

Genome size variation in Peruvian Andean maize landraces

José R. Linares Gonzales^{1,2}, Olga Bracamonte², Graciela E. González¹

1.- Instituto de Ecología, Genética y Evolución (IEGEB, Consejo Nacional de Investigaciones Científicas y Técnicas-CONICET)-Laboratorio de Citogenética y Evolución-LaCyE. Facultad de Ciencias Exactas y Naturales, Universidad de Buenos Aires, CABA, Argentina.

2.- Laboratorio de Citogenética Luis Alberto Tellería Cáceres. Facultad de Ciencias Biológicas, UNMSM, Lima, Perú.

INTRODUCTION & AIM

Maize (*Zea mays* subsp. *mays*) exhibits intraspecific variability in DNA content, ranging from 40% to 58%. Negative correlations between genome size and cultivation altitude have been observed in Andean landraces from Northwest Argentina and Bolivia. These variations are attributed to differences in the percentage of heterochromatin and the presence of B chromosomes (Fourastié et al., 2017; González and Poggio, 2021).

To investigate whether variation in DNA content is also present in landraces from the secondary center of maize diversification, the genome size of Peruvian Andean maize landraces was estimated, and its relationship with cultivation altitude was analyzed.

MATERIAL

The DNA content of 9 Peruvian Andean maize races from Cuzco and Abancay (Peru) was evaluated (Table). The samples were obtained from Centro Internacional de Cultivos Andinos (CICA) of Universidad Nacional de San Antonio Abad del Cuzco (UNSACC).

Accesion Code	Landrace	2C-value (pg)	Attitude m.a.s.l.	Localidad
CMC-043	Confite Puntigudo	5,39 ± 0,07	2939	Calca, Cuzco, Cuzco
CMC-527	Paro	5,47 ± 0,13	3143	Curahuasi, bancay, Apurímac
CMC-042	Confite Morocho	5,44 ± 0,14	2776	Ollantaytambo, Cuzco
CMC-359	Kculli	4,54 ± 0,05	2450	Huanicapa, Abancay, Apurímac
CMC-034	Pisqorunto	5,40 ± 0,89	3483	Tinta, Canchis, Cuzco
CMC-158	Granada	4,58 ± 0,03	2909	Chacora, Abancay, Apurímac
CMC-37	Chullpi	5,40 ± 0,04	3193	Quispicanchis, Cuzco, Cuzco
CMC-001	Cuzco Gigante	5,41 ± 0,07	2860	Yucay, Urubamba, Cuzco
	Cuzco Amarillo			
CMC-009	Cristalino	4,57 ± 0,04	3279	San Jerónimo, Cuzco, Cuzco

METHODS

At least 10 individuals per landrace were randomly selected. The estimation of nuclear DNA content was carried out by Flow Cytometry in FCEN-UBA. The measured nuclei were stained with propidium iodide (PI) and *Pisum sativum* cv. Ctirad (2C = 9.09 pg) was used as standard (Dolezel and Greilhuber, 2010). 2C DNA content was estimated by comparing the peak produced by the sample with the standard (Fig. 1). Data analysis was performed using Flowing Software version 2.5.1 (Turku Center for Biotechnology, University of Turku, Finland).

A one-way analysis of variance (ANOVA) was conducted using Excel (Microsoft Office 10), where the null hypothesis was the equality of mean DNA content between landraces, with a significance level of 0.05. Additionally, the correlation coefficient between altitude and DNA content was calculated.

RESULTS & DISCUSSION

Genome size was estimated in 9 Andean landraces (Table).

Inter- and intraracial variations in DNA content were observed, although the percentage of variation (13.21%) was lower than that reported by other authors.

The mean 2C value was 5.14 ± 0.42 pg. This value ranging from 4.54 ± 0.05 pg (landrace Kculli) to 5.44 ± 0.14 pg (landrace Confite Morocho) (Table).

The ANOVA test yielded a p-value of less than 0.05, indicating significant differences in mean DNA content among the studied landraces.

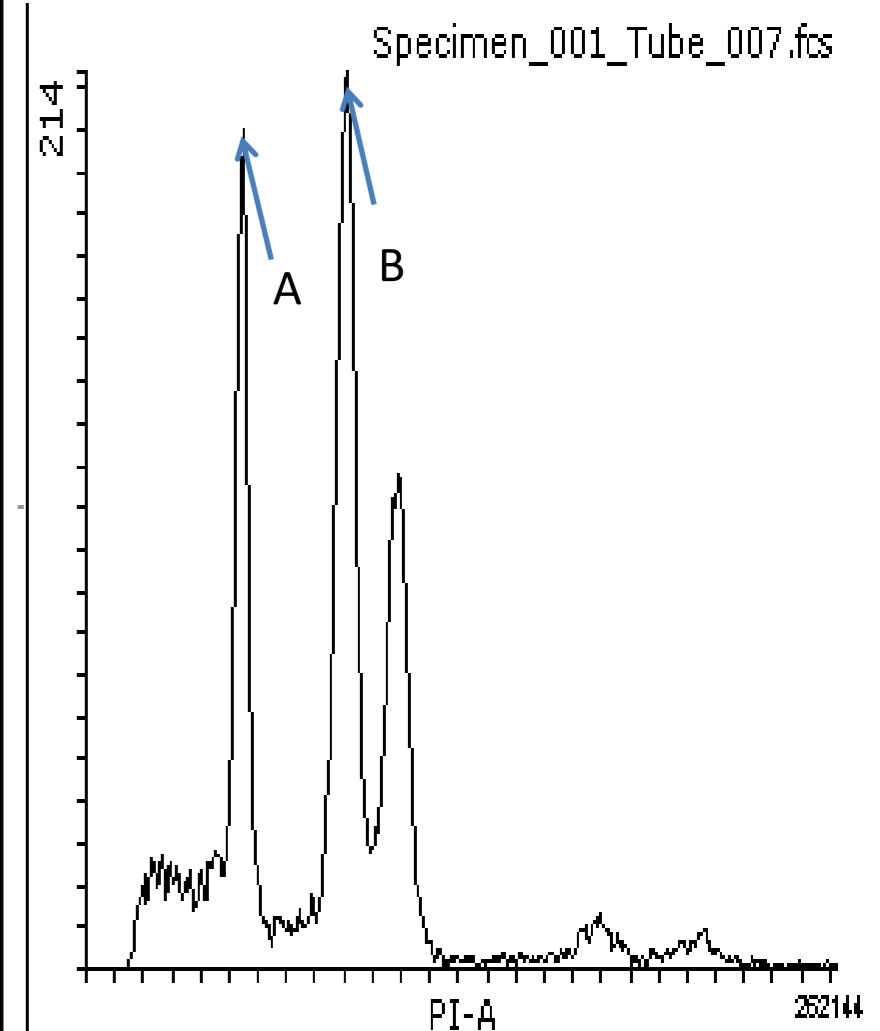
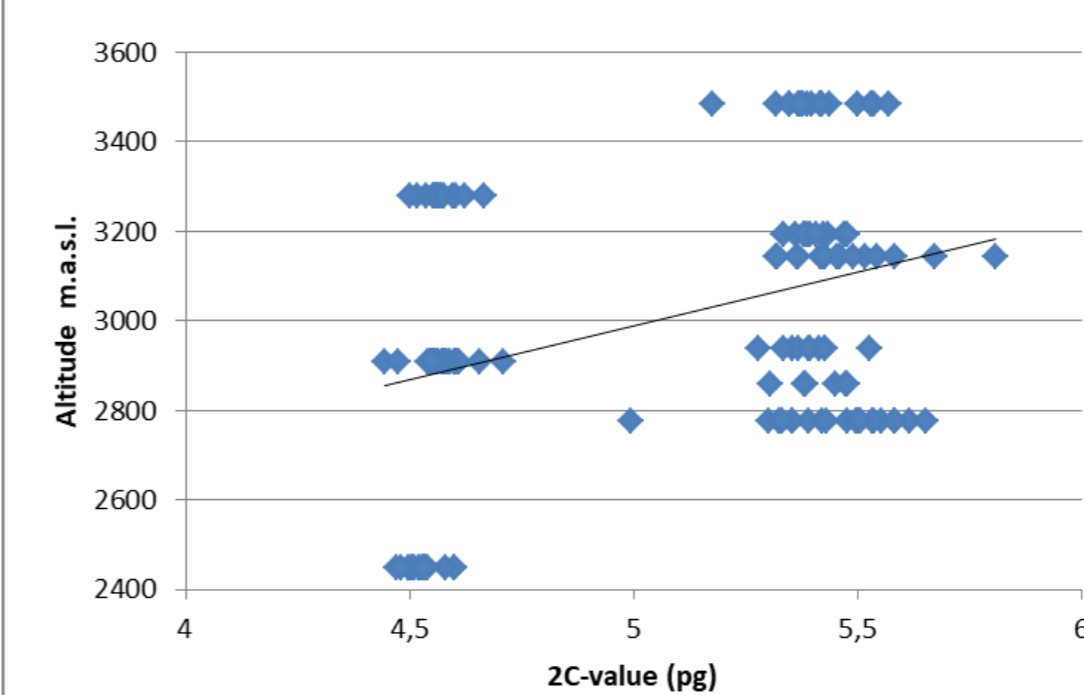


Fig. 1: Example of histograms showing the emission curves of PI from individuals of the Granada landrace (A) and from the standard (B).

The correlation coefficient was 0.35 (Fig. 2); therefore, no correlation between genome size and cultivation altitude was found. The smaller percentage of variation in genome size observed compared to previous reports, along with the lack of correlation with cultivation altitude, could be attributed to the narrow altitudinal range here sampled.

The variation in genome size found here may be due to the percentage of heterochromatin variation and the different doses of B chromosomes present in the Peruvian landraces (Linares et al., 2023).

Fig. 2: Scatter plot of the cultivation altitude (masl) and DNA content



CONCLUSIONS

1. There is variation in genome size among Peruvian Andean maize, and the mean 2C-values showed significant differences between the analyzed landraces.
2. There is no correlation between genome size variation in Peruvian Andean maize landraces and cultivation altitude.

FUTURE WORK / REFERENCES

Future studies will expand the altitudinal range. Genome size will be estimated in Peruvian landraces cultivated at low altitudes in order to integrate and correlate all data.

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