Polygenic traits (QTLs)

History

- Johansen (1909) explained continuous variation in quantitative traits by the segregation of numerous genes modified by the environment.
- Biometric studies were used to study the overall effect of these numerous genes (% of explained variance, number of factors, etc.)
- In 1923, Sax demonstrated for the first time linkage between a qualitative marker (seed color) and a quantitative locus (size of the seed).
- Today the genome can be screened for QTLs using molecular maps.

Strategies to detect QTLs

The basic principle is to divide the population in the genotypic classes based on the marker (e.g. AA AB and BB) and then determine if there is correlation between the marker and the trait effect (ANOVA or Correlation)

Example

Plant	1	2	3	4	5	6	7	8	9	10
Genotype	A	H	H	H	B	B	A	H	H	A
Coding	2	1	1	1	0	0	2	1	1	2
Height	50	45	47	43	40	43	52	46	44	53

Correlation Genotype vs. Height ***R*=0.92**

Point analysis

- Based on one marker at a time and therefore, does not require a complete map
- Crossovers between the QTL and the closest marker decrease the probability to detect a significant effect

Interval analysis (Mapmaker QTL, Lander and Botstein 1989)

- Simultaneous use of linked markers to determine their effect and the effect of possible recombinant genotypes within the interval
- Increases the possibility to detect a QTL
- Provides an unbiased estimation of the effect of the QTL over the trait

For markers located at less than 10 cM there is not much difference between the Point analysis and the interval analysis. However, the interval analysis is significantly better for larger intervals.

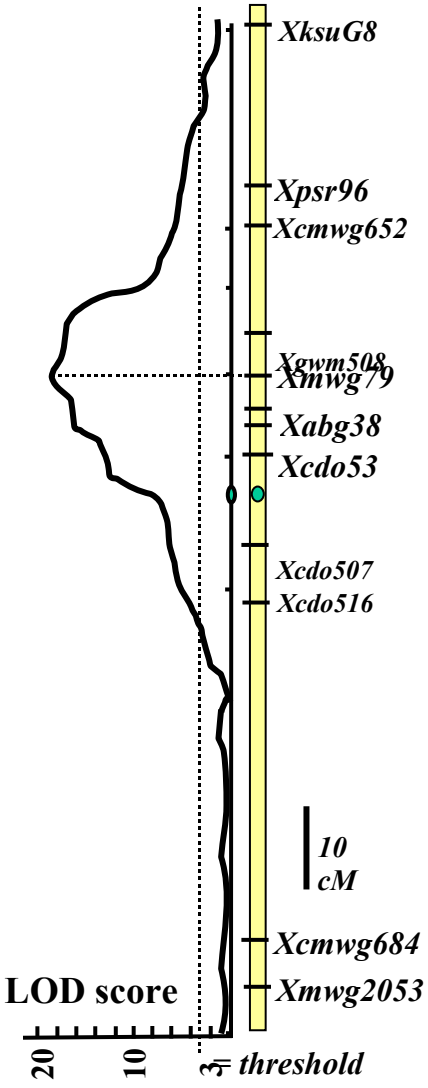
Polygenic traits (QTLs) (2)

Mapping of extreme genotypes

- In this strategy only the extreme individuals of the population are mapped
- If only those individuals, which values higher than **one** SD of the mean are used: 33% of the population and 81 % of the linkage information
- If only those individuals, which values higher than **two** SD of the mean are used: 5% of the population and 28 % of the linkage information

Disadvantages

- Can not use lineal regression because it will overestimate the phenotypic effects
- Only one character can be analyzed
- Is less efficient to determine the effect of each QTL



LOD scores for QTLs

To test the hypothesis of the presence of a QTL the following LOD score is calculated:

Pb. of the observed data from a linked QTL

Log (10) ----------
Pb. of the observed data from a random sample

A LOD score is calculated every 2 cM along the complete chromosome and represented in a graphical way (left Fig.)

LOD Threshold

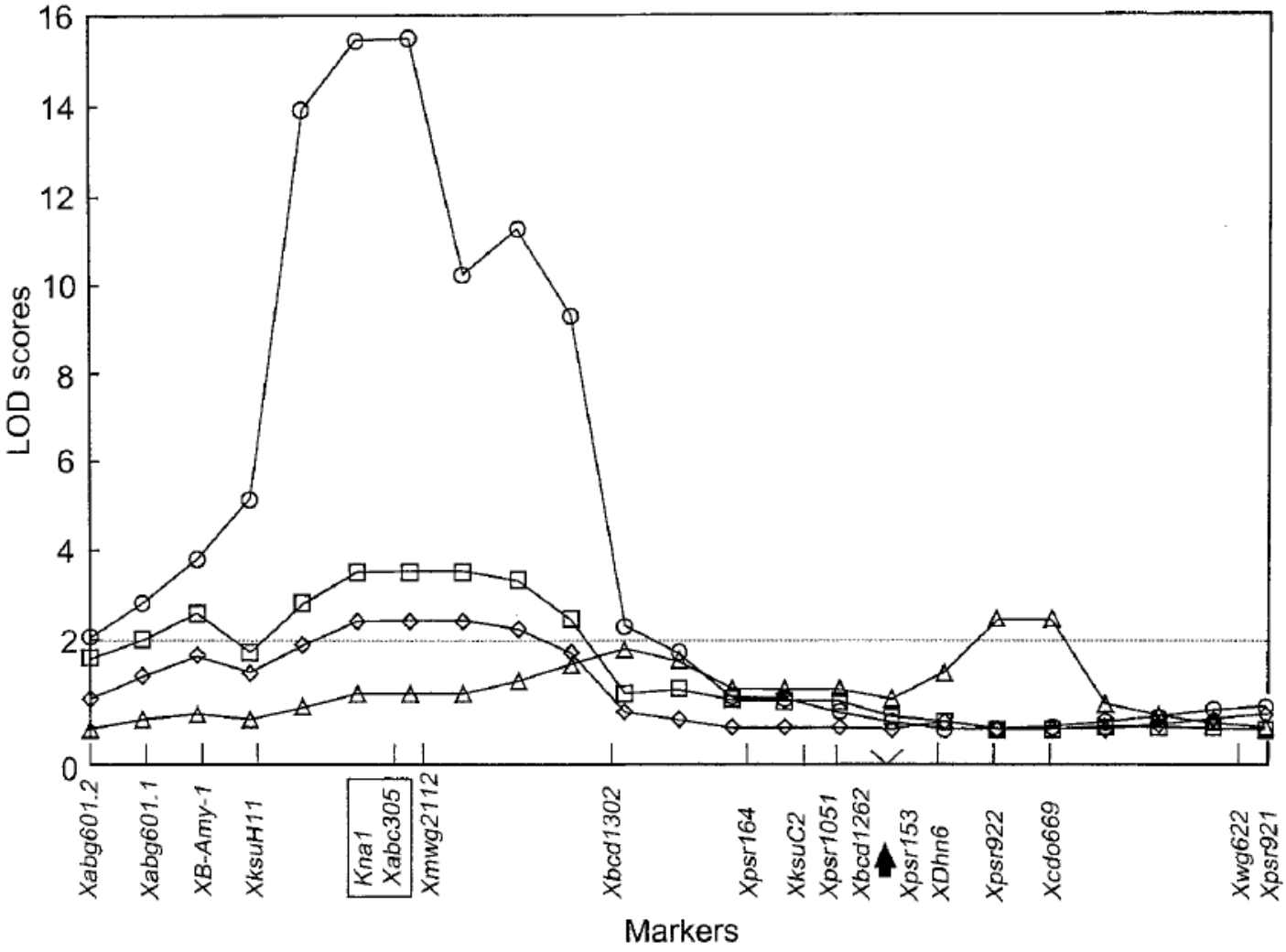
The threshold depends of the length and density of the map. The longer the map, the higher is the probability to find an artificial QTL just by chance, therefore a higher LOD score is required to keep the 5% confidence along the complete map.

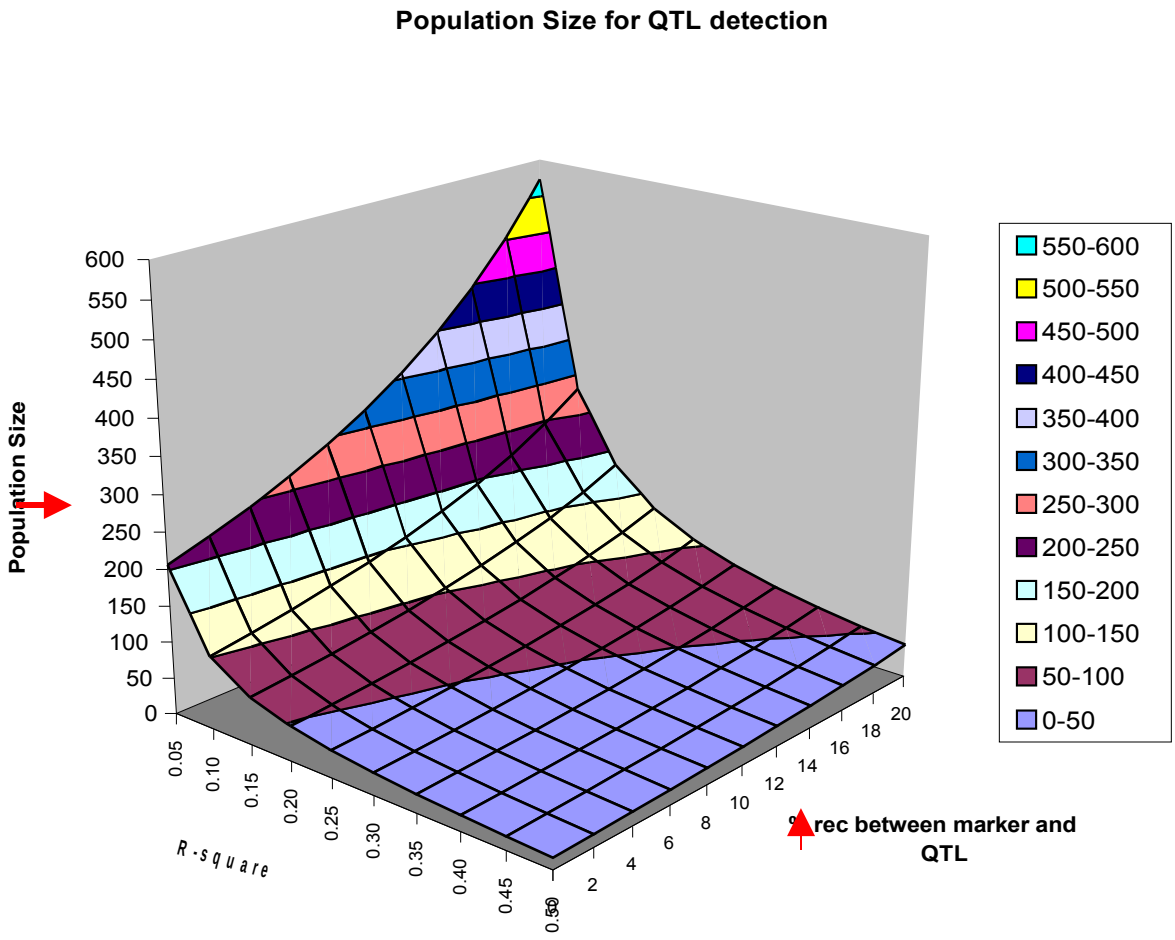
- For one interval, 5% confidence = LOD 0.83
- For one chromosome 5% confidence ≈LOD 2.0

For complete map 5% confidence

Kna/Na QTL in the field and in tanks

Reducing experimental error increases the precision of your QTL!





Relationship between linkage map marker density, r-square for a QTL and population size (Lynch and Walsh 1998 *Genetics and Analysis for Quantitative Traits* Sinauer Assoc., Sunderland, MA).

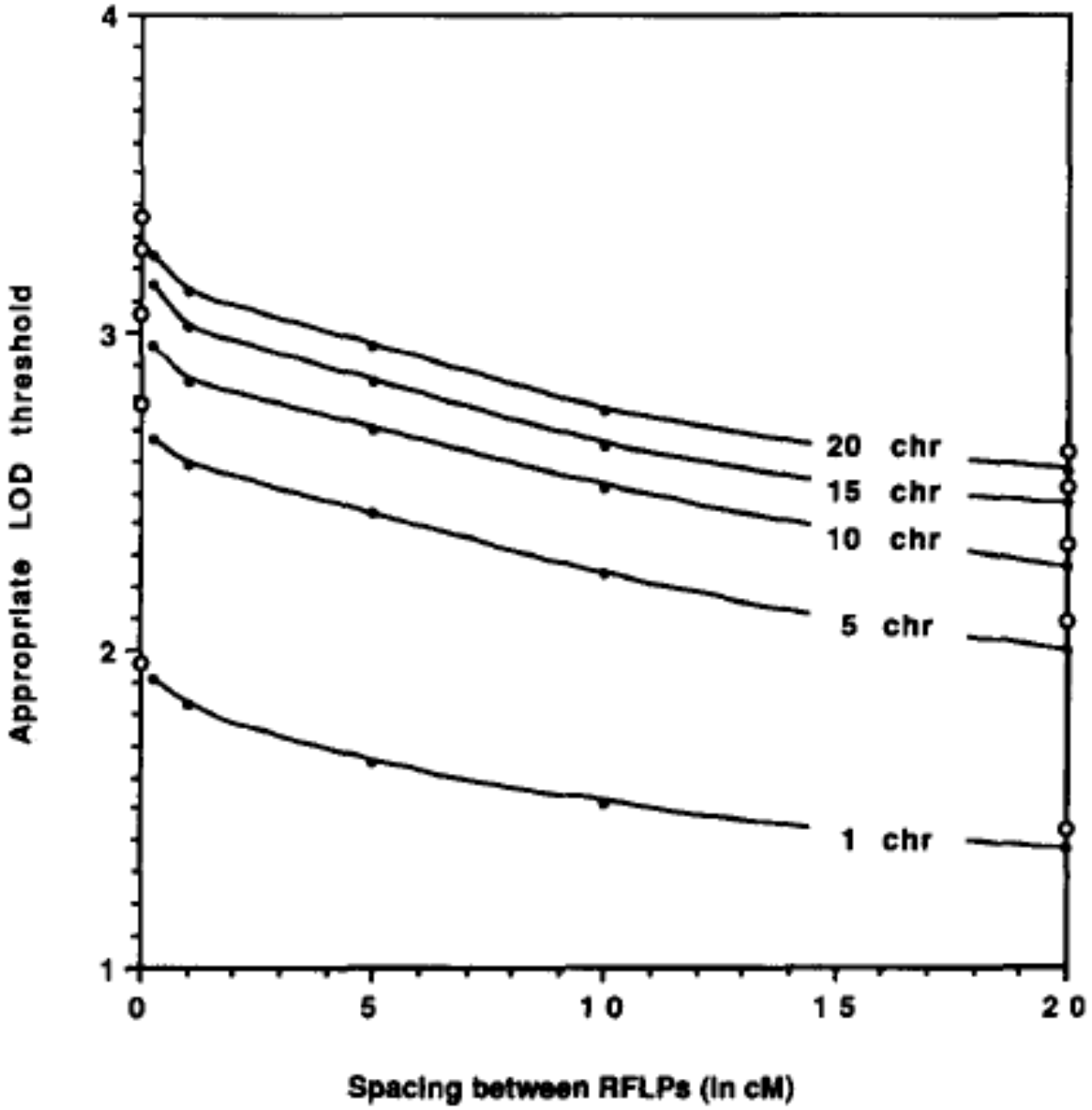


FIGURE 4.—LOD thresholds. Appropriate LOD threshold so that the chance of a false positive occurring *anywhere* in the genome is at most 5%, as a function of genome size and density of RFLPs

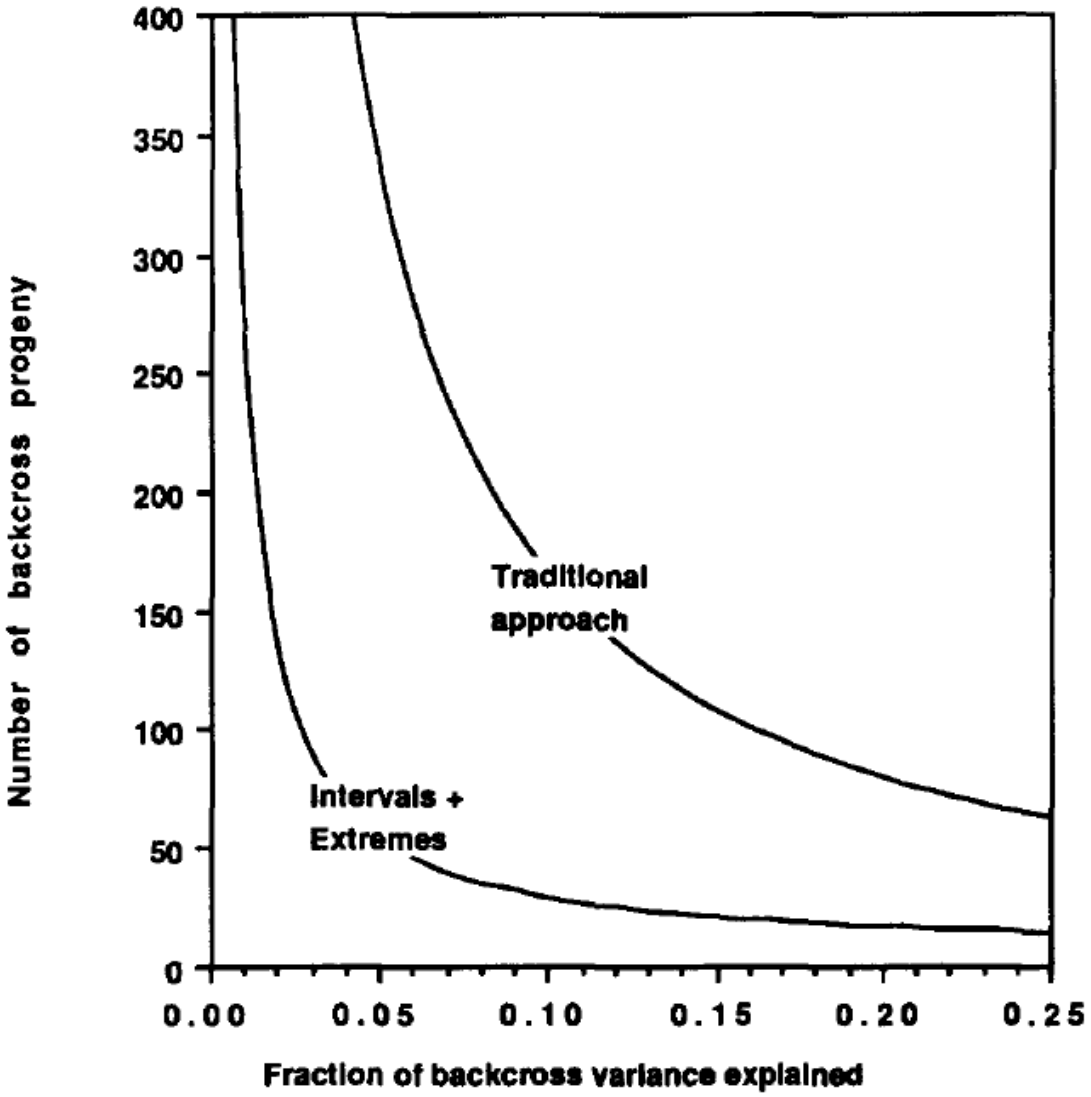


FIGURE 6.—Required progeny size. The number of backcross progeny that must be genotyped to map a QTL, based on the fraction of the backcross variance explained by the segregation of the QTL. The upper curve shows the traditional approach in which all progeny are genotyped and single markers analyzed. In the lower curve, only progeny with 5% most extreme phenotypes are genotyped and interval mapping is used to analyze the data. The calculations are based on use of a complete 20 cM RFLP map, a 50% chance of detection for QTLs in the middle of intervals, and a LOD threshold of 2.5. Note that for a QTL with phenotypic effect δ, the fraction of the backcross variance explained is $\delta^2/16$