

Approaches in QTL mapping of Fusarium head blight resistance in wheat

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Introduction

Why map QTL ?

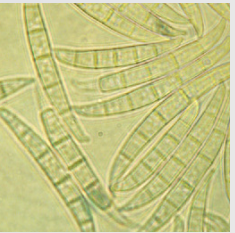
Determine locations and effects of 'genes' that contribute to a quantitative trait

Find out which genotypes possess the same/different R-QTL

Find out about association (correlation, linkage, pleiotropy) with other traits (e.g. earliness, height, quality, yield, ...)

Develop tools for marker assisted selection, in the ideal case 'perfect markers'

Prerequisite for map based gene isolation and functional gene analysis



Principal of classical (QTL) mapping

Parent 1 x Parent 2

Contrasting phenotypes
Near homozygous

Principal of classical (QTL) mapping

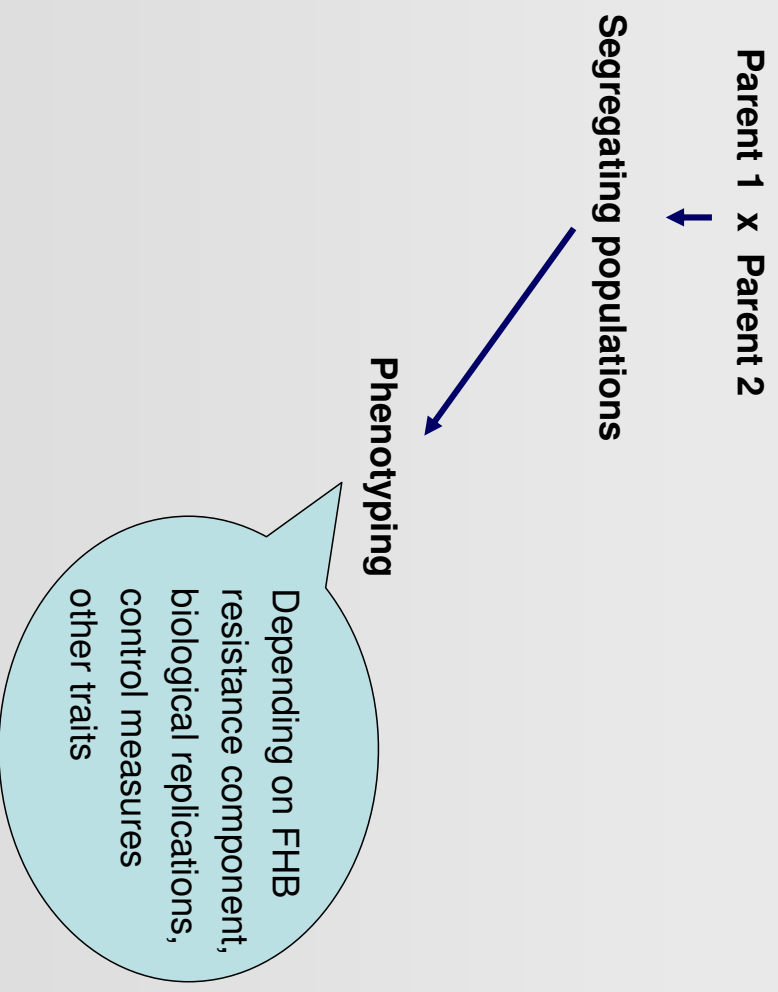
Parent 1 x Parent 2



Segregating populations

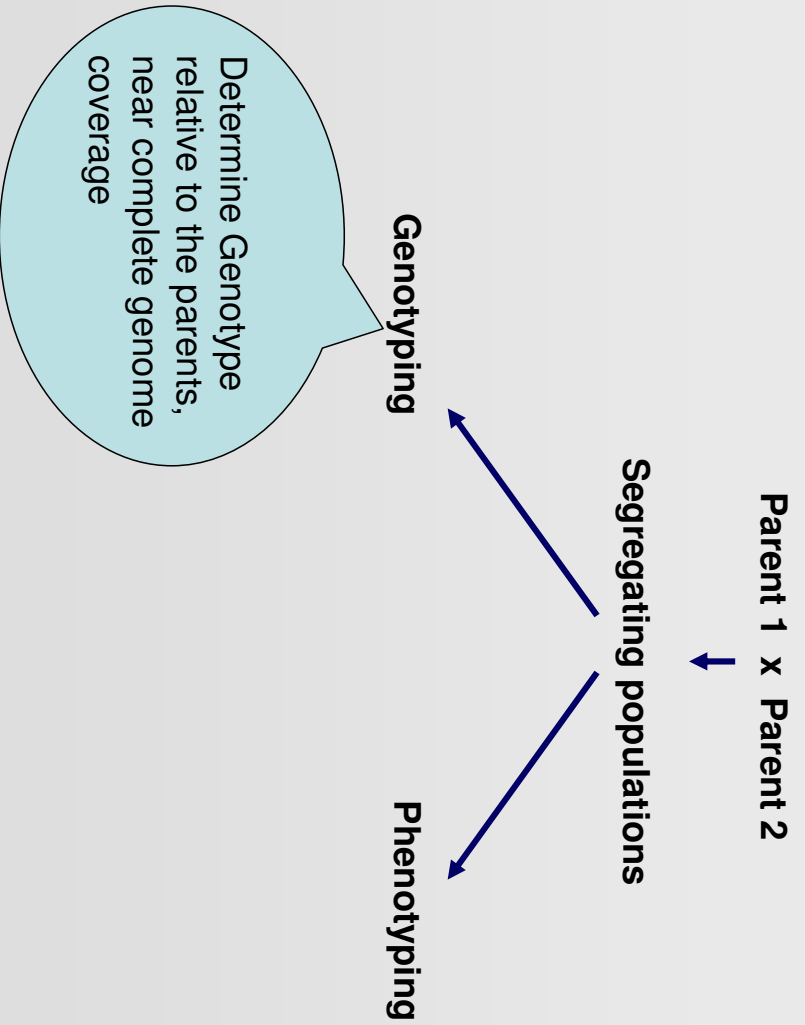
Many lines (> 150),
random sample,
stable (immortal)
(RILs, DHS)

Principal of classical (QTL) mapping



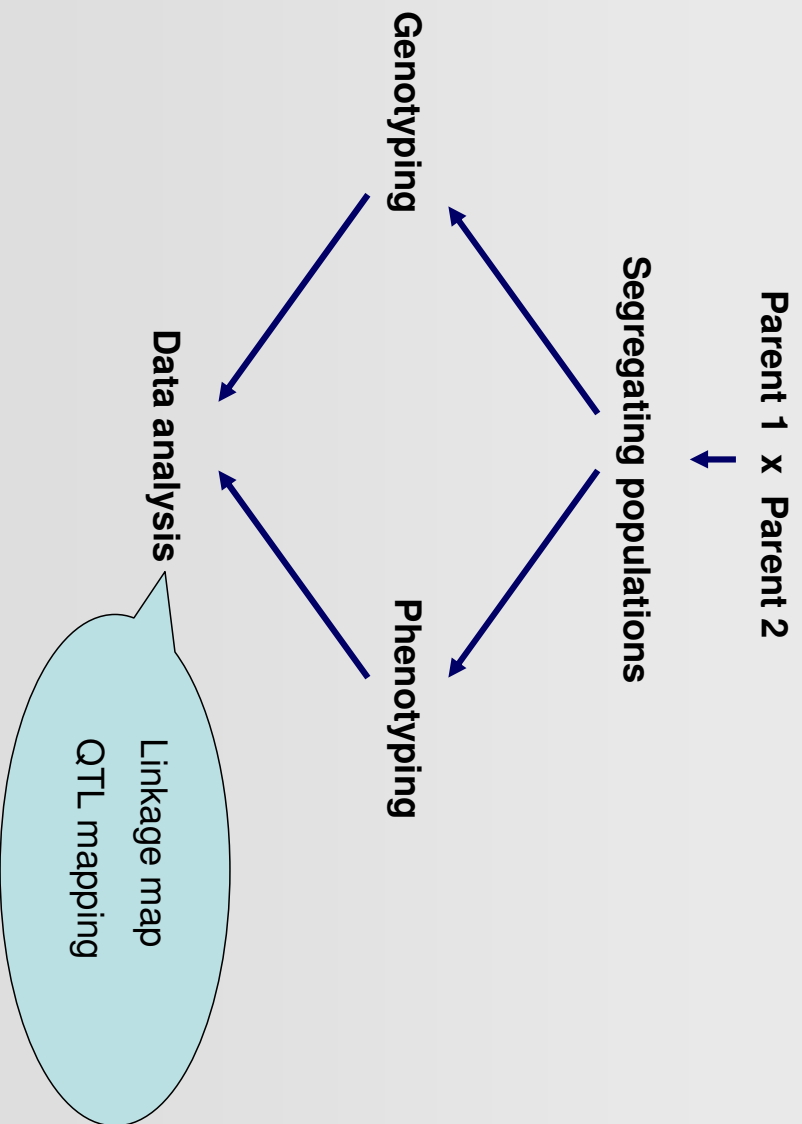
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Principal of classical (QTL) mapping

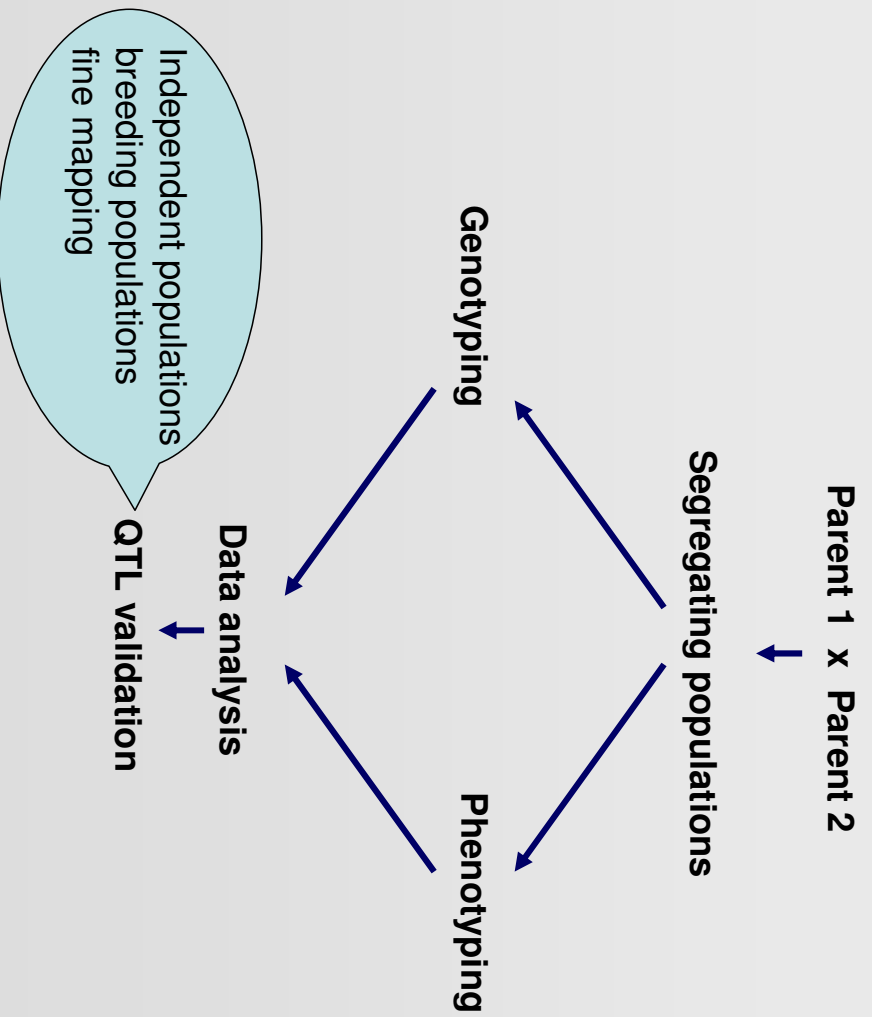


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Principal of classical (QTL) mapping



Principal of classical (QTL) mapping



Principal of association mapping

