, genetic drift, natural selection and relevant to vector born disease. On population genetics review articles have been written (Crow and Kimura 1970, Crow 1987, Charlesworth Charles worth 2017, Chakraborty 2006) and Mendel (1866), Hardy (1908), and Weinberg (1908) documented the development of population genetics. Mutation occurs when a DNA gene is damaged or changed in such a way as to alter genetic message carried by that gene result from DNA copying mistakes made during cell division, exposure to ionizing radiation, exposure to chemicals called mutagens or infection by viruses. The effect of genetic drift are most pronounced

small populations. It is mechanism of evolution. It refers to random fluctuations in the frequencies of alleles from generation to generation due to chance events. In natural selection is the process through which population of living organisms adapt and change. Reproduction, heredity, variation in fitness or organism, variation in individual characters among members of the population. Dispersal is one of the central process in the plants and evolution of plant population. The spatial dynamics plants populations are determined to a large degree by the movement of seeds. At regional scales seeds dispersal ranges will set the possibilities for colonization of new sites, and will influence the probability of extinctions of local population (Brown and Kodric 1977). Dispersal distances are measured

by trapping seeds at various distance from the source (Huiskeset *et.al.* 1995; Ruckelshaus 1996;Thirde and Augspurger1996). Study of dispersal would greatly benefit from integration of ecological and population genetics approaches. Integrate ecological and population genetics approaches to study dispersal should start with a definition of dispersal as distinct from gene flow. Evolution of the risk of escape of genetically modified organisms into natural populations (Ellstrand and Hoffman1990) and control of epidemic diseases and invasions of exotic species (Hengeveld 1989; Williamson 1996). Dispersal distance are measured by trapping seeds at various distances from the source (Huiskeset *et.al.*1995; Ruckelshaus 1996; Thiede and Augspurger 1996) by recapturing marked and releases propagules ( Johansson and Nilsson 1993) by using artificial analogues of dispersal propagules Johansson and Nilsson 1991) or by using artificial analogues of dispersal propagules (Nilsson *et.al.* 1991) in this review we highlight how the population genetics take place in plants and animals in this fast growing research field.

## POPULATION GENETICS IN DOMESTIC ANIMALS

The domestic Bactrian camel were treated as one of the principal means of locomotion between the eastern and western cultures in history. However whether they originated from east Asia or central Asia remains elusive.To address the question( Liang et al 2020) performed whole genome sequence of128 camels across Asia.The extant wild and domestic Bactrian camel show remarkable genetic divergence. as they were split from dromedaries.The wild Bactrian camel also contribute little to the ancestry of domestic ones, although they share close habitat in east Asia.

The population of domestic Bactrian camels inhabit the desert and semi desert areas of southern and western Mongolian and northern and western China,while small populations remain in Russia and Kazakhstan.Magnolia has successfully preserved pasture supported animal husbandary under the condition of traditional nomadic life style. For centuries Mongolian herders have maintained five type of livestock Bactrian camels,horses,cattle,sheep and goats.Although the domestication history of the other livestock species is well explored our understanding of Bactrian camel domestication is still incomplete (Chuluunbat *et.al.*2014).The relationship between domestic and wild camels(Camels *ferus*) is comparable to that of domestic and wild horses (Camelus *ferus*) is comparable to that of domestic and wild horses (Equus *ferus przewalskii*).Although closely related Bayesian reconstruction of the demographic history do not support the Przewalskis horse as direct ancestor of the domestic form(Lau *et. al.*2009,Warmuth *et al.*2012).Similarly, the extant wild two humped camels in Mangolia and China have been considered as the ancestors of modern domestic Bactrian camels.However, genetic studies have demonstrated high sequence divergence at mitochondria l(Ji *et. al.*2009) (Silbermayr *et.al.*2010a) and nuclear loci ( Jirimutu *et.al.* 2012),excluding the wild camel as the direct ancestor of modern domestic populations.

The domestic cat is the one of the popular pets in the world.There are an estimated 106.4 million pet cats in Europe,95.6 million pet cats in the United States of America 1 and the united kingdom alone has 10.9 million pet cats2.It is estimated that non pedigreed cats make up the vast majority of this population, with only 8- 10 % of owned cats in the UK being pedigreed cats 34 Evidence presented by both Lipnski *et.al.*5 and Kurushima*et.al.*6proposed that pedigree cats continue to share genetic ancestry with the cat local to these breeds geographic origins.

Over the past 140 years, the plethora of pedigree cat varieties have developed due to mankind's imposed artificial selection on the process of cat domestication.Since the first cat show in London in The First cat show in London 1871 which showcased only five breeds the development of pedigreed cat has increased in popularity (Penny 1871) In the USA the cat Fanciers Association currently recognized 41 breeds for competition and the international cat association accept 57 breeds.Cat breed standards are defined by phenotypic characteristics.Many of these phenotypes such as hair length, coat patterning and colours are single gene traits found at low to moderate levels in the general non pedigreed cat population (Kurushima *et. al.* 2014 ).Cat bread standards are defined by phenotypic characteristics. Many of these phenotypes such as hair length,coat patterning and colours are single gene traits found at low to moderate levels in the general non pedigreed cat population ( Kurushima *et. al.* 2014 ).The genetics profile of the loci coding coat characteristics such as colour pattern length as well as for skeletal anomalies have been examined for many domestic cat in north America ( Anderson and Jenkins 1979,Blumenberg 1977,1983,Blumenberg and McDonald 1978,Fagen 1978,Glass 1981,Kerr 1984, Kerr and Halpine 1986 Klein *et. al.*1988, Lloyd 1985,Todd 1964,1966 1969 Todd and Todd 1976).

## POPULATION GENETICS IN FISHES

Fishes are the most diverse vertebrates the recorded fishes have reached more than 32000 species which are over one half of the world 60,000 living vertebrate species (Nelson *et.al.* 2016).According to their lived habitats fishes are commonly classified as continental fishes or marine fishes.Continental fishes include freshwater fishes, peripheral freshwater fishes,marine fishes and salt water fishes.Marine fishes are divided into coastal fishes,ocean fishes and deep sea fishes.Some fishes need to migrate between fresh water and marine water during their life cycle are called anadromous and catadromous fishes (Reis *et.al.*2016).Therefore ,fish biology not only investigates the diversity,phylogenesis,morphology,physiology,reproduction and behaviour but also explore ecological distribution and analyzes the influence of many environmental factors.Fishes are increasingly faced with altered environmental conditions and disturbance resulting from human activities. In particular over harvesting habitat destruction, pollution,and the introduction of non native species have led to a global decline in marine and freshwater fish biodiversity (Leidy and Moyle1998, Pauly and Zeller 2016).A land mark study by Dewoody and Avise (2000) analyzed 32 fish species and provided one of the first quantitative comparison of genetic diversity in fishes occupying different habitats.The study suggested that genetic diversity was higher in marine fishes relative to fresh water fishes.

## POPULATION GENETICS IN PLANTS

Plant popularity genetics focuses on the genetic foundations of the process that have led to documentable improvements in cultivated plants since the earliest domestications took place perhaps 13000 years ago. All human civilizations have depended heavily on inbreeding plants particularly wheat,barley,soybeans and other inbreedings legumes,as well as out breeding vegetatively propagated species white potatoes,yams as their dietary standbys.Maize joined wheat,rice, and barley as a truly major crop worldwide only after its conversion to self pollination combined with hybridization between favorably interacting in bred lines increased yield of maize several fold in the twentieth century ( Robert A.W.1999).

Genetic diversity among plant population in a given species allows to plant to adapt to various environmental conditions.,such as fluctuation in climate and soil conditions.Food security is an urgent concern because of the growing world population. A recent estimate suggests that the world population will reach 9 billion or more by 2050 (United nation 2012) and meeting the demands of this estimated global population is expected to required a 70% increase or at least a doubling in food production (Smith *et.al* 2013,Royal 2009).Excellent reviews of population genetics have been written Chakraborty2006,Charlesworth and Charlesworth 2017,Crow1987,Crow and Kimura 1970) documenting the development of population genetics from early achievements by Mendel(1866) ,Hardy( 1908 and Weinberg (1908) up to highly sophisticated theoretical developments mostly by American,British and Japanese Scientists.

Overview of process to be analysed by more than one discipline divided into population of overlapping with the four research fields population ecology (extrinsic tractors from envisioned conditional like habitat fragmentation).Movement ecology (intrinsic factor like anima behavior morphology and spatial modelling.Genetics diversity in a given species allows the plants to adapt to various environmental conditions such as fluctuation in climate and soil conditions. Sources of genetic diversity in a species can be classified into three types first one is cultivars crop that are artificially selected by human based on useful phenotypic traits and second one are natural variation selected by nature over a long period and last one is mutant produced using transgenic technologies.

## CONCLUSION

This review of plant and animals population genetics focuses on the genetic foundation of the processes that have led to documentable improvements in plant and animals. Genetics can be longer be regarded as a very young science. Population genetics as an integral part of theoretical and evolutionary biology and ultra, as a cornerstone of the modern synthesis that bridged the gap between naturalists and geneticists. The integration of population size estimates and demographic dynamics as well as individual behavior allows for testing of adaptations to local environments and understanding times.Population genetics research has transformed from the study of genetic structures in to a much wider and highly multidisciplinary research.

## REFERENCES

1. Anderson M.M. and Jenkins S.H. (1979). Gene frequencies in the domestic cat of Reno, Nevada confirmation of a recent hypothesis. *J. Hered* 70:267-269.
2. Anagram. (1978). Domestic cat demography and population genetics in a Midwestern USA metropolitan area. *Carnivore* 1:60-67.
3. Blumenberg B. (1977). The genetic differences and selection in domestic cat populations of the United Kingdom and former British colonies. *Theor. Appl. Genet.* 49:243-247.
4. Chakerabarty R. (2006) Population genetics: Historical aspects. eLS. Wiley, Chichester, 1-6
5. Charlesworth B., Charlesworth D. (2017) Population genetics from 1966 to 2016. *Heredity (Edinb)* 118:2-9
6. Crow J.F., Kimura M. (1970). An introduction to population genetics theory. Harper and Row, New York
7. Dewoody, J.A. and Avise J.C. (2000). Microsatellite variation in marine freshwaters and anadromous fishes compared with other animals. *Journal of fish biology.* 56:461-473.
8. Glass G. (1981) A preliminary survey of domestic cat gene frequencies in Goodland, Kansas. *Carnivore Genet. Newsletter.* 4:130-132.
9. Hardy G.H. (1908) Mendelian proportions in a mixed population. *Science.* 28:49-50
10. Huiskeset, A.H.L., Koutstaal, B.P., Herman, P.M.J., Beeftink, W.G., Markusse M.M., De Munck, W. (1995). Seed dispersal of halophytes in tidal salt marshes. *Journal of ecology.* 83:559-567
11. Johansson, M.E. and Nilsson, C. (1993) Hydrochory population dynamics and distribution of the clonal equipollent *Ranunculus linva*. *Journal of Ecology.* 81:81-91.
12. Ji R, Cui P., Ding, Geng J., Gao H, Zhang H., Yu J., Hu S., Meng H. (2009). Monophytic origin of domestic Bactrian camel (*Camelus bactrianus*) and its evolutionary relationship with the extant wild camel *Camelus bactrianus ferus*. *Animal genetics.* 40:377-82.
13. Jirimitu (2012). Bactrian Camel Genome Consortium Genome Sequences of wild and domestic bactrian camels. *Nature Communication.*
14. Kurushim J.D., Lipinski M.J. and Lyons L.A. (2014). Variations of cats under domestication genetic assignment of domestic cats to breeds and worldwide random bred populations. *Animal genetics* 44(3):311-324.
15. Kerr S.J. (1984). Mutant allele frequencies in rural Wisconsin cats. *J. Hered* 75:203-206.
16. Kerr S.J. and Halpine T. (1986). Mutant allele frequencies in the cat populations of Omaha Nebraska. *J. Hered.* 77:460-462.
17. Klein K.K., Smith S., Schmidt J., Shostak J. and Kerr S.J. (1988). Mutant allele frequencies in upper Midwestern cat in the United States. *J. Hered.* 79:389-393.
18. Lloyd A.T. (1985) Geographic distribution of mutant alleles in domestic pet population of New England and the Canadian writings. *J. Biogeos.* 12:315-322.
19. Lau A.N., Peng L., Goto H., Chemnick L., Ryder O.A., Makova K.D. (2009) Horse domestication and conservation genetics of Przewalski's horse inferred from sex chromosomal and autosomal sequences. *Molecular biology and evolution.* 26:199-208.
20. Leidy, R.A. and Moyle, P.B. (1998). Conservation status of the world's fish fauna. An overview in Fidler P.L., Kereiva P.M. (Eds) *Conservatory biology.* 187-227.
21. Mendel G.J. (1866) Versuche über Pflanzen-Hybriden. *Naturforsch. Verh. Brunn.* 4:3-47

22. Munck,W.(1995).Seed dispersal of halophytes in tidal salt marshes.Journal of ecology. 83:559-567
- 23.Nilsson C.,Gardfjell M.Grelsson,G.(1991)Importance of hydrochory in structuring plant communities along riversCanadian Journal of Botany. 69:2631-2633.
- 24.Penny D. (1871) Cat show on July
- 25.Pauly,D.and Zeller,D.(2016).Catch reconstruction reveal that global marine fisheries catches are higher than reported and declining Nature Communication Communicatio. 7:10244.
- 26.Ruckelshaus,M.H.(1996).Estimation of genetic neighborhood parameters from pollen and seed dispersal in the marine angiosperm *Zostera marina* L. Evolution. 50:856-864
- 27.Robert W.A.(1999).History of plant population genetics. Annual review of genetics 33(1):1-27
- 28.Royal Society.Reaping the benefits (2009).Science and the sustainable intensification of global agriculture.London Royal Society.
- 29.Reis,R.E.,Albert,J.S.,Di Dario,F.,Mincarone,M.M.PetryP.,Rochna,I.A.(2016).Fish biodiversity and conservation in South America.J.Fish biol.89:12-47.
- 30.Silbermayr K.,Orozco-ter Wengel. P.,Enkhbileg D.,Walzer C.,Vogi C.Schwarzenberger F.,KaczenskyP.,Burger P.A. (2010a).High mitochondrial differentiation levels between wild and domestic Bactrian camels a basis for rapid detection of maternal hybridization. Animal genetics.41
- 31.Smith P.,Gregoty P.J.(2013).Climate change and sustainable food production.Proc.Nuts. Soc.72:21-28
- 32.Weinberg W.(1908) Über den Nachweis der Vererbung beim Menschen.Jahreshefte des Vereins für Vaterländische Naturkunde in Württemberg. 64:369-382
- 33.Todd N.B.(1964).Gene frequencies of Bostons catsheredity19:47-51.
- 34.Todd N.B. (1966).Gene frequencies in the cat populations of New York City.J. Hered 57:185-187.
- 35.Todd N.BB(1969). Cat gene frequencies in Chicago and other populations of the united States.J. Hered.60:273-277.
- 36.Todd N.B.and Todd L.M.( 1976).Mutant allele frequencies among domestic cat in some eastern areas of Canada J.Hered 67:368-372
- 37.Thirds, D.A. and Augs purger, C.K.(1996) Interspecific variation in seed dispersion of *Lepidium campestre*.American Journal of Botany. 83,856-866.
- 38.Warmuth V.,ErikssonA.Bower M.A.,(2012). Reconstruction and origin and spread of horse domestication in the Eurasian steppe.Proceedings of the National Academy of Science of the united states of America.22:8206
- 39.United Nations(2012).World Population prospects.New yark