EXPLANATION OF FIELD HEADINGS, ABBREVIATIONS, VARIABLE NAMES.

FIELD HEADING	EXPLANATION
RACE	From natural or planted population
PRRABR	Abbreviation for provenance region
PROVREG	Provenance region
PROVNO	Provenance number
TRIALREG	Trial region
TRIAL	Trial number
PLTYR	Planting year of trial
AGE	Age at time of assessment
NAME	Name of character *) see below
OVALLM	Trial average
LSMEAN	Average for provenance
OVSTD	Standar error for trial mean
STDERR	Standard error for provenance mean
ERMS	Error mean-square
PRMS	Provenance mean square
PRKOEF	Average number of replicates
PRVCOM	Provenance variance component
HERIT	Average provenance heritability
HERIT01	Average provenance heritability between 0 and +1
ESTDEV	Difference between LSMEAN and OVALMEAN in original units
GENEST	Difference between LSMEAN and OVALMEAN reduced by heritability
GAI	Intermediate values for calculation of genetic deviation
GAIAVG	Intermediate values for calculation of genetic deviation
GENDEV	Genetic deviation, ie. the genetic estimate in percent of trial average

NOTE: *In all the following graphs and tables results are presented as %-deviation from trial mean ! - In the summary table in the article results are presented partly as %-deviation, partly as deviation in the original unit of measurement.*

*) See the document "ASSESSMENT" for definition of characters.

BREAKS	The squre root of the number of large branches or forks (multiplied by -1 to denote the large numbers of branches or breaks is a negative property). The genetic deviation is in principle back-tranformed, i.e. big values are negative properties and vice versa
SURVN	The proportion of live trees
HEALTH3	The proportion of trees in good health
DIAMBAW	The basal-area-weighted plot mean diameter
STEMAREA	The total cross-sectional area at breast-height (square-cm) per plot (the variation is similar to variation for basal area per hectare)
PERG	The average of all persistence classes
FORMG	The average of all form classes
PILO	The average of pilodyn-readings

Simple means are available for trials **GP041 & GP042** , but their designs do no permit calculation of genetic estimates.

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