

Steps towards Dessert Fruit Varieties with Quantitative Host Resistance – Report on Strategy, Experiences and Results of Poma Culta Apple Breeding

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Abstract

Dessert apple varieties with polygenic broad-based field resistance are a desirable breeding goal. It is expected that disease resistance achieved in this way will be maintained in the long term. Due to the high genetic heterozygosity of the apple genome, such breeding is complex and requires a special strategy. Most characteristics are based on the quantitative expression of many genes. Since Mendel's rules of inheritance are only valid where individual genes can be directly assigned to a trait, the result of a cross has a limited predictability.

Based on the experience of two decades of Poma Culta apple breeding, concrete examples are used to show where the difficulties lie, and which strategy is considered promising. How can the high disease tolerance of otherwise inferior varieties be combined with the quality and yield potential of today's dessert apple varieties?

The way to achieve this requires crossing planning over several generations to specifically increase homozygosity while avoiding inbreeding depression, careful selection of crossing partners by means of a breeding value assessment and a sufficiently high number of progenies.

Keywords: apple breeding, breeding strategy, quantitative host resistance

Introduction

Nowadays, apple breeding usually works with qualitative host resistance based on single resistance genes. For apple scab (*Venturia inaequalis*) and powdery mildew (*Podosphaera leucotricha*) several resistance genes are known and used. For most other diseases in apple no single resistance genes have yet been identified.

In breeding Poma Culta is focussing on quantitative host resistance (definition and terminology according to Miedaner, 2011), and is therefore taking a different approach to most of its fellow breeders. Field-resistant landraces are used as resistance donors. Quantitative resistance is based on the complex interaction of various genes. It means not an absolute resistance but the greatest possible tolerance to infection. It is considered valuable because it is assumed that there is little risk of a sudden breakthrough, and the resistance should main over long periods of time. Agroscope Wädenswil has identified a whole series of highly resistant genotypes in its inventory of old Swiss local varieties. These have been used for breeding in a joint project between Agroscope, FiBL and Poma Culta (PGREL, 2023).

This raises the questions of whether this approach is effective and how long will it take to develop commercial varieties?

I would like to discuss these questions using two examples of selection in crossbred progenies.

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Example 1: Removal of seedlings from three exemplary selected cross progenies

Question: How many seedlings remain at the end of the juvenile phase for the next selection step?

Materials and method: Seeds were sown in winter 2020/21 and the germination rate was between 85% and 95% for all six progenies compared. The plants were grown in the greenhouse and inoculated with a mixture of apple scab spores (scab leaves from the site) at the age of three true leaves. As soon as clear symptoms appeared, all seedlings with sporulating infections were removed. Subsequently, all healthy and vigorous seedlings were planted out in the open-field.

At the end of June of the second vegetation year, the infestation with apple scab was assessed again and infested plants were removed. Powdery mildew-infested plants were also removed. Further selections were made for vigour, architecture, leaf health and more diseases. Finally, at the end of October, the seedlings were determined to be grafted in the following winter on the rootstock M9 for the further selection process.

Table 1: Examples of different types of seedling removal in the first selection step in the juvenile phase. Highlighted in green: Group 1 with resistant parent

Offspring	Number of Sown Seeds (= 100%)	Germin. rate (%)	Left after Scab Selection (%)	Planted in the open field (%)	Left after 2nd. Scab Selection (%)	Left after further selections (%)	Grafted on M9 (%)	Grafted on M9 (numb. of Genotypes)
Bt22Zih.21A	240	95.00	42.92	42.29	31.67	23.33	12.08	29
AK15BU9.21D	300	94.67	55.33	54.33	29.33	16.33	12.00	36
BO17Zih.21D	183	93.99	49.73	49.00	20.22	13.11	9.29	17
Bu9Bo17.21D	200	85.50	22.00	18.50	3.50	2.00	2.00	4
Bt22Eu19.21A	216	94.44	7.41	7.41	6.02	2.31	1.39	3
Bu9Eu19.21D	300	89.00	26.00	12.67	1.67	1.00	0.67	2

Results: As Table 1 and Figure 1 show, there are two groups of typical reduction processes in seedling selection. Group 1 is reduced by around half during scab selection after inoculation. Of the transplanted seedlings, around half are again infested with scab in the following year. Due to the other selection criteria, only around 10% of the seedlings reach the next stage of fruiting on M9. In group 2, there is a very drastic reduction after inoculation due to scab, and after further selections only one percent or less of the seedlings remain for the next stage.

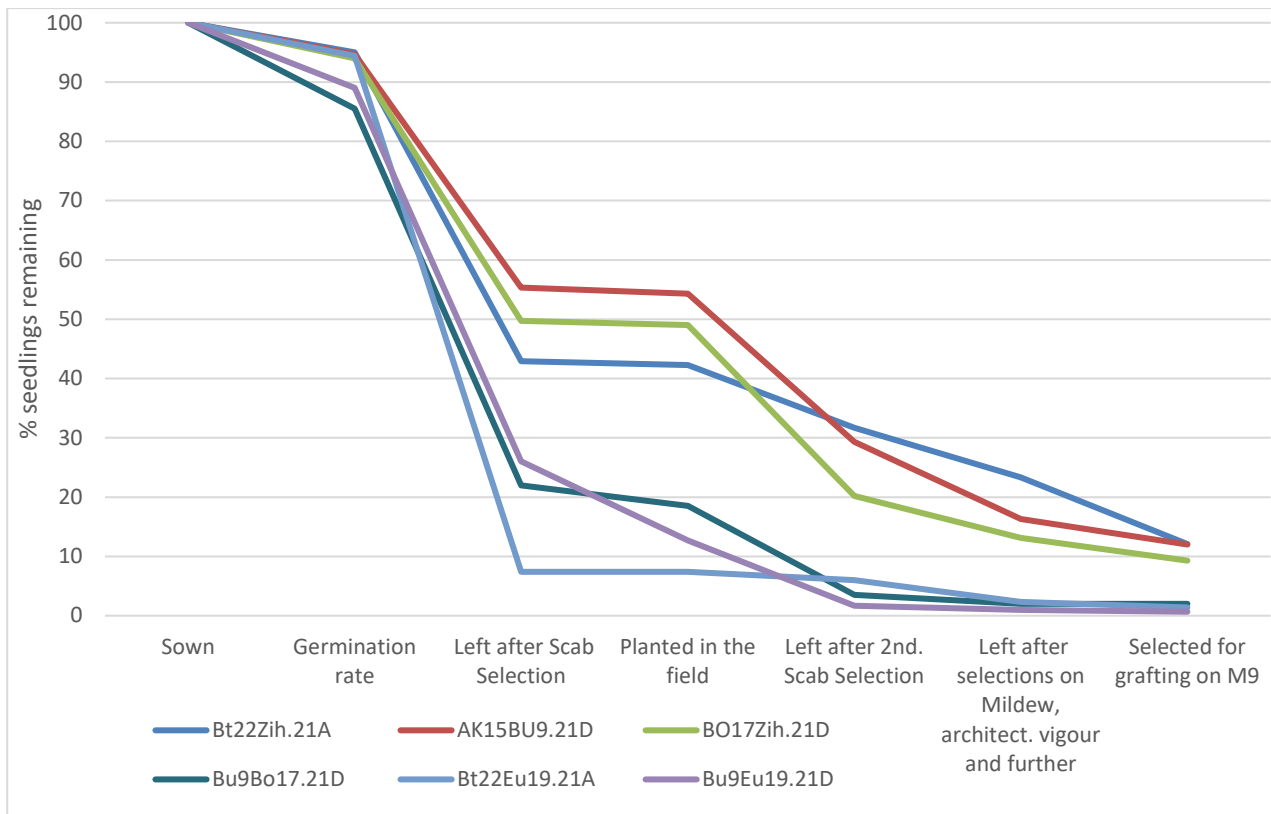


Figure 1: Examples of different types of seedling removal in the first selection step in the juvenile phase

Discussion: Experience shows that the behaviour of group 2 is typical for crosses between susceptible parents. Such cross combinations are very unpromising in terms of resistance properties. Group 1, on the other hand, has one parent with high quantitative resistance, which is reflected in some of the progeny.

The subsequent selection stages are concerned with quality and agronomic characteristics. As there are very high requirements here, the highest possible number of resistant genotypes should be available for further selection. The following options are available to increase this number:

- Increasing the initial number of seeds: This is often only possible to a limited extent for various reasons, e.g. young mother tree with few fruits.
- Through the consistent use of resistant progeny, in which in the further selection stages improvements in the categories of quality and agronomic properties were also identified, it is to be expected that more interesting progeny can be found in subsequent generations of crosses.

Example 2: Apple scab selection of cross progeny from highly quantitative resistant parents

Question: What is the incidence of quantitative resistance in the offspring if both parents exhibit it to a high degree?

Materials and method: Four genotypes from the Agroscope Wädenswil Top-30 collection (PGREL, 2023) were used to make crosses of each with each. The progeny (5 times 144 each, 1 time 120) of the six cross combinations were inoculated with an apple scab spore mixture (100K/ml). After three weeks, the percentage of seedlings without visible scab symptoms was determined.

Results: Progeny with scab infections were found in all six crossing pairs. In the best combination Np-Bu 67% were without scab symptoms, in the worst Bu-Sa 19%. Combinations with the Sa genotype were all among the worst. Combinations with the genotype Gf were in the middle range. Combinations with Np were between very good and the second worst. The Bu genotype showed the best combination with Np, the second best with Gf and the worst with Sa.

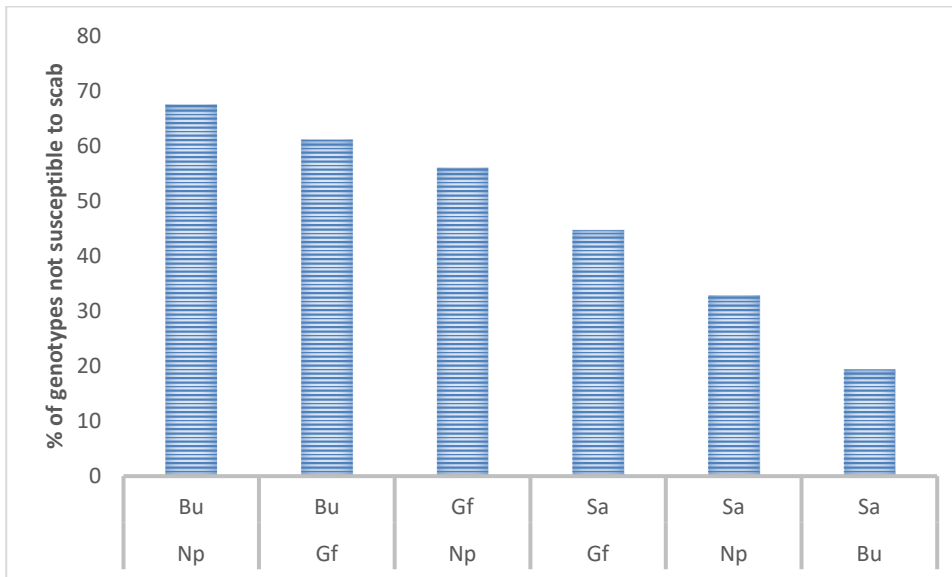


Figure 2: Incidence of non-scab susceptible genotypes in the progeny of different combinations of highly quantitative resistant crossbred parents

Discussion: The results give rise to the following conclusions:

- The resistance is only passed on to some of the offspring, even if both parents have this phenotype.
- The different results of the six combinations suggest that the genetic anchoring of resistance is different in each genotype and is passed on with different incidence. It would be interesting to summarise the results of a larger number of crosses in order to make a corresponding estimate of the breeding value of a genotype.
- Crossbreeding combinations can fit better or less well. The "genetic complementation" then leads to different incidences of resistance in the offspring.
- The question remains to what extent genotypes with a better genetic anchoring of resistance could be identified among the offspring, which would make them particularly interesting as parents for further crosses.

Strategy

The relevant traits in apple breeding can be roughly divided into three categories:


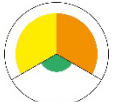

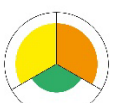
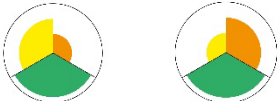
Q Quality: All characteristics related to fruit quality such as aroma, crispness, firmness, juiciness, fruit colouring and size, shelf life, etc.

A Agronomic properties: yield, vigour, tree architecture, flowering and ripening times, etc.

R Resistance: Resistance to diseases and (pests)

(Note: One further important category "abiotic stress" should also be mentioned but is omitted here for reasons of clarity).

Table 2: Gradual improvement of the properties of all categories over several generations of crossbreeding

Genotypes	symbolised	Quality	Agronomic properties	Resistance	for use as
the perfect apple		top	top	top	breeding goal
common commercial varieties		top	top	potential for improvement	donors for quality and agronomic properties
highly tolerant old genotypes		large deficiency	large deficiency	high	donors for resistances
genotypes from strict selection for quality and agronomic traits		highly improved	highly improved	potential for improvement	advanced breeding material for next crosses
genotypes from strict selection for resistance		improved	improved	high, possibly better anchored	advanced breeding material for next crosses

Outlook

Poma Culta has around two dozen F2 and F3 genotypes from the crossing procedure described above. These show excellent characteristics but also deficiencies in all three categories and are used for further crosses. It is to be expected that after one or two further generations, candidate varieties will emerge from this material.

Collaboration with other breeding initiatives for the mutual utilisation of a common gene pool could further increase the chances of success. In addition, closer collaboration with genetics experts would be helpful in optimising the crossing partners.

References

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