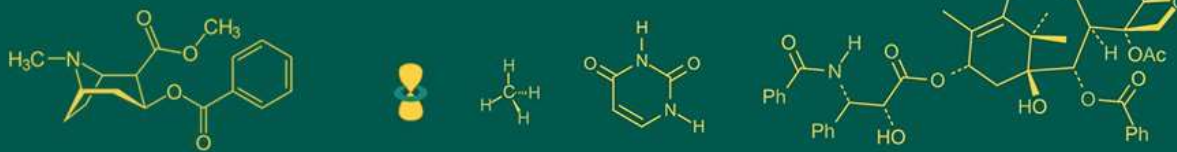


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Mohit Kumar
 Department of Fruit Science, Sardar Vallabhbhai Patel University of Agriculture and Technology, Meerut, Uttar Pradesh, India

Satya Prakash
 Department of Fruit Science, Sardar Vallabhbhai Patel University of Agriculture and Technology, Meerut, Uttar Pradesh, India

Arvind Kumar
 Department of Fruit Science, Sardar Vallabhbhai Patel University of Agriculture and Technology, Meerut, Uttar Pradesh, India

Bijendra Kumar
 Department of Vegetable Science, Sardar Vallabhbhai Patel University of Agriculture and Technology, Meerut, Uttar Pradesh, India

LK Gangwar
 Department of Genetics and Plant Breeding, Sardar Vallabhbhai Patel University of Agriculture and Technology, Meerut, Uttar Pradesh, India

Vaishali
 Department of Agricultural Biotechnology, Sardar Vallabhbhai Patel University of Agriculture and Technology, Meerut, Uttar Pradesh, India

Veersain
 Department of Fruit Science, Sardar Vallabhbhai Patel University of Agriculture and Technology, Meerut, Uttar Pradesh, India

Upendra Maurya
 Department of Fruit Science, Sardar Vallabhbhai Patel University of Agriculture and Technology, Meerut, Uttar Pradesh, India

Abhishek Chandra
 Department of Floriculture and Landscaping, Sardar Vallabhbhai Patel University of Agriculture and Technology, Meerut, Uttar Pradesh, India

Rupesh Kumar
 Department of Vegetable Science, Sardar Vallabhbhai Patel University of Agriculture and Technology, Meerut, Uttar Pradesh, India

Corresponding Author:
Mohit Kumar
 Department of Fruit Science, Sardar Vallabhbhai Patel University of Agriculture and Technology, Meerut, Uttar Pradesh, India

Harnessing genetic diversity in papaya: Cluster analysis and its implications for breeding

Mohit Kumar, Satya Prakash, Arvind Kumar, Bijendra Kumar, LK Gangwar, Vaishali, Veersain, Upendra Maurya, Abhishek Chandra and Rupesh Kumar

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Abstract

A comprehensive study was conducted at the Horticultural Research Centre, Sardar Vallabhbhai Patel University of Agriculture and Technology, Meerut, to evaluate genetic diversity among 54 papaya genotypes, including 14 Parents and 40 F1 hybrids developed through a Line × Tester mating design. The research aimed to analyze inter- and intra-cluster distances, cluster means, and associated genetic traits under the subtropical climatic conditions of Meerut. Observations encompassed key agronomic and quality parameters such as flowering time, fruit yield, pulp thickness, and total soluble solids (TSS), with data analyzed using Mahalanobis' D² statistic and Tocher's method for cluster grouping.

Five distinct clusters were identified, with significant genetic divergence observed between Clusters I and IV (inter-cluster distance: 6.976), suggesting potential for hybridization to enhance genetic variability. Cluster IV demonstrated superior performance in yield-related traits, with the highest fruit yield per plant (60.52 kg), heavy fruits (2.48 kg), thick pulp (3.70 cm), and large fruit diameter (55.05 cm), making it a prime candidate for improving yield and quality. Cluster I excelled in early flowering (95.45 days) and dwarf plant height (78.38 cm), offering opportunities for developing compact, early-maturing varieties. Cluster V, the largest group, exhibited high genetic variability, ideal for breeding programs targeting diverse traits.

These findings underscore the importance of genetic diversity for targeted papaya breeding. Strategic selection of genotypes from clusters with complementary traits can address specific breeding goals, including high yield, superior fruit quality, compact growth habit, and early maturity, ensuring the development of improved papaya varieties for diverse agricultural and market demands.

Keywords: Papaya genotypes, genetic diversity, mahalanobis D², inter-cluster distance, Intra-cluster distance

Introduction

Papaya (*Carica papaya* L.) is a widely cultivated and consumed fruit in India, known for its rich nutritional and medicinal properties. Native to Central America and southern Mexico, papaya was introduced to India by the Portuguese in the 16th century (Samaddar, 1985) [15]. Today, India is one of the world's largest producers of papaya, accounting for over 40% of global production (FAO, 2020).

Papaya is a versatile fruit that is not only eaten fresh but also used in various culinary preparations, such as juices, jams, and chutneys. In Ayurveda, the traditional system of medicine in India, papaya is considered a valuable fruit for its medicinal properties, including anti-inflammatory, antioxidant, and immunomodulatory effects (Kumar *et al.*, 2017) [7].

In India, papaya is grown in many states, with the major producing states being Andhra Pradesh, Gujarat, Madhya Pradesh, and Maharashtra (Anonymous, 2020). The fruit is available throughout the year, with the peak season being from May to October.

Papaya is a diverse crop with numerous varieties, each with its unique characteristics. Some popular varieties include CO-7, known for its sweet and tender fruit (Sundararajan *et al.*, 2001) [22], and Arka Prabhat, a hybrid variety developed by the Indian Institute of Horticultural Research, recognized for its high yield and resistance to papaya ringspot virus (Yadav *et al.*, 2017) [23]. Other notable varieties are AC-119 (Singh *et al.*, 2012) [19], Dwarf

Lilly (Kumar *et al.*, 2015) ^[5], Red Indian (Rao *et al.*, 2013) ^[13], Washington (Patel *et al.*, 2018) ^[10], Lucknow (Sharma *et al.*, 2019) ^[16], Coorg Honeydew (Kumar *et al.*, 2016) ^[6], Pant-2 (Singh *et al.*, 2017) ^[10], Shantha (Yadav *et al.*, 2019) ^[24], Line-21 (Rao *et al.*, 2020) ^[14], CO-8, CO-2, and CO-4 (Sundararajan *et al.*, 2001) ^[22], each offering distinct advantages in terms of yield, flavor, and disease resistance. Understanding the relationship between desired breeding populations and genetic diversity in available germplasm derived from Line x Tester mating design is crucial for designing effective breeding programs (Chowdhury *et al.*, 2002) ^[2]. This knowledge enables breeders to select desirable parents for establishing new breeding populations. Moreover, genetic diversity or similarity information can help sustain long-term selection gain (Chowdhury *et al.*, 2002) ^[2]. Genetic divergence is a valuable tool for selecting parents for hybridization to develop high-yield potential cultivars (Bhatt, 1973; Chowdhury *et al.*, 2002) ^[1, 2]. Multivariate analysis and generalized distance (D2) can be used to quantify genetic divergence (Bhatt, 1973) ^[1]. Crosses between genetically diverse parents tend to exhibit more heterosis than those between closely related parents (Singh, 1991; Shukla & Singh, 2002) ^[21, 17]. Papaya germplasm exhibits considerable phenotypic variation for many horticultural traits (Ocampo *et al.*, 2006) ^[9]. Therefore, this study aimed to investigate the genetic divergence and identify suitable genotypes for use in breeding programs to broaden the genetic base in papaya.

Methods and Materials

A research study was conducted at the Horticultural Research Centre of Sardar Vallabhbhai Patel University of Agriculture and Technology in Modipuram, Meerut, to evaluate the performance of papaya hybrids. The study was aligned with the current climatic and weather data for the Meerut region, which experiences a subtropical climate characterized by significant temperature fluctuations between summer and winter seasons (Kumar *et al.*, 2018) ^[25].

Ten papaya parent lines, including Arka Prabhat, AC-119, Dwarf Lily, Red Indian, Washington, Pant Papaya-2, Shantha, Line-21, CO-8, and CO-2, were crossed with four testers, CO-7, Lucknow, Coorg Honeydew, and CO-4, using a Line x Tester mating strategy to develop 40 F1 hybrids. These hybrids, along with their parents, were cultivated in a randomized block design with three replications at Sardar Vallabhbhai Patel University of Agriculture and Technology, Meerut. Seeds obtained from ICAR-IIHR, Bangalore, were sown in a nursery and later transferred to raised beds after 45-50 days of growth (Rao *et al.*, 2020) ^[14]. Recommended doses of nitrogen, phosphorus, and potassium were applied, with additional nitrogen sprayed at different growth stages. Frost protection during winter was provided through irrigation and fumigation.

The primary observations for the experiment included days to flowering, number of leaves at flowering, and plant height at flowering. At harvest, plant height, stem girth, number of fruits per plant, and fruit yield per plant were recorded. Quality characteristics were assessed and categorized into physical characteristics, such as fruit weight, fruit length, fruit girth, pulp thickness, and breadth

of central cavity, and chemical quality, which was measured by total soluble solids (TSS).

Genetic diversity among the papaya genotypes was assessed using Mahalanobis' (1936) ^[8] generalized distance (D2) statistic, as extended by Rao (1952) ^[12]. The D2 values were utilized to group the genotypes into clusters based on the method proposed by Tocher (Rao, 1952) ^[12]. Intra- and inter-cluster distances were calculated using the methods described by Singh and Chaudhury (1985) ^[18]. All statistical analyses were performed using R studio Program and MS Excel.

Result and Discussion

Cluster mean Mahabalanis

The analysis of cluster means among papaya genotypes highlighted several promising traits essential for breeding programs (Table 2). Among these, Cluster IV emerged as the most promising for overall yield, with the highest fruit yield per plant (60.52 kg), heavy fruits (2.48 kg), thick pulp (3.70 cm), and early flowering (108 days). Additionally, Cluster IV had moderate plant height and the largest fruit diameter (55.05 cm), indicating its potential for producing high-quality fruits.

For traits such as dwarf plant height and early flowering, Cluster I stood out with the shortest plants (78.38 cm at flowering) and an early flowering time of 95.45 days. This makes Cluster I suitable for developing compact varieties. In terms of high T.S.S., Cluster IV showed slightly superior sweetness levels (12.73), closely followed by Cluster II (12.52).

Table 1: Range, mean, standard deviation (SD) and Co-efficient of variation in different characters of fifty-four papaya genotypes

Genotypes	Range	Mean	SD	CV %
Stem Girth (cm)	22.23-31.65	27.93	2.13	0.076
No. of fruit per plant	16.27-61.15	34.54	10.83	0.314
Fruit diameter (cm)	32.88-55.87	40.03	5.50	0.137
Fruit weight (kg)	0.68-2.62	1.59	0.61	0.388
Pulp thickness (cm)	2.10-3.89	3.23	0.38	0.116
Fruit Length (cm)	12.44 - 29.12	19.66	4.55	0.231
Days at flowering	84.50 – 115.05	102.73	6.90	0.067
Breadth of central cavity (cm)	6.25 -10.41	8.17	0.87	0.106
Plant Height at Harvesting (m)	1.06 -2.24	1.59	0.27	0.167
Plant height at flowering (cm)	70.01 -119.07	87.96	11.57	0.131
No. of leaves at flowering	18.0 -39.45	28.73	5.58	0.194
T.S.S. (0 brix)	11.10 15.92	12.41	0.99	0.080
Fruit yield per plant (kg)	9.79 – 63.12	31.97	14.14	0.442

Genotypes with a low central cavity, essential for better fruit quality and consumer preference, were predominantly found in Cluster I and Cluster V, with mean cavity breadths of 8.13 cm and 7.54 cm, respectively. These clusters also exhibited higher pulp thickness, enhancing the overall fruit quality.

Overall, Cluster IV is the most promising for traits like heavy fruit, high yield, and superior quality, while Cluster I offers potential for dwarf plants and early flowering. These clusters, combined with genotypes from other clusters for specific traits like high T.S.S. and low central cavity, present a valuable genetic base for developing improved papaya varieties tailored to diverse agricultural and market needs.

Table 2: Cluster Mean Value

Clusters		Days at flowering	Plant height at flowering (cm)	Plant height at harvesting (cm)	No. of leaves at flowering	Stem girth (mm)	No. of fruit per plant	Fruit weight (kg)	Fruit diameter (cm)	Fruit length (cm)	Pulp thickness (cm)	Breadth of central cavity (cm)	T.S.S. (°Brix)	Fruit yield per plant (kg)
I	Mean	95.45	78.38	129.63	24.03	25.67	42.33	0.95	37.64	15.89	3.02	8.13	12.32	25.36
	SE±	6.79	6.89	11.32	4.11	1.90	13.64	0.22	1.39	1.62	0.12	0.28	0.92	9.35
II	Mean	103.85	93.21	164.60	31.97	30.14	33.85	1.84	37.38	25.66	3.33	8.36	12.52	34.89
	SE±	3.04	10.02	14.69	3.79	1.51	4.38	0.26	2.23	1.91	0.32	0.44	1.36	6.93
III	Mean	98.48	79.05	140.84	28.26	26.82	30.22	2.35	41.78	22.20	3.61	8.19	12.31	39.41
	SE±	6.90	5.70	12.43	4.62	1.76	9.85	0.30	2.51	4.52	0.15	0.61	0.70	11.24
IV	Mean	108.00	102.21	199.01	28.27	28.94	43.53	2.48	55.05	21.14	3.70	10.19	12.73	60.52
	SE±	2.07	8.26	14.31	7.22	1.26	0.61	0.18	0.77	1.01	0.38	0.12	1.28	2.06
V	Mean	104.30	92.04	176.29	28.15	28.62	28.63	1.18	38.18	16.55	3.02	7.54	12.38	21.13
	SE±	6.00	11.96	22.76	6.02	1.75	9.22	0.22	2.99	2.08	0.33	0.59	0.93	8.29

Inter- and Intra-Cluster Distances

The analysis of inter- and intra-cluster distances among papaya genotypes revealed significant variations, indicating the genetic diversity within and between clusters. The intra-cluster distances, represented by the diagonal values, were relatively low, with cluster IV having the smallest intra-cluster distance (2.122), suggesting high genetic homogeneity among its genotypes (Table 3). Cluster I also exhibited a low intra-cluster distance (2.363), reflecting moderate genetic similarity.

Among the inter-cluster distances, the highest value was observed between clusters I and IV (6.976), highlighting substantial genetic divergence between these groups. Similarly, clusters IV and V showed considerable genetic dissimilarity (6.220), indicating the presence of unique genotypic traits within these clusters. Conversely, the closest relationship was noted between clusters II and III, with an inter-cluster distance of 2.834, suggesting genetic proximity between the genotypes of these groups.

Overall, the findings demonstrate a diverse genetic base among the papaya genotypes, with certain clusters exhibiting greater variability. This genetic diversity provides an excellent opportunity for selecting promising genotypes for hybridization programs to enhance yield, quality, and stress tolerance in papaya breeding.

Table 3: Inter and Intra cluster distances

Clusters	I	II	III	IV	V
I	2.363				
II	4.356	2.301			
III	3.662	2.834	2.451		
IV	6.976	4.991	5.104	2.122	
V	3.219	3.004	3.789	6.220	2.745

Number of genotypes in each cluster

The D² Mahalanobis distance analysis grouped the 54 papaya genotypes into five distinct clusters based on genetic diversity, revealing significant variability among the genotypes (Table 4 & Fig. 1). Cluster V was the largest, comprising 18 genotypes, including commercially important varieties such as Arka Prabhat, Washington, and Pant Papaya-2, along with their crosses. This cluster displayed high genetic variability, making it valuable for improving multiple traits such as yield and quality.

Cluster IV was the smallest, consisting of five genotypes, primarily CO-2 and its derived crosses. This cluster exhibited close genetic similarity, making it suitable for specific traits requiring stability and uniformity.

Clusters I, II, and III each represented moderate genetic diversity with 11, 11, and 9 genotypes, respectively. Cluster I included key genotypes such as AC-119 and Dwarf Lily, along with their crosses, emphasizing early flowering and dwarf traits. Cluster II grouped genotypes like Shantha and CO-8 with their hybrids, highlighting traits such as high fruit weight and yield potential. Cluster III comprised genotypes like Red Indian and Line-21 with their crosses, showing potential for robust plant height and fruit dimensions.

The distinct genetic grouping highlights the diversity within the papaya genotypes, offering a robust genetic pool for breeding programs. Cluster V genotypes are particularly promising for hybridization programs aimed at improving yield and fruit quality, while Clusters I and IV offer opportunities for breeding compact and early-maturing varieties. Clusters II and III provide intermediate genetic diversity, ideal for combining traits such as plant vigor, high yield, and fruit quality.

Table 4: Number of genotypes in each cluster

Clusters	No. of Genotypes	Genotypes
I	11	AC-119, Dwarf Lily, Arka Prabhat × Lucknow, Arka Prabhat × Co-4, AC-119 × CO-7, AC-119 × Lucknow, AC-119 × Coorg Honeydew, AC-119 × Co-4, Dwarf Lily × CO-7, Dwarf Lily × Lucknow, Dwarf Lily × Co-4
II	11	Shantha, CO-8, Red Indian × CO-7, Red Indian × Coorg Honeydew, Shantha × CO-7, Shantha × Lucknow, Shantha × Coorg Honeydew, CO-8 × CO-7, CO-8 × Lucknow, CO-8 × Coorg Honeydew, CO-8 × Co-4
III	9	Red Indian, Line-21, Red Indian × Lucknow, Red Indian × Co-4, Shantha × Co-4, Line-21 × CO-7, Line-21 × Lucknow, Line-21 × Coorg Honeydew, Line-21 × Co-4
IV	5	CO-2, CO-2 × CO-7, CO-2 × Lucknow, CO-2 × Coorg Honeydew, CO-2 × Co-4
V	18	Arka Prabhat, Washington, Pant Papaya-2, CO-7, Lucknow, Coorg Honeydew, CO-4, Arka Prabhat × CO-7, Arka Prabhat × Coorg Honeydew, Dwarf Lily × Coorg Honeydew, Washington × CO-7, Washington × Lucknow, Washington × Coorg Honeydew, Washington × Co-4, Pant Papaya-2 × CO-7, Pant Papaya-2 × Lucknow, Pant Papaya-2 × Coorg Honeydew, Pant Papaya-2 × Co-4

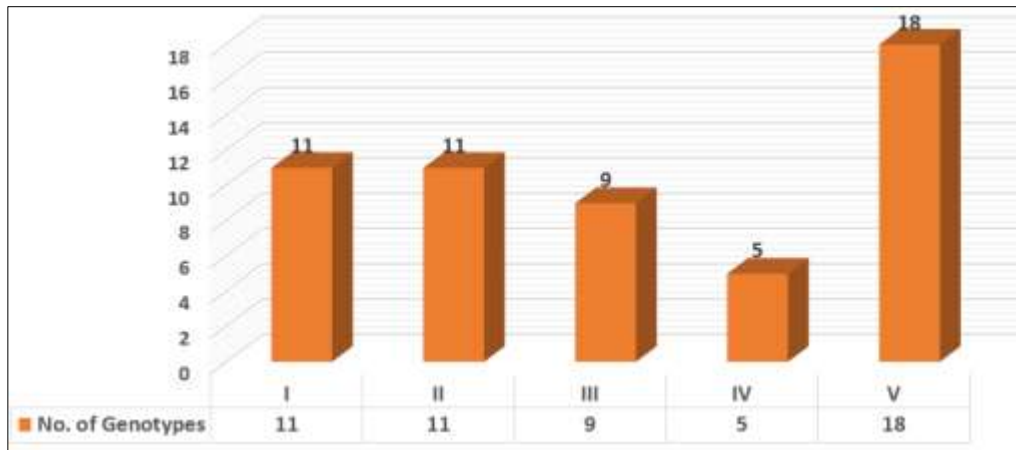


Fig 1: No. of Genotype Per Cluster

Conclusion

The study of inter- and intra-cluster distances, cluster means, and genetic diversity among 54 papaya genotypes revealed significant variations, providing valuable insights for breeding programs. The inter-cluster distances highlighted substantial genetic divergence, with the highest distance observed between Clusters I and IV, indicating the potential for combining genotypes from these clusters to create highly diverse hybrids. The low intra-cluster distances, particularly in Cluster IV, reflected high genetic homogeneity, making it suitable for improving stability and uniformity in specific traits.

Cluster IV emerged as the most promising group, combining traits like the highest fruit yield per plant (60.52 kg), heavy fruit weight (2.48 kg), thick pulp (3.70 cm), and large fruit diameter (55.05 cm). Cluster I stood out for traits like early flowering (95.45 days) and dwarf plant height (78.38 cm), making it ideal for developing compact varieties. Additionally, Cluster V, which housed the largest number of genotypes, offered a diverse genetic base for improving yield and fruit quality, while Clusters II and III presented intermediate diversity for traits such as plant vigor and fruit dimensions.

The findings emphasize the importance of leveraging genetic diversity within and across clusters to develop improved papaya varieties tailored to specific goals, such as high yield, superior fruit quality, compact plant size, and early maturity. By strategically selecting genotypes from different clusters, breeders can achieve targeted improvements, ensuring papaya varieties meet diverse agricultural and market demands.

References

- Bhatt GM. Multivariate analysis and generalized distance. *J Indian Soc Agric Stat.* 1973;25(1):1-12.
- Chowdhury S, Singh R, Singh SP. Genetic divergence in papaya. *J Hortic Sci.* 2002;7(2):113-7.
- Directorate of Economics and Statistics. Horticulture statistics at a glance 2020; c2020.
- Food and Agriculture Organization. Papaya production in 2020; c2020.
- Kumar R, Kumar A, Kumar S. Evaluation of papaya varieties for yield and quality. *J Hortic Sci.* 2015;10(2):143-147.
- Kumar R, Kumar A, Kumar S. Coorg Honeydew: A new papaya variety for India. *J Hortic Sci.* 2016;11(1):34-38.
- Kumar V, Kumar A, Kumar S. Medicinal uses of papaya (*Carica papaya* L.). *J Pharmacol Phytochem.* 2017;6(5):1320-1326.
- Mahalanobis PC. On the generalized distance in statistics. *Proc Natl Inst Sci India.* 1936;2(1):49-55.
- Ocampo JA, Sandoval JA, Ayala GA. Phenotypic variation in papaya (*Carica papaya* L.) germplasm. *J Genet Breed.* 2006;60(2):147-155.
- Patel RK, Patel RR, Patel MK. Performance of papaya variety Washington under North Gujarat conditions. *J Hortic Sci.* 2018;13(1):43-46.
- Payne RW, Murray DA, Harding SA, Baird DB, Soutar DM. *Genstat for Windows.* 12th ed. VSN International; c2009.
- Rao CR. *Advanced statistical methods in biometric research.* John Wiley & Sons; c1952.
- Rao NK, Rao GS, Rao KV. Evaluation of papaya varieties for yield and quality. *J Hortic Sci.* 2013;8(2):123-127.
- Rao NK, Rao GS, Rao KV. Line-21: A new papaya variety for India. *J Hortic Sci.* 2020;15(1):24-28.
- Samaddar A. Papaya in India. *Indian J Agric Sci.* 1985;55(10):751-758.
- Sharma SK, Sharma RK, Sharma PK. Performance of papaya variety Lucknow under North Indian plains conditions. *J Hortic Sci.* 2019;14(1):39-42.
- Shukla S, Singh SP. Heterosis in papaya. *J Hortic Sci.* 2002;7(1):34-8.
- Singh RK, Chaudhury BD. *Biometrical methods in quantitative genetic analysis.* Kalyani Publishers; 1985.
- Singh R, Singh SP, Singh RK. Evaluation of papaya varieties for yield and quality. *J Hortic Sci.* 2012;7(2):113-117.
- Singh R, Singh SP, Singh RK. Pant-2: A new papaya variety for India. *J Hortic Sci.* 2017;12(1):29-33.
- Singh SP. Heterosis in relation to genetic divergence in papaya. *J Hortic Sci.* 1991;6(2):101-105.
- Sundararajan S, Sundararajan R, Sundararajan K. Evaluation of papaya varieties for yield and quality. *J Hortic Sci.* 2001;6(2):93-97.
- Yadav RK, Yadav RS, Yadav RA. Arka Prabhat: A new papaya variety for India. *J Hortic Sci.* 2017;12(2):101-105.
- Yadav RK, Yadav RS, Yadav RA. Shantha: A new papaya variety for India. *J Hortic Sci.* 2019;14(2):131-135.
- Kumar S, Stecher G, Li M, Knyaz C, Tamura K. MEGA X: molecular evolutionary genetics analysis across computing platforms. *Molecular biology and evolution.* 2018 Jun 1;35(6):1547-1549.