



Conventional and genome-enabled farmer-participatory selection in large-scale breeding programmes: a pea case study

Paolo Annicchiarico



Centre for Animal Production and Aquaculture, Lodi, Italy



Challenges for integrating farmers' selection in large-scale breeding programs

(1) **High numbers of tested lines** are usually needed, to select simultaneously for various traits

It takes $N = (1 / s)^m$ tested lines (s = selection rate, m = no. of selected traits), to find one ideal line

E.g., assuming $s = 0.10$ and $m = 4$: $N = (1 / 0.10)^4 = 10,000$ tested lines (which is hardly workable)



(2) **A few contrasting selection sites** are adopted when targeting large regions, to cope with large $G \times E$ interactions

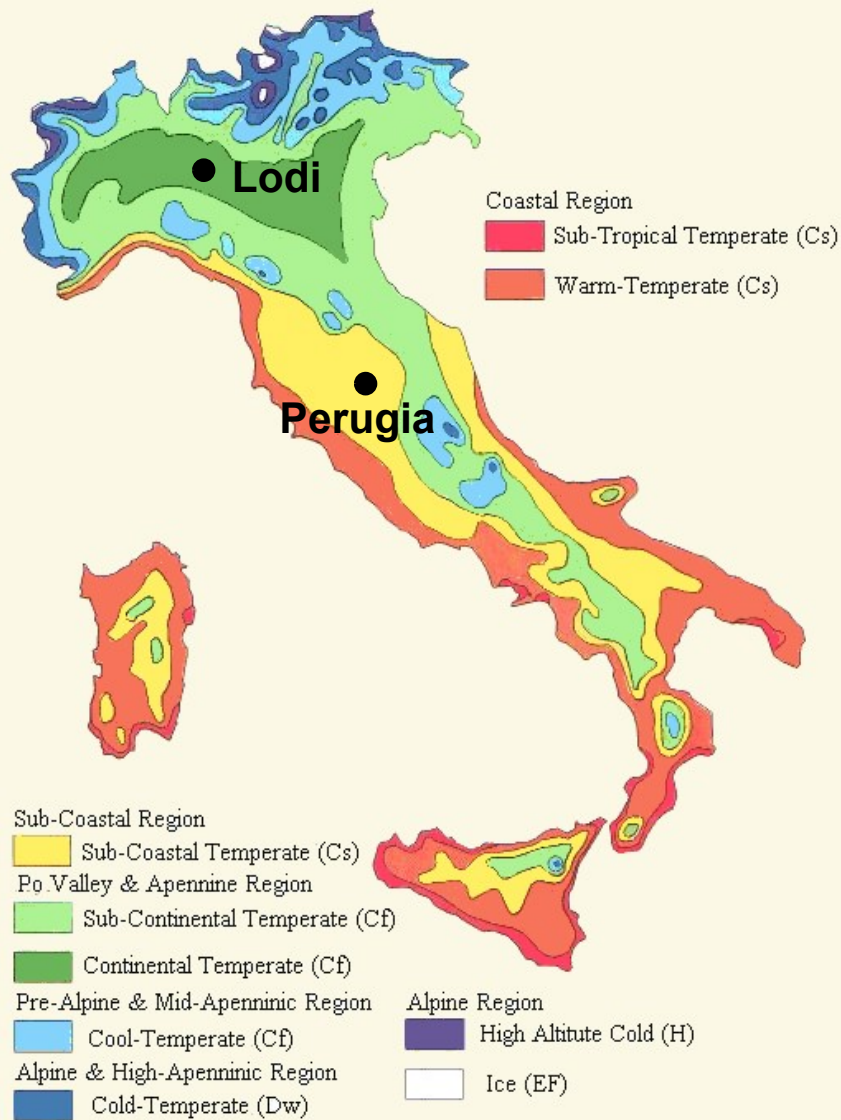
(3) **Advanced countries: breeding programs have efficient experimental equipment for plot sowing and harvesting, while on-farm trials can hardly test many lines**



Especially in advanced countries, due to (1), (2), (3): **centralized farmer participatory breeding** may be convenient (with good match of selection and target environments)

Due to the high costs of (1), (2): **genomic selection** may be useful

Pea for Italian organic farming: testing of 306 lines in 2 contrasting sites



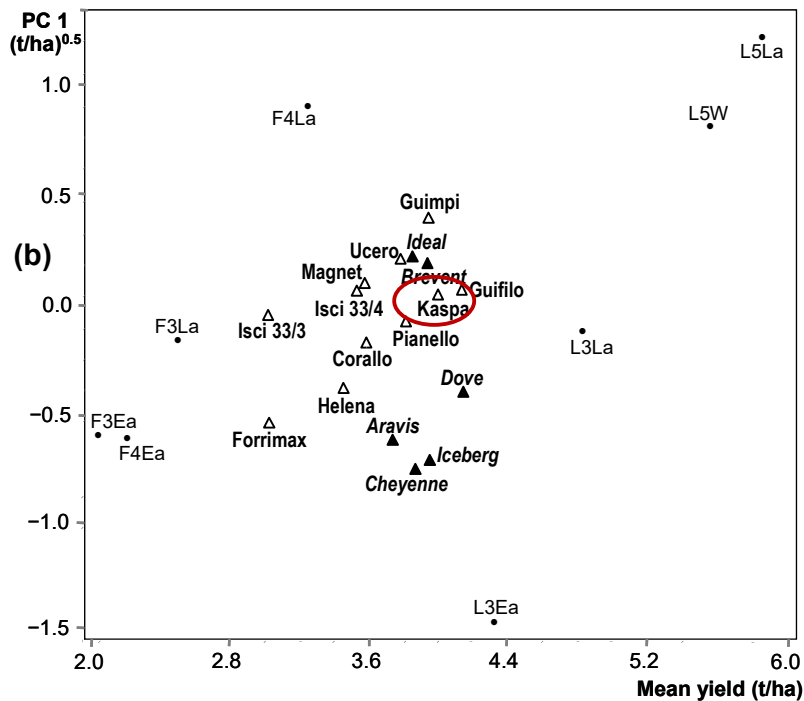
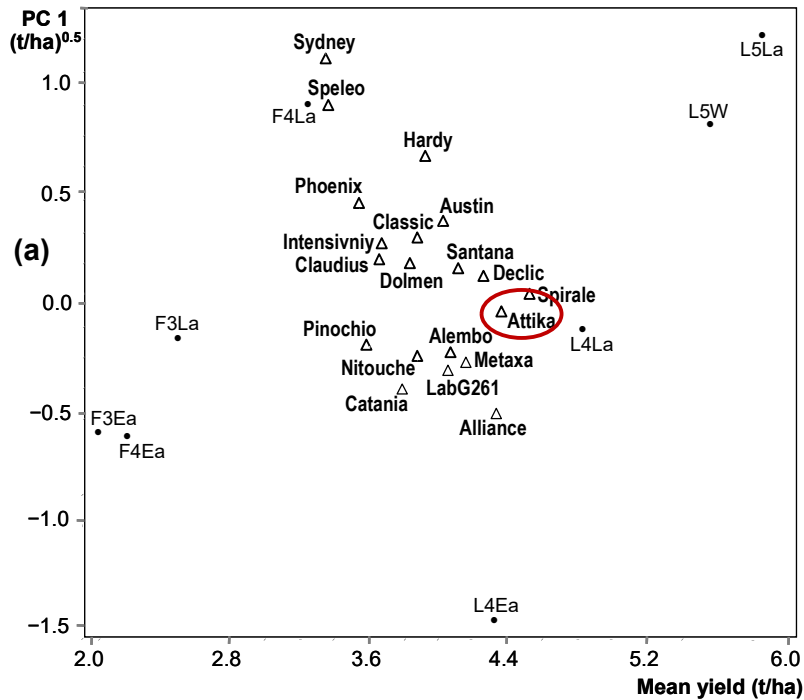
Carefully-chosen parent genotypes

Selection of 2 parents with high and stable yield across 4 subcontinental-climate and 4 Mediterranean environments of Italy (AMMI-1 biplot)

Annicchiarico & Iannucci (2008) Field Crops Res. 108: 133-142

Three connected crosses of elite cultivars

- Kaspa x Attika: 100 lines
- Attika x Isard: 102 lines
- Kaspa x Isard: 104 lines



Comparison of farmers vs. breeders for importance of pea traits (5 = very high; 0 = nil)



AIAB contributing farmers from North (above) and Centre Italy (below)



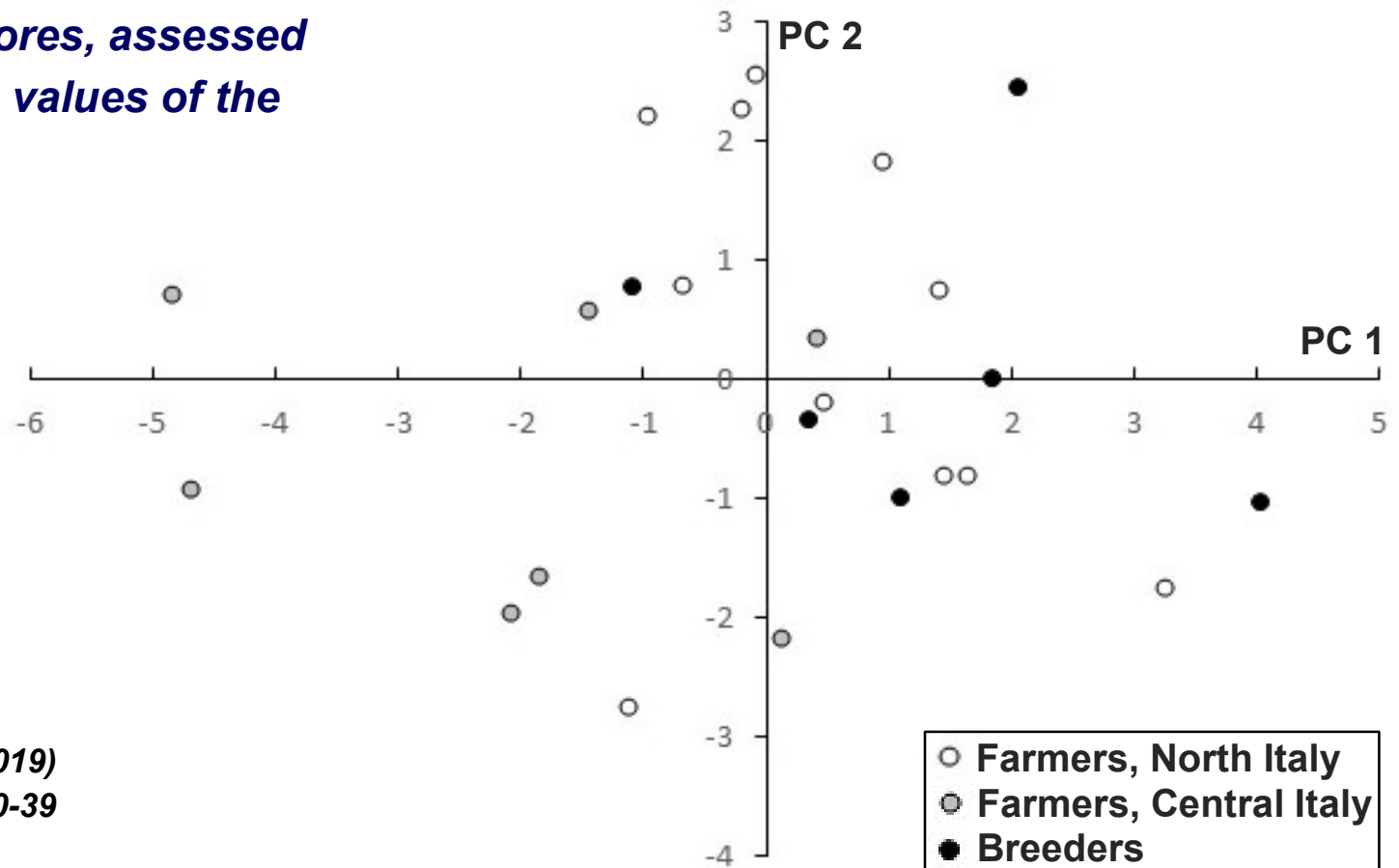
**Annicchiarico et al. (2019)
Field Crops Res. 232: 30-39**

Trait	Breeder	Farmer	P
	No. = 6	No. = 20	
Visual acceptability score	5	5	ns ←
Grain yield	4.83	4.61	ns ←
Biomass	3.33	1.86	*
Cold tolerance	4.08	4.03	ns ←
Lodging tolerance	4.58	4.22	ns ←
Antracnose tolerance	3.75	2.22	*
Fusarium tolerance	3.08	2.19	ns
Early flowering	3.33	2.83	ns
Early maturity	3.17	3.17	ns
Plant height (flowering)	2.83	2.33	ns
Semi-leaflessness	4.50	2.56	*
Seed size	0.83	0.86	ns
Yellow seed	1.00	0.00	*
Green seed	0.67	1.19	ns
Brown seed	0.33	0.14	ns
Grain protein content	3.92	4.22	ns ←
First pod height	3.67	3.45	ns

These values were used as weights to define farmers' and breeders' selection indexes

$$I_i = w_1 T_{1i} + w_2 T_{2i} + \dots + w_n T_{ni} \quad w_n = \text{weight, and } T_{ni} = \text{standardized value of line } i, \text{ for trait } T_n$$

**Similarity of breeders and farmers
for trait priority scores, assessed
by a PCA on score values of the
individuals**



*Annicchiarico et al. (2019)
Field Crops Res. 232: 30-39*



**Set of farmers (left) and
individual breeders (right)
attributing the visual
acceptability score**



Correlation between farmers' acceptability score, breeders' acceptability score and grain yield over 2 sites of 306 pea lines

Item	Breeders' score	Grain yield
Farmers' score (range: 2.6 - 6.8)	0.78 ***	0.66 ***
Breeders' score (range: 1.6 - 7.3)		0.60 ***

Annicchiarico et al. (2019) Field Crops Res. 232: 30-39

Mean yield and farmers' acceptability in independent environments of pea germplasm selected over 2 environments according to 5 selection criteria

Germplasm ^a	Average of four trials, organic management		One trial, conventional management
	Grain yield (t/ha)	Farmer acceptability score (1=lowest, 9=highest)	Grain yield (t/ha)
Selected by farmers' selection index	1.824 a	4.68 a	5.966 ab
Selected by breeders' selection index	1.726 b	4.36 b	5.227 b
Selected by farmer + breeder indexes	1.811 a	4.65 a	5.882 ab
Selected by grain yield	1.819 a	4.63 a	6.025 ab
Selected by farmer acceptability score	1.780 ab	4.61 a	6.227 a
Three parent cultivars	1.285 c	3.53 c	3.489 c
Three commercial cultivars	1.301 c	3.08 d	–

^a For each criterion, selection of 3 top-performing lines from each of 3 crosses based on pooled data from 2 organically-managed test environments (Lodi and Perugia). Column means with different letter differ at $P < 0.05$.

DNA characterization for genomic selection

Genotyping-by-Sequencing (GBS) using ApeKI restriction enzyme

Obtained up to 7521 polymorphic SNP markers for genomic selection

Genomic selection model

$$Y_i = \sum x_{ij} \beta_j + e_i$$

Y_i = breeding value for line i

x_{ij} = genotypic value for SNP marker j of line i

β_j = effect of SNP marker j

e_i = residual (unknown) effects

Savings by genomic selection relative to phenotypic selection (for inbred crops)

- 5-7 fold **lower cost per evaluated line** (for GBS-based selection)
- 2-3 fold **shorter selection cycle** (e.g. compared to 2-year phenotypic selection)
- if predicting farmers' acceptability: lower farmers' commitment in visits, etc.

Correlation of pea line value for 8 selection criteria (as observed or genomically-modelled in 2 environments) with grain yield in independent environments

Selection criterion^a	Average of four trials, organic management	One trial, conventional management
Farmer selection index	0.458^d	0.268^d
Breeder selection index	0.370^d	0.242^d
Farmer + breeder selection indexes	0.418^d	0.257^d
Grain yield	0.348^d	0.328^d
Farmer acceptability score	0.645	0.409
Breeder acceptability score	0.479	0.342^d
Genomic selection for grain yield	0.679	0.453
Genomic selection for farmer acceptability score	0.769	0.564

^a Phenotypic values or genomic predictions based on data from 2 organically-managed test environments (Lodi and Perugia). Organic trials, 31 lines; conventional trial, 306 lines.

^d Correlation lower ($P < 0.05$) than for genomic selection for farmer acceptability score.

Mean yield and farmer acceptability of 'Pantera rosa' (issued by the farmer-participatory selection; under registration) vs. other cultivars

Cultivar	Grain yield (t/ha)^a	Farmer acceptability score (1=lowest, 9=highest)^b
Pantera rosa	4.56	6.3
Spacial	3.56	5.2
Attika	2.69	3.1
Isard	3.43	4.0
Kaspa	3.12	4.7

^a Averaged across 7 organically- or conventionally-managed environments.

^b Averaged across 4 organically-managed environments.

Conclusions

- ***Breeders and farmers did not agree completely on priority traits to select for***
- ***A farmer selection index outperformed a breeder index for yield and acceptability of selected lines***
- ***Selection based on a farmer acceptability score performed nearly as well as yield-based selection***
- ***Genomic predictions were particularly accurate for a farmer acceptability score***
- ***Genomic selection for a farmer score ranked 1st in a preliminary comparison of selection criteria***
- ***The centralized farmer participatory selection produced an excellent new variety***

Thanks for your attention !



FP7-EraNet REFORMA “Resilient, water- and energy-efficient forage and feed crops for Mediterranean agricultural systems” <http://reforma.entecra.it/>



FP7-Core Organic COBRA “Coordinating organic plant breeding activities for diversity” <http://www.coreorganic2.org/>



I gratefully acknowledge:

The scientific contribution by M. Romani, L. Pecetti, N. Nazzicari, B. Ferrari (CREA); L. Russi (Univ. Perugia); E.C. Brummer, Y. Wei (Univ. California)

The cooperation by:

C. Micheloni, D. Ponzini, V. Vizioli (AIAB)

A. Baroni, I. Begliomini, S. Brambilla, L. Brambilla, F. Bossi, A. Briatti, R. Ciechi, T. Comolli, R. De Cielli, G. De Paolis, E. Di Porzio, P. Galuffo, G. Garuffi, R. Lovati, D. Mocchiutti, S. Pettinacci, E. Pietromarchi, A. Pitton, C. Rocca, M. Rubeca, E. Tavazzani, C. Vailati and F. Viganò (Farmers)

D. Bacilieri (Florisem), P. Legrand (Semfor), B. Parisi (CIN), P. Viola (ApsovSementi)

The technical assistance by A. Passerini, S. Proietti, P. Gaudenzi (CREA); F. Vecchietti, S. Vergoni (Univ. Perugia)