Latitudinal genome size variation in *Capsella bursa-pastoris*

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Introduction

Genome sizes vary not only greatly between species of the Brassicaceae family but also within species themselves[1]. This is considered to play an important role in plant phenotypic evolution[2]. The Sheperd's Purse (*Capsella bursa-pastoris* (L.) Medik., Brassicaceae) is one of the most widespread flowering plants of the world[3]. Previous studies showed variation on several life history traits like onset of flowering and germination behaviour[4].

The aim of this study was to determine the level of variation within the genome size of *C. bursa-pastoris* estimated via Flow Cytometry of plants from different locations from **North and South America** and **Europe and Asia** (fig. 1) in a latitudinal context.

Materials and Methods

Nuclear DNA content was estimated from 725 plants grown from seeds sampled from **91** American (*n* = 358 samples) and **101** Eurasian (*n* = 367 samples) wild populations relatively to *Petroselinum crispum* as an internal reference standard. Estimation was performed with the *CyStain® UV Precise P* reagents with the CyFlow® Ploidy Analyser (Sysmex Partec GmbH, Görlitz, Germany): GAIN: 540 V, velocity: 0,4 µl/s, 365 nm UV-LED, 532 nm excitation, 532 nm emission. FCM measurements were replicated 3 times.

2C DNA content was calculated from gated fluorescence histograms: (G1 peak of *C. bursa-pastoris* / *P. crispum* standard) x 2C DNA content of *P. crispum* (4.46pg[5]).

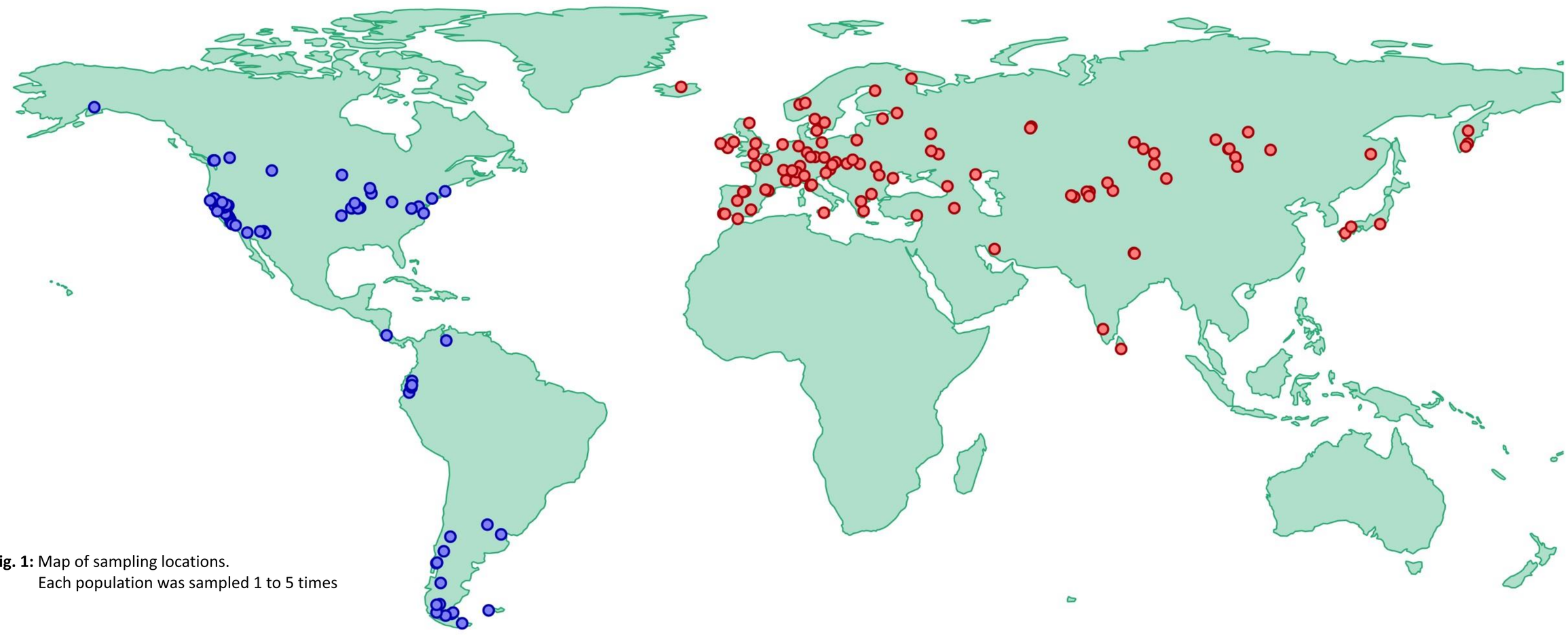

Fig. 1: Map of sampling locations.
Each population was sampled 1 to 5 times

Results

Tab. 1: Descriptive statistics

2C DNA content	America	Eurasia	All samples
min	0.8546 pg	0.8467 pg	0.8467 pg
max	1.0460 pg	1.0570 pg	1.0570 pg
mean	0.9027 pg	0.9288 pg	0.9159 pg
median	0.8922 pg	0.9300 pg	0.9168 pg
sd	0.0294 pg	0.0308 pg	0.0328 pg

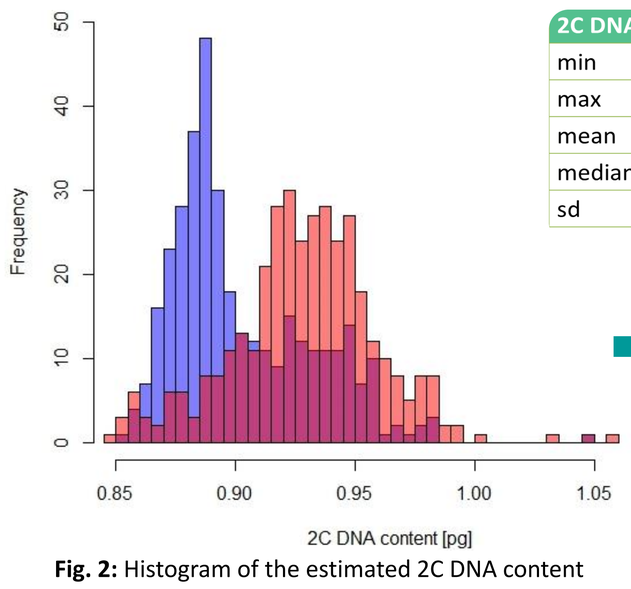

Fig. 2: Histogram of the estimated 2C DNA content

- DNA content varied from min to max in 24.84% indicating two means without normal distribution (Shapiro-Wilk p = 1.031e-09; fig. 2).

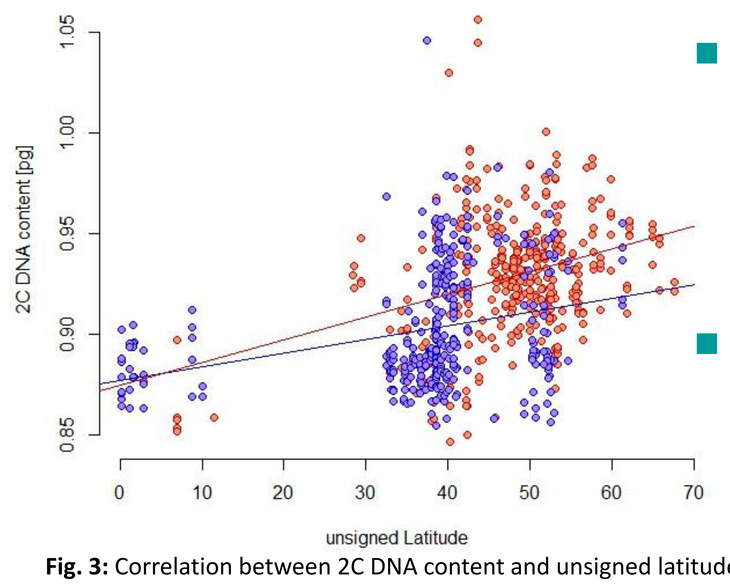

Fig. 3: Correlation between 2C DNA content and unsigned latitude

- Plants from equator near regions tend to have smaller genomes in both groups (spearman ρ = 0.4729**; fig. 3).
- The altitude of sampling locations showed no significant correlation with genome size.

Outlook

Intraspecific genome size variation depends on environmental climatic factors, biogeography and demographic history. It is assumed that it is primarily found in young radiating species[6] and explained by variation in amounts of transposonal elements and repetitive sequences[7].

What to do next?

- Why do we see two distinct groups?
- Gather sequence information of samples (RAD-Seq in progress…). Loss of certain genes?

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