

## Data importation

### 1. Endpoint dataframe

#### A. Exploration of data

Exploration tables using the rstatix, janitor and skimr packages

Data visualization

#### B. Normality hypothesis and outlier detection

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Number of data observations per day for the traits of the timeseries datasets

#### A. Exploration of the timeseries dataframe

#### B. Exploration of the S\_timeseries dataframe

#### C. Exploration of the T\_timeseries dataframe

# M3P Data Analysis

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Set the right working directory.

```
setwd("C:/Users/elise/Documents/Mémoire/Main/Data/Templates/M3P")
```

## Data importation

Import the data sets extracted from the Data Preparation R Markdown.

```
list.files()
```

```
## [1] "endpoint.txt"
## [2] "plant_info.txt"
## [3] "S_timeseries.txt"
## [4] "T_timeseries.txt"
## [5] "timeseries.txt"
## [6] "timeseries_Leaf_number.txt"
## [7] "timeseries_Ligulated_leaf_number.txt"
## [8] "timeseries_Plant_emergence.txt"
## [9] "timeseries_Plant_transpiration.txt"
## [10] "timeseries_Soil_water_potential.txt"
## [11] "timeseries_Water.txt"
```

```
plant_info <- read.table("plant_info.txt", header = TRUE, sep = "\t")
endpoint <- read.table("endpoint.txt", header = TRUE, sep = "\t")
timeseries <- read.table("timeseries.txt", header = TRUE, sep = "\t")
timeseries_Plant_emergence <- read.table("timeseries_Plant_emergence.txt", header = TRUE, sep = "\t")
timeseries_Plant_transpiration <- read.table("timeseries_Plant_transpiration.txt", header = TRUE, sep = "\t")
timeseries_Soil_water_potential <- read.table("timeseries_Soil_water_potential.txt", header = TRUE, sep = "\t")
timeseries_Ligulated_leaf_number <- read.table("timeseries_Ligulated_leaf_number.txt", header = TRUE, sep = "\t")
timeseries_Water <- read.table("timeseries_Water.txt", header = TRUE, sep = "\t")
timeseries_Leaf_number <- read.table("timeseries_Leaf_number.txt", header = TRUE, sep = "\t")
S_timeseries <- read.table("S_timeseries.txt", header = TRUE, sep = "\t")
```

Convert the columns to factor and date formats.

```
# plant_info
plant_info <- lapply(plant_info, factor)

# endpoint
matching_cols <- intersect(names(endpoint), names(plant_info))
endpoint[, matching_cols] <- lapply(endpoint[, matching_cols], factor)
endpoint$Date <- date(endpoint$Date)
endpoint$Timestamp <- NA

# timeseries_Plant_transpiration
matching_cols <- intersect(names(timeseries_Plant_transpiration), names(plant_info))
timeseries_Plant_transpiration[, matching_cols] <- lapply(timeseries_Plant_transpiration[, matching_cols], factor)
timeseries_Plant_transpiration$Timestamp <- as.POSIXct(timeseries_Plant_transpiration$Timestamp, format = "%Y-%m-%d %H:%M:%S")
timeseries_Plant_transpiration$Date <- date(timeseries_Plant_transpiration$Date)

# timeseries_Leaf_number
matching_cols <- intersect(names(timeseries_Leaf_number), names(plant_info))
timeseries_Leaf_number[, matching_cols] <- lapply(timeseries_Leaf_number[, matching_cols], factor)
timeseries_Leaf_number$Timestamp <- as.POSIXct(timeseries_Leaf_number$Timestamp, format = "%Y-%m-%d %H:%M:%S")
timeseries_Leaf_number$Date <- date(timeseries_Leaf_number$Date)

# timeseries_Soil_water_potential
matching_cols <- intersect(names(timeseries_Soil_water_potential), names(plant_info))
timeseries_Soil_water_potential[, matching_cols] <- lapply(timeseries_Soil_water_potential[, matching_cols], factor)
timeseries_Soil_water_potential$Timestamp <- as.POSIXct(timeseries_Soil_water_potential$Timestamp, format = "%Y-%m-%d %H:%M:%S")
timeseries_Soil_water_potential$Date <- date(timeseries_Soil_water_potential$Date)

# timeseries_Ligulated_Leaf_number
matching_cols <- intersect(names(timeseries_Ligulated_Leaf_number), names(plant_info))
timeseries_Ligulated_Leaf_number[, matching_cols] <- lapply(timeseries_Ligulated_Leaf_number[, matching_cols], factor)
timeseries_Ligulated_Leaf_number$Timestamp <- as.POSIXct(timeseries_Ligulated_Leaf_number$Timestamp, format = "%Y-%m-%d %H:%M:%S")
timeseries_Ligulated_Leaf_number$Date <- date(timeseries_Ligulated_Leaf_number$Date)

# timeseries_Water
matching_cols <- intersect(names(timeseries_Water), names(plant_info))
timeseries_Water[, matching_cols] <- lapply(timeseries_Water[, matching_cols], factor)
timeseries_Water$Timestamp <- as.POSIXct(timeseries_Water$Timestamp, format = "%Y-%m-%d %H:%M:%S")
timeseries_Water$Date <- date(timeseries_Water$Date)

# timeseries_Plant_emergence
matching_cols <- intersect(names(timeseries_Plant_emergence), names(plant_info))
timeseries_Plant_emergence[, matching_cols] <- lapply(timeseries_Plant_emergence[, matching_cols], factor)
timeseries_Plant_emergence$Timestamp <- as.POSIXct(timeseries_Plant_emergence$Timestamp, format = "%Y-%m-%d %H:%M:%S")
timeseries_Plant_emergence$Date <- date(timeseries_Plant_emergence$Date)
```

```
# timeseries
matching_cols <- intersect(names(timeseries), names(plant_info))
timeseries[, matching_cols] <- lapply(timeseries[, matching_cols], factor)
timeseries$Timestamp <- as.POSIXct(timeseries$Timestamp, format = "%Y-%m-%d %H:%M:%S")
timeseries$Date <- date(timeseries$Date)

# S_timeseries
matching_cols <- intersect(names(S_timeseries), names(plant_info))
S_timeseries[, matching_cols] <- lapply(S_timeseries[, matching_cols], factor)
S_timeseries$Timestamp <- as.POSIXct(S_timeseries$Timestamp, format = "%Y-%m-%d %H:%M:%S")
S_timeseries$Date <- date(S_timeseries$Date)

# T_timeseries
# No data
```

Collect the variables of every data template and print the names of the variables. This serves as a double check.

```
platform <- "M3P"

# endpoint
df <- endpoint[, colSums(is.na(endpoint)) < nrow(endpoint)]
genotype_index <- which(colnames(df) == "Genotype")
variables <- "DW_plant_g"

# timeseries
variables_t <- c("Plant_biomass_g", "Leaf_number", "Ligulated_leaf_number", "Plant_emergence", "Plant_transpiration", "Soil_water_potential", "Water")

# S_timeseries
df_S_timeseries <- S_timeseries[, colSums(is.na(S_timeseries)) < nrow(S_timeseries)]
genotype_index <- which(colnames(df_S_timeseries) == "Genotype")
variables_S <- colnames(df_S_timeseries[, c(5:(genotype_index - 1))]) # We remove the three first columns that are "Unit.ID", "Time" and "Date"

# T_timeseries
# No data for M3P

print(paste(platform, ": The variables for endpoint are", paste(variables, collapse = ", "), sep = " "))
```

```
## [1] "M3P : The variables for endpoint are DW_plant_g"
```

```
print(paste(platform, ": The variables for timeseries are", paste(variables_t, collapse = ", "), sep = " "))
```

```
## [1] "M3P : The variables for timeseries are Plant_biomass_g, Leaf_number, Ligulated_leaf_number, Plant_emergence, Plant_transpiration, Soil_water_potential, Water"
```

```
print(paste(platform, ": The variables for S_timeseries are", paste(variables_S, collapse = ", "), sep = " "))
```

```
## [1] "M3P : The variables for S_timeseries are S_Height_cm, S_Leaf_area_cmsquared"
```

Add a column `Plant_type` with three levels, H L and T. This variable is useful to test for heterosis effects.

```
endpoint$Plant_type <- substr(endpoint$Genotype, nchar(as.character(endpoint$Genotype)), nchar(as.character(endpoint$Genotype)))
timeseries$Plant_type <- substr(timeseries$Genotype, nchar(as.character(timeseries$Genotype)), nchar(as.character(timeseries$Genotype)))

timeseries_Plant_transpiration$Plant_type <- substr(timeseries_Plant_transpiration$Genotype, nchar(as.character(timeseries_Plant_transpiration$Genotype)), nchar(as.character(timeseries_Plant_transpiration$Genotype)))
timeseries_Water$Plant_type <- substr(timeseries_Water$Genotype, nchar(as.character(timeseries_Water$Genotype)), nchar(as.character(timeseries_Water$Genotype)))
timeseries_Soil_water_potential$Plant_type <- substr(timeseries_Soil_water_potential$Genotype, nchar(as.character(timeseries_Soil_water_potential$Genotype)), nchar(as.character(timeseries_Soil_water_potential$Genotype)))
timeseries_Plant_emergence$Plant_type <- substr(timeseries_Plant_emergence$Genotype, nchar(as.character(timeseries_Plant_emergence$Genotype)), nchar(as.character(timeseries_Plant_emergence$Genotype)))
timeseries_Ligulated_leaf_number$Plant_type <- substr(timeseries_Ligulated_leaf_number$Genotype, nchar(as.character(timeseries_Ligulated_leaf_number$Genotype)), nchar(as.character(timeseries_Ligulated_leaf_number$Genotype)))
timeseries_Leaf_number$Plant_type <- substr(timeseries_Leaf_number$Genotype, nchar(as.character(timeseries_Leaf_number$Genotype)), nchar(as.character(timeseries_Leaf_number$Genotype)))

S_timeseries$Plant_type <- substr(S_timeseries$Genotype, nchar(as.character(S_timeseries$Genotype)), nchar(as.character(S_timeseries$Genotype)))
```

# 1. Endpoint dataframe

## A. Exploration of data

Exploration tables using the `rstatix`, `janitor` and `skimr` packages

```
endpoint %>%
  count(Genotype)
```

```
##      Genotype  n
## 1    EPPN1_H 14
## 2    EPPN1_L 15
## 3   EPPN10_H 14
## 4   EPPN10_L 15
## 5   EPPN11_H 14
## 6   EPPN11_L 15
## 7   EPPN12_H 14
## 8   EPPN12_L 14
## 9   EPPN13_H 14
## 10  EPPN13_L 13
## 11  EPPN14_H 14
## 12  EPPN14_L 15
## 13  EPPN15_H 13
## 14   EPPN2_H 14
## 15   EPPN2_L 15
## 16 EPPN20_T 15
## 17   EPPN3_H 14
## 18   EPPN3_L 15
## 19   EPPN4_H 14
## 20   EPPN4_L 14
## 21   EPPN5_H 14
## 22   EPPN5_L 15
## 23   EPPN6_H 14
## 24   EPPN6_L 15
## 25   EPPN7_H 14
## 26   EPPN7_L 15
## 27   EPPN8_H 14
## 28   EPPN8_L 15
## 29   EPPN9_H 14
## 30   EPPN9_L 15
```

```
endpoint %>%
  tabyl(Genotype, Column) %>%
  adorn_totals("row") %>%
  adorn_percentages("row") %>%
  adorn_pct_formatting() %>%
  adorn_ns() %>%
  adorn_title("combined")
```

##	Genotype/Column	1	2	3	4	5	6	
##	EPPN1_H	0.0% (0)	7.1% (1)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	
##	EPPN1_L	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	6.7% (1)	6.7% (1)	
##	EPPN10_H	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	7.1% (1)	
##	EPPN10_L	0.0% (0)	6.7% (1)	0.0% (0)	6.7% (1)	0.0% (0)	0.0% (0)	
##	EPPN11_H	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	
##	EPPN11_L	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	
##	EPPN12_H	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	7.1% (1)	7.1% (1)	
##	EPPN12_L	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	7.1% (1)	0.0% (0)	
##	EPPN13_H	7.1% (1)	7.1% (1)	0.0% (0)	0.0% (0)	7.1% (1)	7.1% (1)	
##	EPPN13_L	0.0% (0)	7.7% (1)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	
##	EPPN14_H	0.0% (0)	7.1% (1)	7.1% (1)	7.1% (1)	7.1% (1)	0.0% (0)	
##	EPPN14_L	0.0% (0)	6.7% (1)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	
##	EPPN15_H	7.7% (1)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	
##	EPPN2_H	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	
##	EPPN2_L	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	6.7% (1)	6.7% (1)	
##	EPPN20_T	0.0% (0)	0.0% (0)	6.7% (1)	0.0% (0)	0.0% (0)	0.0% (0)	
##	EPPN3_H	0.0% (0)	0.0% (0)	0.0% (0)	7.1% (1)	0.0% (0)	0.0% (0)	
##	EPPN3_L	6.7% (1)	0.0% (0)	6.7% (1)	6.7% (1)	0.0% (0)	0.0% (0)	
##	EPPN4_H	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	
##	EPPN4_L	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	
##	EPPN5_H	0.0% (0)	0.0% (0)	7.1% (1)	7.1% (1)	0.0% (0)	0.0% (0)	
##	EPPN5_L	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	6.7% (1)	
##	EPPN6_H	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	7.1% (1)	0.0% (0)	
##	EPPN6_L	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	
##	EPPN7_H	0.0% (0)	0.0% (0)	7.1% (1)	7.1% (1)	0.0% (0)	0.0% (0)	
##	EPPN7_L	6.7% (1)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	
##	EPPN8_H	14.3% (2)	7.1% (1)	7.1% (1)	0.0% (0)	0.0% (0)	0.0% (0)	
##	EPPN8_L	0.0% (0)	0.0% (0)	6.7% (1)	6.7% (1)	0.0% (0)	0.0% (0)	
##	EPPN9_H	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	7.1% (1)	
##	EPPN9_L	6.7% (1)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	
##	Total	1.6% (7)	1.6% (7)	1.6% (7)	1.6% (7)	1.6% (7)	1.6% (7)	
##	7	8	9	10	11	12	13	14
##	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	7.1% (1)	7.1% (1)	7.1% (1)	0.0% (0)
##	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	6.7% (1)
##	7.1% (1)	7.1% (1)	0.0% (0)	0.0% (0)	0.0% (0)	7.1% (1)	0.0% (0)	0.0% (0)
##	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	6.7% (1)	0.0% (0)	0.0% (0)	0.0% (0)
##	0.0% (0)	0.0% (0)	7.1% (1)	7.1% (1)	0.0% (0)	0.0% (0)	0.0% (0)	7.1% (1)
##	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	13.3% (2)	6.7% (1)	0.0% (0)
##	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	7.1% (1)
##	7.1% (1)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)
##	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)
##	0.0% (0)	0.0% (0)	0.0% (0)	7.7% (1)	7.7% (1)	0.0% (0)	0.0% (0)	0.0% (0)
##	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)
##	0.0% (0)	6.7% (1)	0.0% (0)	6.7% (1)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)
##	7.7% (1)	7.7% (1)	7.7% (1)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)
##	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	7.1% (1)	7.1% (1)	7.1% (1)	0.0% (0)
##	6.7% (1)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)
##	0.0% (0)	0.0% (0)	6.7% (1)	6.7% (1)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)
##	0.0% (0)	0.0% (0)	0.0% (0)	7.1% (1)	0.0% (0)	0.0% (0)	7.1% (1)	7.1% (1)
##	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)
##	7.1% (1)	7.1% (1)	7.1% (1)	0.0% (0)	7.1% (1)	0.0% (0)	0.0% (0)	0.0% (0)
##	0.0% (0)	14.3% (2)	7.1% (1)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)
##	0.0% (0)	0.0% (0)	0.0% (0)	7.1% (1)	0.0% (0)	0.0% (0)	0.0% (0)	7.1% (1)
##	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	6.7% (1)	6.7% (1)

##	0.0% (0)	0.0% (0)	7.1% (1)	7.1% (1)	7.1% (1)	0.0% (0)	0.0% (0)	0.0% (0)
##	0.0% (0)	0.0% (0)	6.7% (1)	0.0% (0)	6.7% (1)	6.7% (1)	0.0% (0)	0.0% (0)
##	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	7.1% (1)	7.1% (1)	0.0% (0)
##	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	6.7% (1)	6.7% (1)
##	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)
##	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)
##	7.1% (1)	7.1% (1)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)
##	6.7% (1)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)
##	1.6% (7)	1.6% (7)	1.6% (7)	1.6% (7)	1.6% (7)	1.6% (7)	1.6% (7)	1.6% (7)
##	15	16	17	18	19	20	21	22
##	0.0% (0)	0.0% (0)	0.0% (0)	7.1% (1)	7.1% (1)	7.1% (1)	0.0% (0)	0.0% (0)
##	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	6.7% (1)	0.0% (0)	6.7% (1)	0.0% (0)
##	0.0% (0)	7.1% (1)	14.3% (2)	7.1% (1)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)
##	0.0% (0)	6.7% (1)	6.7% (1)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)
##	7.1% (1)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	7.1% (1)	7.1% (1)	0.0% (0)
##	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	6.7% (1)
##	7.1% (1)	7.1% (1)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)
##	7.1% (1)	7.1% (1)	7.1% (1)	7.1% (1)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)
##	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	7.1% (1)	0.0% (0)	0.0% (0)	0.0% (0)
##	0.0% (0)	0.0% (0)	0.0% (0)	7.7% (1)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)
##	0.0% (0)	7.1% (1)	7.1% (1)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)
##	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	6.7% (1)	0.0% (0)	0.0% (0)	6.7% (1)
##	0.0% (0)	0.0% (0)	0.0% (0)	7.7% (1)	7.7% (1)	0.0% (0)	0.0% (0)	0.0% (0)
##	7.1% (1)	7.1% (1)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	7.1% (1)
##	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)
##	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	6.7% (1)	6.7% (1)	0.0% (0)	0.0% (0)
##	0.0% (0)	0.0% (0)	0.0% (0)	7.1% (1)	0.0% (0)	0.0% (0)	7.1% (1)	7.1% (1)
##	0.0% (0)	0.0% (0)	6.7% (1)	6.7% (1)	0.0% (0)	6.7% (1)	6.7% (1)	0.0% (0)
##	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	7.1% (1)	7.1% (1)
##	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)
##	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)
##	0.0% (0)	0.0% (0)	0.0% (0)	6.7% (1)	6.7% (1)	0.0% (0)	0.0% (0)	6.7% (1)
##	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)
##	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	6.7% (1)	6.7% (1)	0.0% (0)	0.0% (0)
##	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	7.1% (1)	7.1% (1)	0.0% (0)	0.0% (0)
##	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	6.7% (1)
##	0.0% (0)	0.0% (0)	7.1% (1)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)
##	6.7% (1)	6.7% (1)	0.0% (0)	0.0% (0)	0.0% (0)	6.7% (1)	0.0% (0)	0.0% (0)
##	7.1% (1)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	7.1% (1)	7.1% (1)	7.1% (1)
##	6.7% (1)	6.7% (1)	6.7% (1)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)
##	1.6% (7)	1.9% (8)	1.9% (8)	1.9% (8)	1.9% (8)	1.9% (8)	1.6% (7)	1.9% (8)
##	23	24	25	26	27	28	29	30
##	0.0% (0)	0.0% (0)	7.1% (1)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)
##	6.7% (1)	6.7% (1)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)
##	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)
##	0.0% (0)	0.0% (0)	0.0% (0)	6.7% (1)	6.7% (1)	0.0% (0)	0.0% (0)	0.0% (0)
##	0.0% (0)	0.0% (0)	7.1% (1)	7.1% (1)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)
##	6.7% (1)	0.0% (0)	0.0% (0)	6.7% (1)	0.0% (0)	0.0% (0)	0.0% (0)	6.7% (1)
##	0.0% (0)	0.0% (0)	0.0% (0)	7.1% (1)	7.1% (1)	0.0% (0)	0.0% (0)	7.1% (1)
##	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)
##	7.1% (1)	7.1% (1)	7.1% (1)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)
##	0.0% (0)	7.7% (1)	7.7% (1)	0.0% (0)	0.0% (0)	0.0% (0)	7.7% (1)	0.0% (0)
##	0.0% (0)	7.1% (1)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	7.1% (1)	0.0% (0)
##	0.0% (0)	6.7% (1)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	6.7% (1)
##	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	7.7% (1)	0.0% (0)	0.0% (0)	0.0% (0)
##	7.1% (1)	7.1% (1)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)	0.0% (0)



##	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	6.7%	(1)	13.3%	(2)	6.7%	(1)	0.0%	(0)
##	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	13.3%	(2)
##	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	7.1%	(1)
##	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)
##	7.1%	(1)	7.1%	(1)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)
##	0.0%	(0)	0.0%	(0)	14.3%	(2)	7.1%	(1)	7.1%	(1)	0.0%	(0)	0.0%	(0)	0.0%	(0)
##	0.0%	(0)	0.0%	(0)	7.1%	(1)	7.1%	(1)	7.1%	(1)	7.1%	(1)	0.0%	(0)	0.0%	(0)
##	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	6.7%	(1)	0.0%	(0)	0.0%	(0)
##	7.1%	(1)	0.0%	(0)	0.0%	(0)	0.0%	(0)	7.1%	(1)	7.1%	(1)	0.0%	(0)	7.1%	(1)
##	6.7%	(1)	0.0%	(0)	0.0%	(0)	6.7%	(1)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)
##	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	7.1%	(1)	7.1%	(1)	0.0%	(0)
##	0.0%	(0)	6.7%	(1)	6.7%	(1)	0.0%	(0)	6.7%	(1)	0.0%	(0)	0.0%	(0)	0.0%	(0)
##	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	7.1%	(1)	7.1%	(1)	7.1%	(1)
##	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	6.7%	(1)	6.7%	(1)	0.0%	(0)
##	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	7.1%	(1)	0.0%	(0)
##	6.7%	(1)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	6.7%	(1)	0.0%	(0)
##	1.9%	(8)	1.9%	(8)	1.9%	(8)	1.6%	(7)	1.9%	(8)	1.9%	(8)	1.9%	(8)	1.9%	(8)
##	31		32		33		34		35		36		37		38	
##	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	7.1%	(1)	7.1%	(1)	0.0%	(0)
##	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	6.7%	(1)	20.0%	(3)	6.7%	(1)
##	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)
##	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	6.7%	(1)
##	0.0%	(0)	7.1%	(1)	7.1%	(1)	7.1%	(1)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)
##	6.7%	(1)	6.7%	(1)	6.7%	(1)	0.0%	(0)	0.0%	(0)	6.7%	(1)	0.0%	(0)	0.0%	(0)
##	7.1%	(1)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	7.1%	(1)	0.0%	(0)	0.0%	(0)
##	0.0%	(0)	7.1%	(1)	7.1%	(1)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)
##	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	7.1%	(1)	7.1%	(1)	7.1%	(1)	0.0%	(0)
##	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	7.7%	(1)	0.0%	(0)	0.0%	(0)
##	0.0%	(0)	0.0%	(0)	0.0%	(0)	7.1%	(1)	7.1%	(1)	0.0%	(0)	0.0%	(0)	0.0%	(0)
##	6.7%	(1)	6.7%	(1)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)
##	7.7%	(1)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)
##	0.0%	(0)	0.0%	(0)	7.1%	(1)	7.1%	(1)	7.1%	(1)	0.0%	(0)	0.0%	(0)	0.0%	(0)
##	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	6.7%	(1)	0.0%	(0)
##	6.7%	(1)	0.0%	(0)	6.7%	(1)	6.7%	(1)	0.0%	(0)	0.0%	(0)	0.0%	(0)	6.7%	(1)
##	0.0%	(0)	7.1%	(1)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	7.1%	(1)
##	6.7%	(1)	6.7%	(1)	6.7%	(1)	6.7%	(1)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)
##	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)
##	7.1%	(1)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)
##	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	7.1%	(1)
##	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	13.3%	(2)	6.7%	(1)	6.7%	(1)	0.0%	(0)
##	7.1%	(1)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)
##	0.0%	(0)	0.0%	(0)	0.0%	(0)	6.7%	(1)	6.7%	(1)	0.0%	(0)	0.0%	(0)	0.0%	(0)
##	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)
##	0.0%	(0)	0.0%	(0)	0.0%	(0)	6.7%	(1)	6.7%	(1)	6.7%	(1)	0.0%	(0)	13.3%	(2)
##	0.0%	(0)	7.1%	(1)	7.1%	(1)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	7.1%	(1)
##	0.0%	(0)	6.7%	(1)	0.0%	(0)	0.0%	(0)	6.7%	(1)	0.0%	(0)	0.0%	(0)	0.0%	(0)
##	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	7.1%	(1)	0.0%	(0)
##	0.0%	(0)	0.0%	(0)	6.7%	(1)	6.7%	(1)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)
##	1.9%	(8)	1.9%	(8)	1.9%	(8)	1.9%	(8)	1.9%	(8)	1.9%	(8)	1.9%	(8)	1.9%	(8)
##	39		40		41		42		43		44		45		46	
##	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	7.1%	(1)	0.0%	(0)	0.0%	(0)	0.0%	(0)
##	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)
##	7.1%	(1)	0.0%	(0)	7.1%	(1)	7.1%	(1)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)
##	6.7%	(1)	6.7%	(1)	6.7%	(1)	0.0%	(0)	6.7%	(1)	0.0%	(0)	0.0%	(0)	0.0%	(0)
##	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)
##	0.0%	(0)	6.7%	(1)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)

#	#	47	48	49	50	51	52	53	54							
##	0.0%	(0)	0.0%	(0)	7.1%	(1)	0.0%	(0)	7.1%	(1)	0.0%	(0)	7.1%	(1)	0.0%	(0)
##	6.7%	(1)	6.7%	(1)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)
##	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	7.1%	(1)
##	0.0%	(0)	6.7%	(1)	6.7%	(1)	6.7%	(1)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)
##	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)
##	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	6.7%	(1)	6.7%	(1)	6.7%	(1)
##	0.0%	(0)	0.0%	(0)	7.1%	(1)	7.1%	(1)	0.0%	(0)	0.0%	(0)	0.0%	(0)	7.1%	(1)
##	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	7.1%	(1)	7.1%	(1)	0.0%	(0)	0.0%	(0)
##	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	7.1%	(1)
##	0.0%	(0)	7.7%	(1)	0.0%	(0)	7.7%	(1)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)
##	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)
##	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)
##	0.0%	(0)	7.7%	(1)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)
##	0.0%	(0)	0.0%	(0)	7.1%	(1)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)
##	6.7%	(1)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	6.7%	(1)	6.7%	(1)	0.0%	(0)
##	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	6.7%	(1)	0.0%	(0)	0.0%	(0)	0.0%	(0)
##	7.1%	(1)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)
##	0.0%	(0)	0.0%	(0)	6.7%	(1)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)
##	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	7.1%	(1)	7.1%	(1)	0.0%	(0)
##	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	7.1%	(1)	0.0%	(0)
##	0.0%	(0)	0.0%	(0)	0.0%	(0)	7.1%	(1)	0.0%	(0)	7.1%	(1)	7.1%	(1)	0.0%	(0)
##	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)
##	7.1%	(1)	7.1%	(1)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)
##	6.7%	(1)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)
##	0.0%	(0)	0.0%	(0)	0.0%	(0)	7.1%	(1)	7.1%	(1)	0.0%	(0)	0.0%	(0)	0.0%	(0)
##	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	6.7%	(1)
##	7.1%	(1)	7.1%	(1)	0.0%	(0)	0.0%	(0)	7.1%	(1)	0.0%	(0)	0.0%	(0)	0.0%	(0)
##	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	6.7%	(1)
##	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	0.0%	(0)	7.1%	(1)	0.0%	(0)	0.0%	(0)
##	0.0%	(0)	0.0%	(0)	0.0%	(0)	6.7%	(1)	6.7%	(1)	0.0%	(0)	0.0%	(0)	0.0%	(0)

```
## 1.4% (6) 1.4% (6) 1.2% (5) 1.4% (6) 1.4% (6) 1.4% (6) 1.4% (6)
## 55 56 57 58 59 60
## 0.0% (0) 0.0% (0) 0.0% (0) 0.0% (0) 0.0% (0) 0.0% (0)
## 0.0% (0) 0.0% (0) 6.7% (1) 0.0% (0) 0.0% (0) 0.0% (0)
## 7.1% (1) 0.0% (0) 0.0% (0) 0.0% (0) 0.0% (0) 7.1% (1)
## 0.0% (0) 0.0% (0) 0.0% (0) 0.0% (0) 0.0% (0) 0.0% (0)
## 0.0% (0) 7.1% (1) 7.1% (1) 7.1% (1) 0.0% (0) 0.0% (0)
## 0.0% (0) 0.0% (0) 0.0% (0) 0.0% (0) 0.0% (0) 0.0% (0)
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## 7.1% (1) 0.0% (0) 0.0% (0) 0.0% (0) 7.1% (1) 0.0% (0)
## 0.0% (0) 0.0% (0) 0.0% (0) 0.0% (0) 0.0% (0) 0.0% (0)
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## 0.0% (0) 0.0% (0) 6.7% (1) 6.7% (1) 6.7% (1) 0.0% (0)
## 0.0% (0) 0.0% (0) 0.0% (0) 7.7% (1) 0.0% (0) 0.0% (0)
## 0.0% (0) 0.0% (0) 0.0% (0) 0.0% (0) 7.1% (1) 7.1% (1)
## 0.0% (0) 0.0% (0) 0.0% (0) 0.0% (0) 0.0% (0) 0.0% (0)
## 6.7% (1) 6.7% (1) 0.0% (0) 0.0% (0) 0.0% (0) 0.0% (0)
## 0.0% (0) 7.1% (1) 7.1% (1) 0.0% (0) 0.0% (0) 0.0% (0)
## 0.0% (0) 0.0% (0) 0.0% (0) 0.0% (0) 6.7% (1) 6.7% (1)
## 7.1% (1) 0.0% (0) 0.0% (0) 0.0% (0) 0.0% (0) 0.0% (0)
## 0.0% (0) 0.0% (0) 0.0% (0) 0.0% (0) 7.1% (1) 7.1% (1)
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## 6.7% (1) 6.7% (1) 0.0% (0) 0.0% (0) 0.0% (0) 6.7% (1)
## 0.0% (0) 0.0% (0) 0.0% (0) 0.0% (0) 0.0% (0) 0.0% (0)
## 0.0% (0) 0.0% (0) 0.0% (0) 0.0% (0) 0.0% (0) 0.0% (0)
## 0.0% (0) 0.0% (0) 0.0% (0) 0.0% (0) 0.0% (0) 0.0% (0)
## 0.0% (0) 0.0% (0) 6.7% (1) 6.7% (1) 0.0% (0) 0.0% (0)
## 0.0% (0) 0.0% (0) 0.0% (0) 0.0% (0) 0.0% (0) 0.0% (0)
## 6.7% (1) 6.7% (1) 0.0% (0) 0.0% (0) 0.0% (0) 0.0% (0)
## 0.0% (0) 0.0% (0) 0.0% (0) 0.0% (0) 7.1% (1) 7.1% (1)
## 0.0% (0) 0.0% (0) 0.0% (0) 0.0% (0) 0.0% (0) 0.0% (0)
## 1.4% (6) 1.4% (6) 1.4% (6) 1.4% (6) 1.4% (6) 1.4% (6)
```

```
endpoint %>%
  tabyl(Genotype, Row) %>%
  adorn_totals("row") %>%
  adorn_percentages("row") %>%
  adorn_pct_formatting() %>%
  adorn_ns() %>%
  adorn_title("combined")
```

##	Genotype/Row	1	2	3	4	5	6
##	EPPN1_H	14.3%	(2) 14.3%	(2) 14.3%	(2) 14.3%	(2) 14.3%	(2)
##	EPPN1_L	13.3%	(2) 13.3%	(2) 13.3%	(2) 13.3%	(2) 13.3%	(2)
##	EPPN10_H	14.3%	(2) 14.3%	(2) 14.3%	(2) 14.3%	(2) 14.3%	(2)
##	EPPN10_L	13.3%	(2) 13.3%	(2) 13.3%	(2) 13.3%	(2) 13.3%	(2)
##	EPPN11_H	14.3%	(2) 14.3%	(2) 14.3%	(2) 14.3%	(2) 14.3%	(2)
##	EPPN11_L	13.3%	(2) 13.3%	(2) 13.3%	(2) 13.3%	(2) 13.3%	(2)
##	EPPN12_H	14.3%	(2) 14.3%	(2) 14.3%	(2) 14.3%	(2) 14.3%	(2)
##	EPPN12_L	14.3%	(2) 14.3%	(2) 14.3%	(2) 14.3%	(2) 14.3%	(2)
##	EPPN13_H	14.3%	(2) 14.3%	(2) 14.3%	(2) 14.3%	(2) 14.3%	(2)
##	EPPN13_L	15.4%	(2) 15.4%	(2) 15.4%	(2) 7.7%	(1) 15.4%	(2)
##	EPPN14_H	14.3%	(2) 14.3%	(2) 14.3%	(2) 14.3%	(2) 14.3%	(2)
##	EPPN14_L	13.3%	(2) 13.3%	(2) 13.3%	(2) 13.3%	(2) 13.3%	(2)
##	EPPN15_H	15.4%	(2) 15.4%	(2) 7.7%	(1) 15.4%	(2) 15.4%	(2)
##	EPPN2_H	14.3%	(2) 14.3%	(2) 14.3%	(2) 14.3%	(2) 14.3%	(2)
##	EPPN2_L	13.3%	(2) 13.3%	(2) 13.3%	(2) 13.3%	(2) 13.3%	(2)
##	EPPN20_T	13.3%	(2) 13.3%	(2) 13.3%	(2) 13.3%	(2) 13.3%	(2)
##	EPPN3_H	14.3%	(2) 14.3%	(2) 14.3%	(2) 14.3%	(2) 14.3%	(2)
##	EPPN3_L	13.3%	(2) 13.3%	(2) 13.3%	(2) 13.3%	(2) 13.3%	(2)
##	EPPN4_H	14.3%	(2) 14.3%	(2) 14.3%	(2) 14.3%	(2) 14.3%	(2)
##	EPPN4_L	14.3%	(2) 14.3%	(2) 14.3%	(2) 14.3%	(2) 7.1%	(1)
##	EPPN5_H	14.3%	(2) 14.3%	(2) 14.3%	(2) 14.3%	(2) 14.3%	(2)
##	EPPN5_L	13.3%	(2) 13.3%	(2) 13.3%	(2) 13.3%	(2) 13.3%	(2)
##	EPPN6_H	14.3%	(2) 14.3%	(2) 14.3%	(2) 14.3%	(2) 14.3%	(2)
##	EPPN6_L	13.3%	(2) 13.3%	(2) 13.3%	(2) 13.3%	(2) 13.3%	(2)
##	EPPN7_H	14.3%	(2) 14.3%	(2) 14.3%	(2) 14.3%	(2) 14.3%	(2)
##	EPPN7_L	13.3%	(2) 13.3%	(2) 13.3%	(2) 13.3%	(2) 13.3%	(2)
##	EPPN8_H	14.3%	(2) 14.3%	(2) 14.3%	(2) 14.3%	(2) 14.3%	(2)
##	EPPN8_L	13.3%	(2) 13.3%	(2) 13.3%	(2) 13.3%	(2) 13.3%	(2)
##	EPPN9_H	14.3%	(2) 14.3%	(2) 14.3%	(2) 14.3%	(2) 14.3%	(2)
##	EPPN9_L	13.3%	(2) 13.3%	(2) 13.3%	(2) 13.3%	(2) 13.3%	(2)
##	Total	14.0%	(60) 14.0%	(60) 14.0%	(60) 13.7%	(59) 13.7%	(59) 13.7%
##	7	8					
##	14.3%	(2) 0.0%	(0)				
##	6.7%	(1) 13.3%	(2)				
##	14.3%	(2) 0.0%	(0)				
##	6.7%	(1) 13.3%	(2)				
##	14.3%	(2) 0.0%	(0)				
##	6.7%	(1) 13.3%	(2)				
##	14.3%	(2) 0.0%	(0)				
##	7.1%	(1) 7.1%	(1)				
##	14.3%	(2) 0.0%	(0)				
##	0.0%	(0) 15.4%	(2)				
##	14.3%	(2) 0.0%	(0)				
##	6.7%	(1) 13.3%	(2)				
##	15.4%	(2) 0.0%	(0)				
##	14.3%	(2) 0.0%	(0)				
##	6.7%	(1) 13.3%	(2)				
##	6.7%	(1) 13.3%	(2)				
##	14.3%	(2) 0.0%	(0)				
##	6.7%	(1) 13.3%	(2)				
##	14.3%	(2) 0.0%	(0)				
##	7.1%	(1) 14.3%	(2)				
##	14.3%	(2) 0.0%	(0)				
##	6.7%	(1) 13.3%	(2)				

```
## 14.3% (2) 0.0% (0)
## 6.7% (1) 13.3% (2)
## 14.3% (2) 0.0% (0)
## 6.7% (1) 13.3% (2)
## 14.3% (2) 0.0% (0)
## 6.7% (1) 13.3% (2)
## 14.3% (2) 0.0% (0)
## 6.7% (1) 13.3% (2)
## 10.2% (44) 6.7% (29)
```

```
endpoint %>%
  count(Genotype)
```

```
##      Genotype  n
## 1  EPPN1_H 14
## 2  EPPN1_L 15
## 3  EPPN10_H 14
## 4  EPPN10_L 15
## 5  EPPN11_H 14
## 6  EPPN11_L 15
## 7  EPPN12_H 14
## 8  EPPN12_L 14
## 9  EPPN13_H 14
## 10 EPPN13_L 13
## 11 EPPN14_H 14
## 12 EPPN14_L 15
## 13 EPPN15_H 13
## 14 EPPN2_H 14
## 15 EPPN2_L 15
## 16 EPPN20_T 15
## 17 EPPN3_H 14
## 18 EPPN3_L 15
## 19 EPPN4_H 14
## 20 EPPN4_L 14
## 21 EPPN5_H 14
## 22 EPPN5_L 15
## 23 EPPN6_H 14
## 24 EPPN6_L 15
## 25 EPPN7_H 14
## 26 EPPN7_L 15
## 27 EPPN8_H 14
## 28 EPPN8_L 15
## 29 EPPN9_H 14
## 30 EPPN9_L 15
```

```
get_summary_stats(data = endpoint,
                  variables,
                  type = "common")
```

```
## Warning: Using an external vector in selections was deprecated in tidyselect 1.1.0.
## i Please use `all_of()` or `any_of()` instead.
##   # Was:
##   data %>% select(variables)
##
##   # Now:
##   data %>% select(all_of(variables))
##
## See <https://tidyselect.r-lib.org/reference/faq-external-vector.html>.
## This warning is displayed once every 8 hours.
## Call `lifecycle::last_lifecycle_warnings()` to see where this warning was
## generated.
```


```
## # A tibble: 1 x 10
##   variable      n  min  max median  iqr mean  sd  se  ci
##   <fct>      <dbl> <dbl> <dbl>  <dbl> <dbl> <dbl> <dbl> <dbl> <dbl>
## 1 DW_plant_g  430    -1  624   215   182  235.  123.  5.96  11.7
```

```
skim(endpoint[variables])
```

Data summary

Name	endpoint[variables]
Number of rows	430
Number of columns	1
Column type frequency:	
numeric	1
Group variables	
None	

Variable type: numeric

skim_variable	n_missing	complete_rate	mean	sd	p0	p25	p50	p75	p100	hist
DW_plant_g	0	1	234.96	123.5	-1	138	215	320	624	

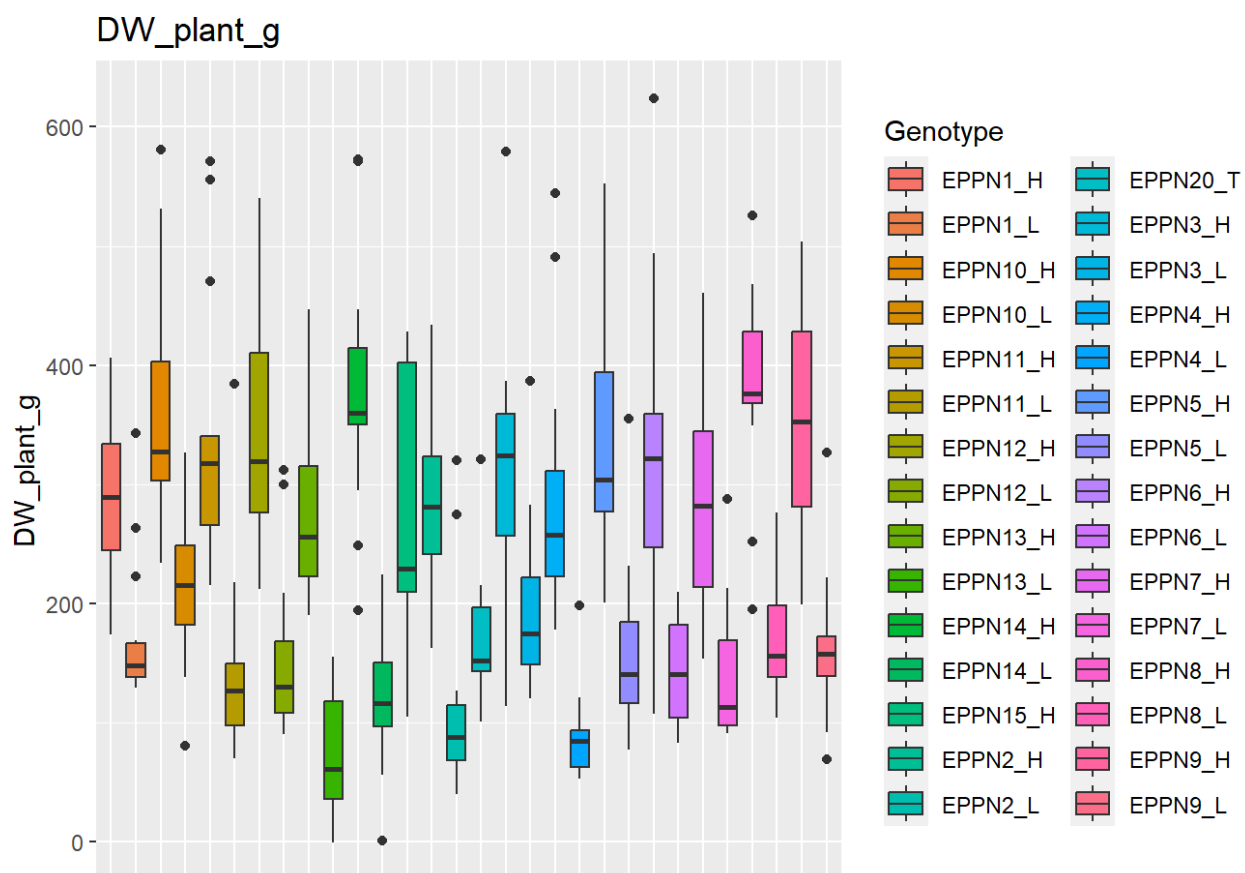
Data visualization

Using several functions that are located in the functions.R script

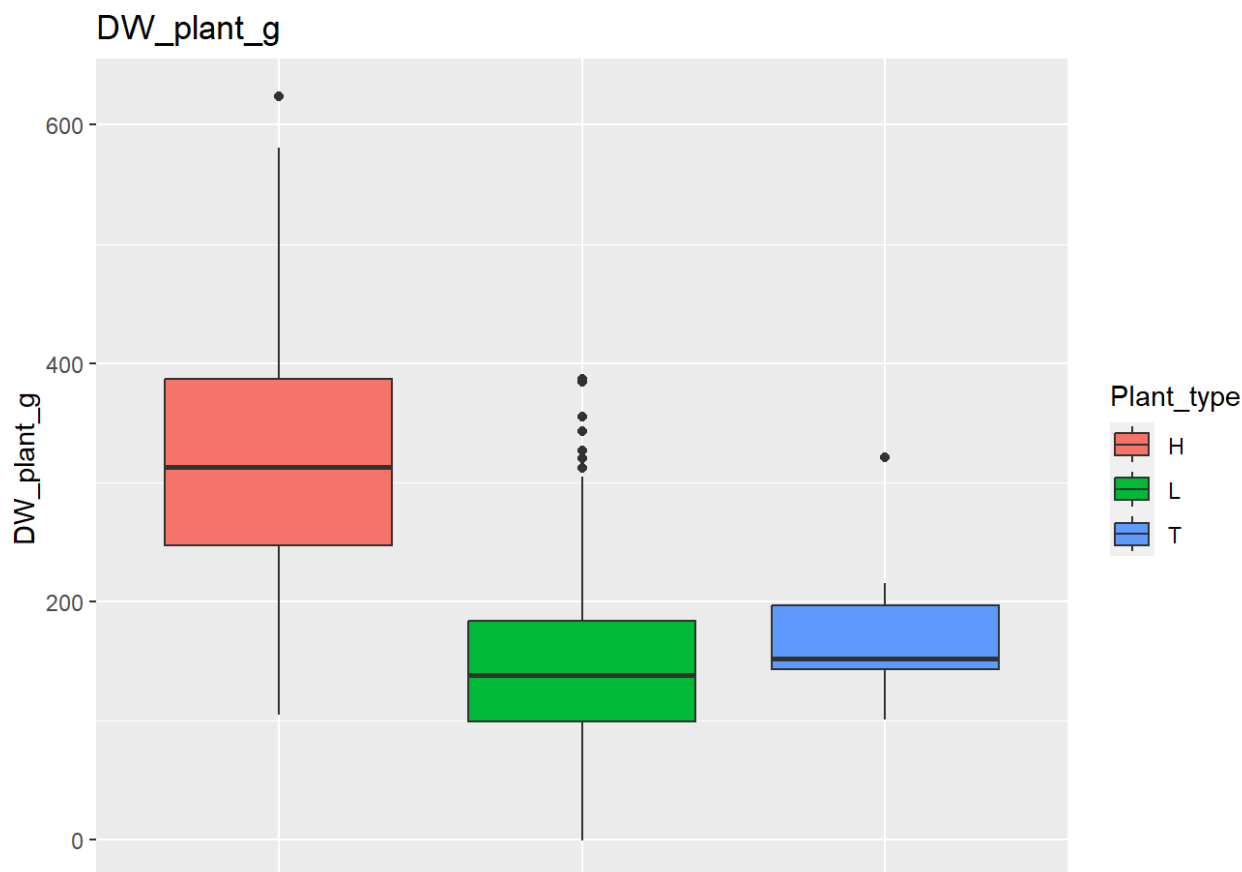
Boxplots

```
create_boxplots(endpoint, variables, "Genotype")
```

```
## Warning: `aes_string()` was deprecated in ggplot2 3.0.0.
## i Please use tidy evaluation idioms with `aes()`.
## i See also `vignette("ggplot2-in-packages")` for more information.
## This warning is displayed once every 8 hours.
## Call `lifecycle::last_lifecycle_warnings()` to see where this warning was
## generated.
```



```
create_boxplots(endpoint, variables, "Plant_type")
```



## Correlation plots

```
print(paste0("No data for ", platform))
```

```
## [1] "No data for M3P"
```

## B. Normality hypothesis and outlier detection

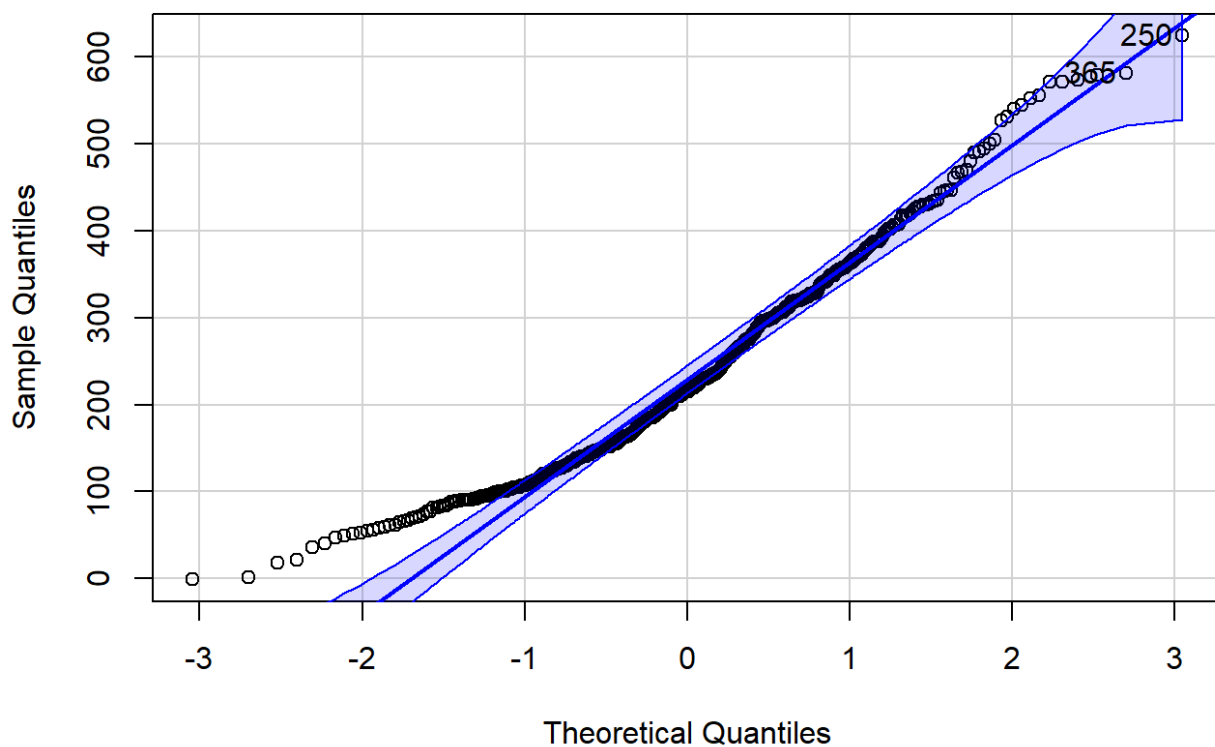
Test for normality hypothesis and plot density histogram. The red curve is the normal distribution, the blue dotted curve is the data density curve.

```
normality_results <- normality_test_histogram(endpoint)
```

```
## Warning: Using `size` aesthetic for lines was deprecated in ggplot2 3.4.0.
## i Please use `linewidth` instead.
## This warning is displayed once every 8 hours.
## Call `lifecycle::last_lifecycle_warnings()` to see where this warning was
## generated.
```



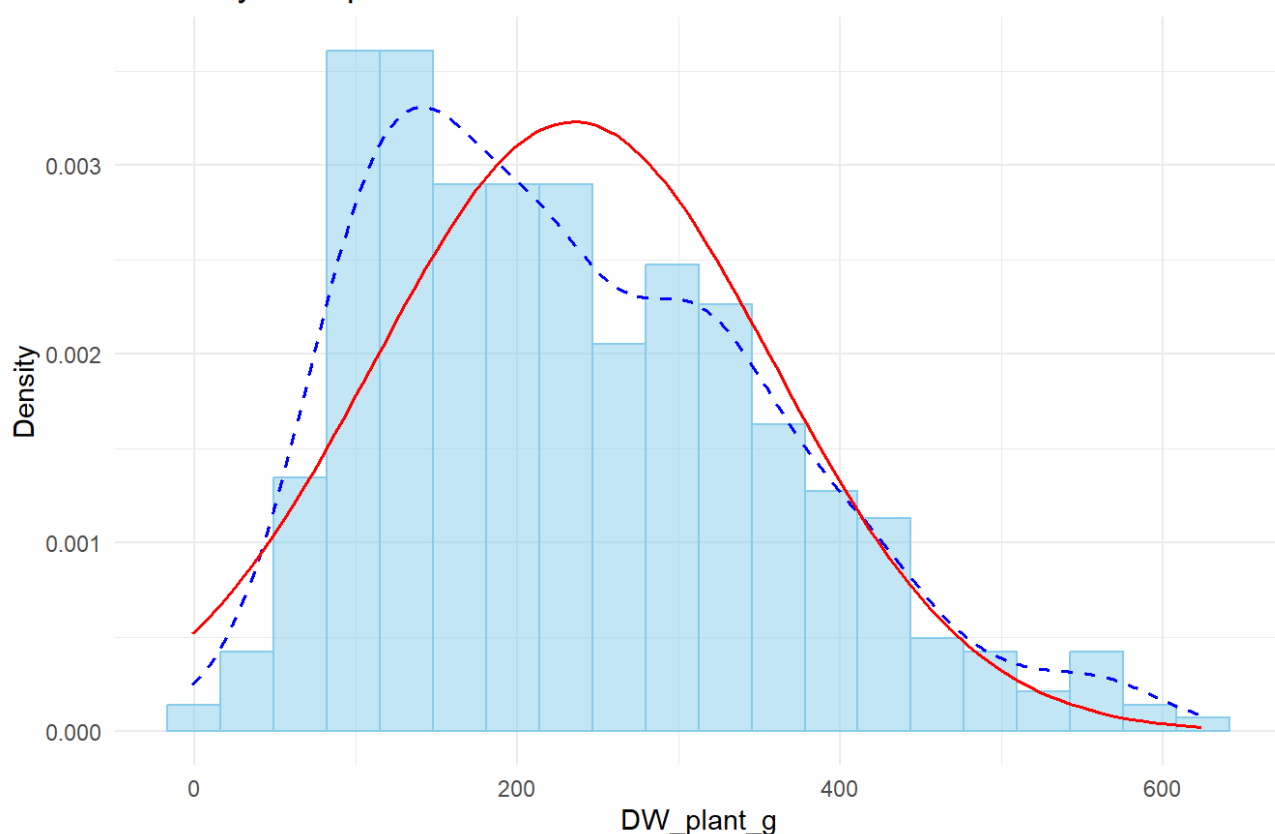
## QQ Plot of DW\_plant\_g



```
## Warning: The dot-dot notation (`..density..`) was deprecated in ggplot2 3.4.0.  
## i Please use `after_stat(density)` instead.  
## This warning is displayed once every 8 hours.  
## Call `lifecycle::last_lifecycle_warnings()` to see where this warning was  
## generated.
```

### Histogram of DW\_plant\_g

Normality Test:  $p = 0$



```
## [1] 250 365
```

Remove the outliers, replacing them with NULL values and normality visual verification.

The function `detect_replace_outliers_by_genotype` checks for outlying values, using the Tukey method.

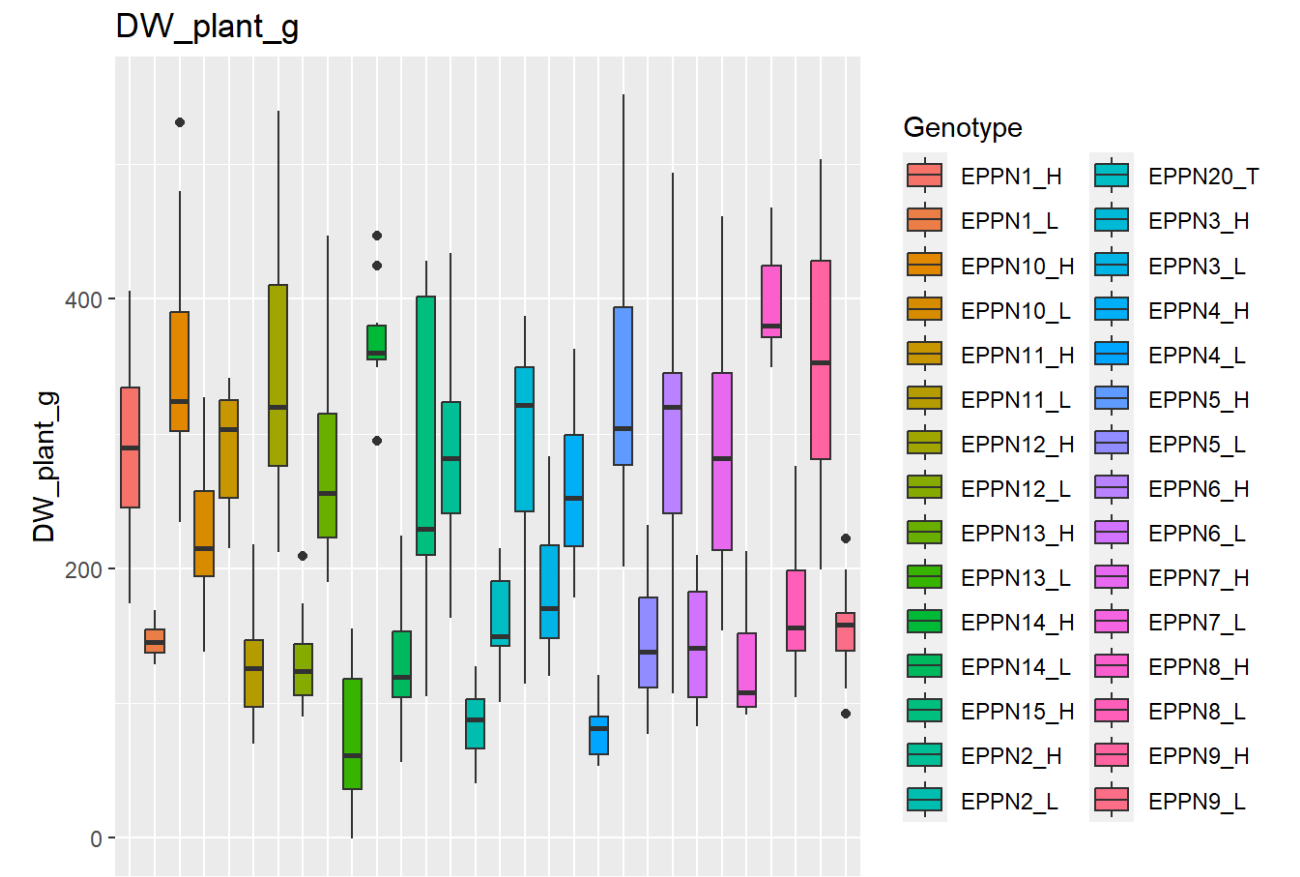
Then run the function on all variables of the dataset.

```
endpoint_clean <- endpoint
# Run the function on the dataset for all the variables
endpoint_clean <- detect_replace_outliers_by_genotype(endpoint_clean)
```

## Boxplots after outlier detection

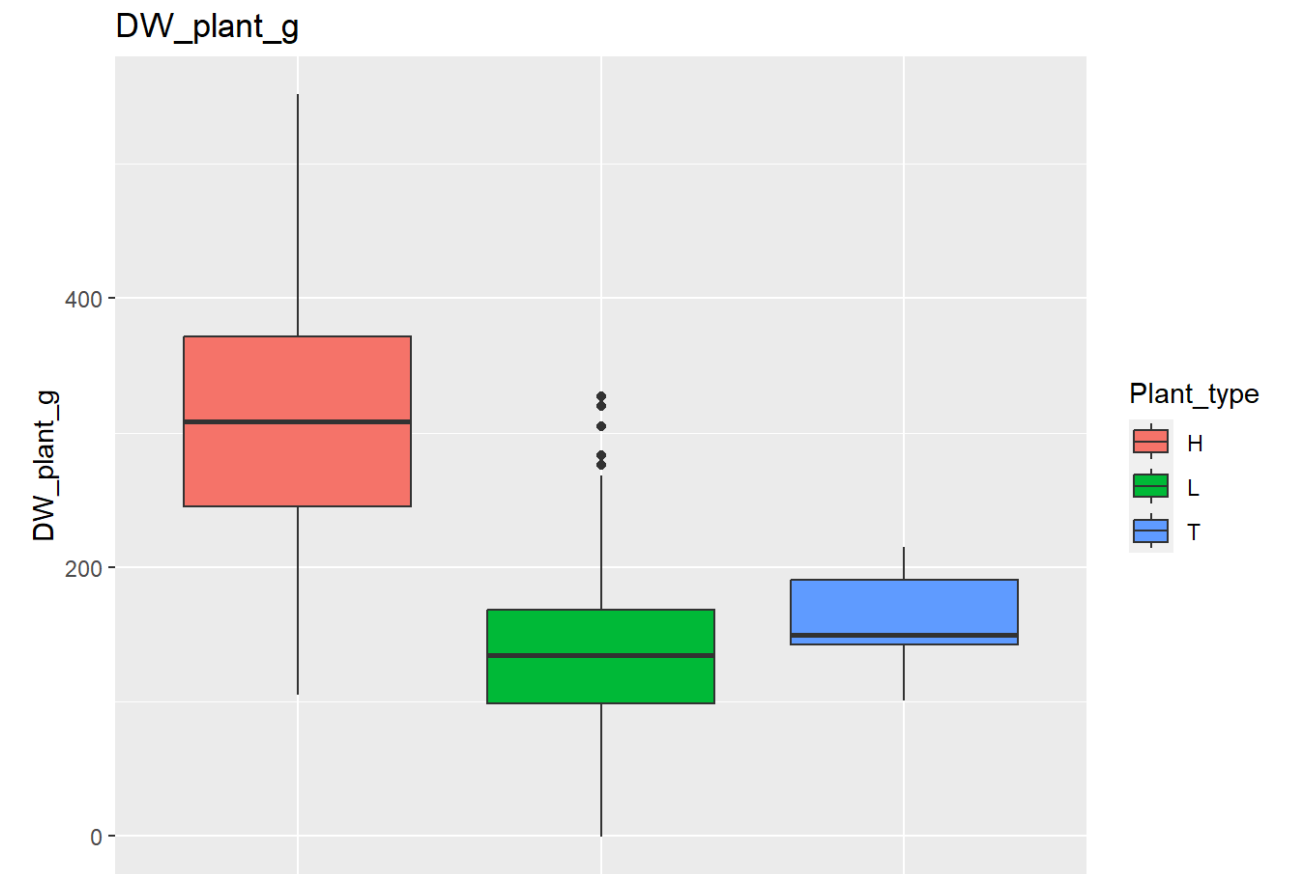
```
create_boxplots(endpoint_clean, variables, "Genotype")
```

```
## Warning: Removed 32 rows containing non-finite values (`stat_boxplot()`).
```



```
create_boxplots(endpoint_clean, variables, "Plant_type")
```

```
## Warning: Removed 32 rows containing non-finite values (`stat_boxplot()`).
```



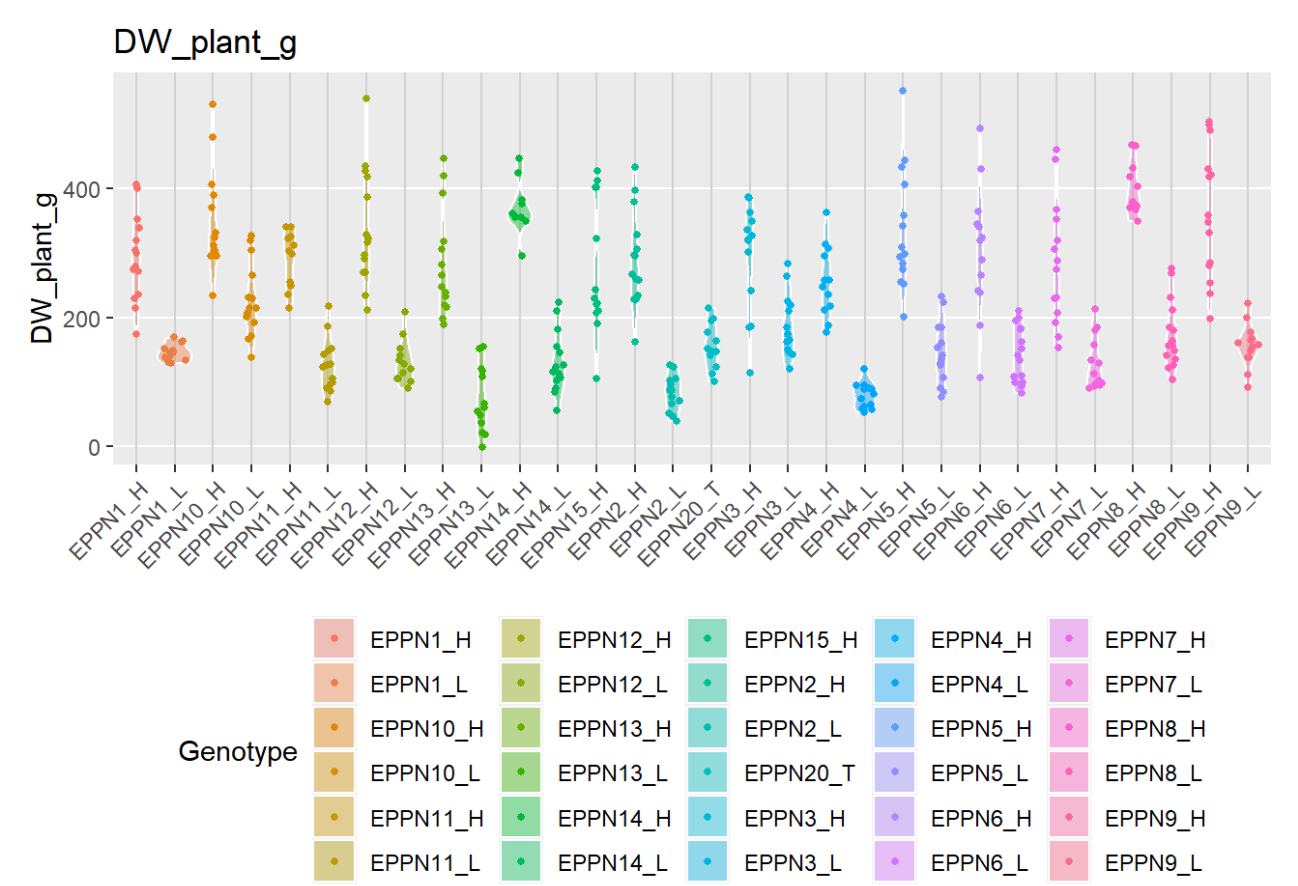
# Violin and sina plots after outlier detection

```
create_violin_plots(endpoint_clean, variables, "Genotype")
```

```
## Warning: The `size` argument of `element_line()` is deprecated as of ggplot2 3.4.0.
## i Please use the `linewidth` argument instead.
## This warning is displayed once every 8 hours.
## Call `lifecycle::last_lifecycle_warnings()` to see where this warning was
## generated.
```

```
## Warning: Removed 32 rows containing non-finite values (`stat_ydensity()`).
```

```
## Warning: Removed 32 rows containing non-finite values (`stat_sina()`).
```



```
create_violin_plots(endpoint_clean, variables, "Plant_type")
```

```
## Warning: Removed 32 rows containing non-finite values (`stat_ydensity()`).
## Removed 32 rows containing non-finite values (`stat_sina()`).
```



Exploration statistics for the variables after outlier detection

```
skim(endpoint_clean[variables])
```

Data summary

Name	endpoint_clean[variables]
Number of rows	430
Number of columns	1
Column type frequency:	
numeric	1
Group variables	
None	

Variable type: numeric

skim_variable	n_missing	complete_rate	mean	sd	p0	p25	p50	p75	p100	hist
DW_plant_g	32	0.93	225.15	113.9	-1	134	210	306.75	552	

```

for (var in variables) {
  cat("\nSummary for:", var, "\n")
  endpoint_clean %>%
    group_by(Genotype) %>%
    summarize(mean      = mean(get(var), na.rm = TRUE),
              std.dev    = sd(get(var), na.rm = TRUE),
              n_missing  = sum(is.na(get(var)))) %>%
    arrange(desc(mean)) %>%
    print(n = Inf)
}

```

```

##
## Summary for: DW_plant_g
## # A tibble: 30 × 4
##   Genotype mean std.dev n_missing
##   <fct>    <dbl>  <dbl>    <int>
## 1 EPPN8_H  400      41.1      3
## 2 EPPN14_H 370.      41.9      4
## 3 EPPN9_H  361.     102.      0
## 4 EPPN10_H 352.      82.1      1
## 5 EPPN12_H 339.      90.9      0
## 6 EPPN5_H  336.      94.1      0
## 7 EPPN6_H  304.     101.      1
## 8 EPPN3_H  294.      85.5      1
## 9 EPPN1_H  293.      67.7      0
## 10 EPPN2_H  291.      74.1      0
## 11 EPPN11_H 291.      44.4      3
## 12 EPPN7_H  286.      96.3      0
## 13 EPPN13_H 284.      83.1      0
## 14 EPPN15_H 277.     104.      0
## 15 EPPN4_H  256.      55.2      2
## 16 EPPN10_L 228.      57.8      1
## 17 EPPN3_L  185.      48.4      1
## 18 EPPN8_L  174.      52.2      0
## 19 EPPN20_T 160.      36.4      1
## 20 EPPN9_L  157.      33.8      2
## 21 EPPN1_L  146.      13.4      3
## 22 EPPN5_L  145.      48.5      1
## 23 EPPN6_L  143.      43.4      0
## 24 EPPN12_L 131.      34.1      2
## 25 EPPN14_L 131.      47.9      1
## 26 EPPN7_L  128.      40.5      1
## 27 EPPN11_L 127.      40.8      1
## 28 EPPN2_L   83.4     27.8      2
## 29 EPPN4_L   79.3     19.6      1
## 30 EPPN13_L  73.8     51.6      0

```

## 2. Exploration of the timeseries data

In this part, we look at the timeseries, S\_timeseries and T\_timeseries datasets, also using several functions, located in the functions.R script.

# Number of data observations per day for the

# traits of the timeseries datasets

```

h1 <- ggplot(timeseries, aes(x = Date)) +
  geom_bar(aes(fill = Genotype), position = "stack", width = 0.96) +
  scale_fill_viridis_d(option = "D") +
  labs(x = "Date", y = "Number of observations", title = "Observations per day for Plant_biomass_g") +
  scale_y_continuous(breaks = seq(from = 0, to = 325, by = 25)) +
  scale_x_date(date_breaks = "2 days", date_labels = "%d-%m-%Y") +
  theme(axis.text.x = element_text(angle = 45, hjust = 1),
        panel.grid.major.x = element_line(color = "lightgray", size = 0.5),
        panel.grid.minor.x = element_blank())

h2 <- ggplot(timeseries_Leaf_number, aes(x = Date)) +
  geom_bar(aes(fill = Genotype), position = "stack", width = 0.96) +
  scale_fill_viridis_d(option = "D") +
  labs(x = "Date", y = "Number of observations", title = "Observations per day for Leaf_number") +
  scale_y_continuous(breaks = seq(from = 0, to = 325, by = 25)) +
  scale_x_date(date_breaks = "2 days", date_labels = "%d-%m-%Y") +
  theme(axis.text.x = element_text(angle = 45, hjust = 1),
        panel.grid.major.x = element_line(color = "lightgray", size = 0.5),
        panel.grid.minor.x = element_blank())

h3 <- ggplot(timeseries_Ligulated_leaf_number, aes(x = Date)) +
  geom_bar(aes(fill = Genotype), position = "stack", width = 0.96) +
  scale_fill_viridis_d(option = "D") +
  labs(x = "Date", y = "Number of observations", title = "Observations per day for Ligulated_leaf_number") +
  scale_y_continuous(breaks = seq(from = 0, to = 325, by = 25)) +
  scale_x_date(date_breaks = "2 days", date_labels = "%d-%m-%Y") +
  theme(axis.text.x = element_text(angle = 45, hjust = 1),
        panel.grid.major.x = element_line(color = "lightgray", size = 0.5),
        panel.grid.minor.x = element_blank())

h4 <- ggplot(timeseries_Plant_emergence, aes(x = Date)) +
  geom_bar(aes(fill = Genotype), position = "stack", width = 0.96) +
  scale_fill_viridis_d(option = "D") +
  labs(x = "Date", y = "Number of observations", title = "Observations per day for Plant_emergence") +
  scale_y_continuous(breaks = seq(from = 0, to = 325, by = 25)) +
  scale_x_date(date_breaks = "2 days", date_labels = "%d-%m-%Y") +
  theme(axis.text.x = element_text(angle = 45, hjust = 1),
        panel.grid.major.x = element_line(color = "lightgray", size = 0.5),
        panel.grid.minor.x = element_blank())

h5 <- ggplot(timeseries_Plant_transpiration, aes(x = Date)) +
  geom_bar(aes(fill = Genotype), position = "stack", width = 0.96) +
  scale_fill_viridis_d(option = "D") +
  labs(x = "Date", y = "Number of observations", title = "Observations per day for Plant_transpiration") +
  scale_y_continuous(breaks = seq(from = 0, to = 325, by = 25)) +
  scale_x_date(date_breaks = "2 days", date_labels = "%d-%m-%Y") +

```



```

    theme(axis.text.x = element_text(angle = 45, hjust = 1),
          panel.grid.major.x = element_line(color = "lightgray", size = 0.5),
          panel.grid.minor.x = element_blank())

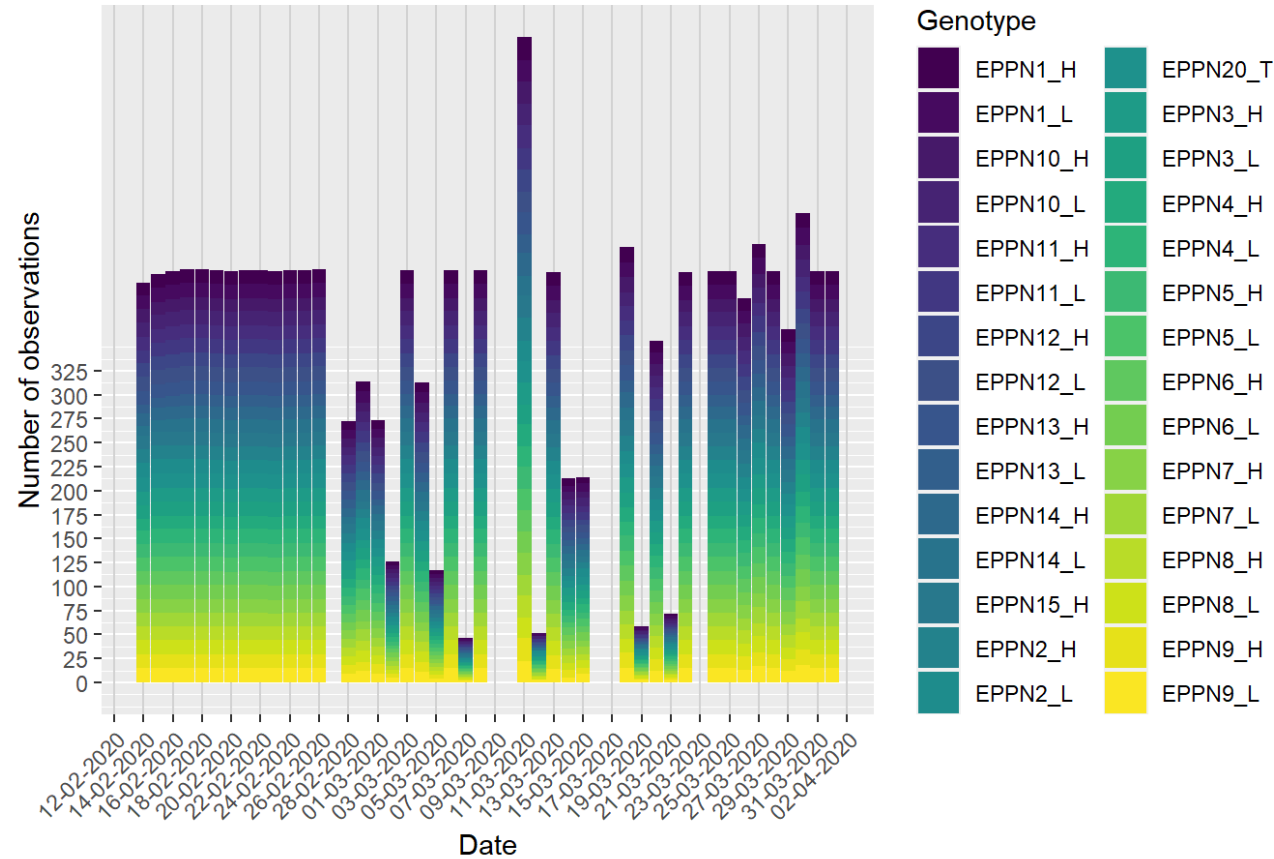
h6 <- ggplot(timeseries_Soil_water_potential, aes(x = Date)) +
  geom_bar(aes(fill = Genotype), position = "stack", width = 0.96) +
  scale_fill_viridis_d(option = "D") +
  labs(x = "Date", y = "Number of observations", title = "Observations per day for Soil
_water_potential") +
  scale_y_continuous(breaks = seq(from = 0, to = 325, by = 25)) +
  scale_x_date(date_breaks = "2 days", date_labels = "%d-%m-%Y") +
  theme(axis.text.x = element_text(angle = 45, hjust = 1),
        panel.grid.major.x = element_line(color = "lightgray", size = 0.5),
        panel.grid.minor.x = element_blank())

h7 <- ggplot(timeseries_Water, aes(x = Date)) +
  geom_bar(aes(fill = Genotype), position = "stack", width = 0.96) +
  scale_fill_viridis_d(option = "D") +
  labs(x = "Date", y = "Number of observations", title = "Observations per day for Wate
r") +
  scale_y_continuous(breaks = seq(from = 0, to = 325, by = 25)) +
  scale_x_date(date_breaks = "2 days", date_labels = "%d-%m-%Y") +
  theme(axis.text.x = element_text(angle = 45, hjust = 1),
        panel.grid.major.x = element_line(color = "lightgray", size = 0.5),
        panel.grid.minor.x = element_blank())

h8 <- ggplot(S_timeseries, aes(x = Date)) +
  geom_bar(aes(fill = Genotype), position = "stack", width = 0.96) +
  scale_fill_viridis_d(option = "D") +
  labs(x = "Date", y = "Number of observations", title = "Observations per day for S_ti
meseries") +
  scale_y_continuous(breaks = seq(from = 0, to = 325, by = 25)) +
  scale_x_date(date_breaks = "2 days", date_labels = "%d-%m-%Y") +
  theme(axis.text.x = element_text(angle = 45, hjust = 1),
        panel.grid.major.x = element_line(color = "lightgray", size = 0.5),
        panel.grid.minor.x = element_blank())
h1

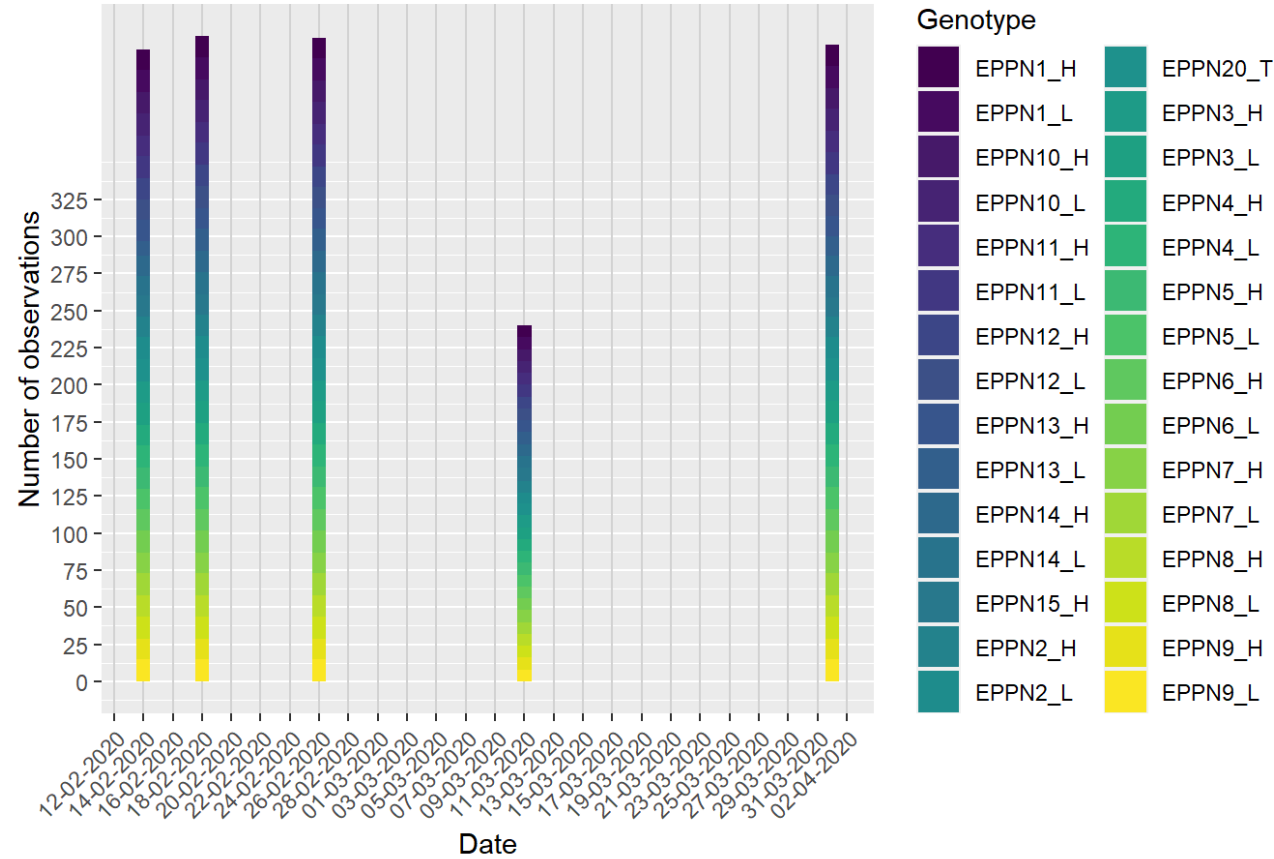
```

Observations per day for Plant\_biomass\_g



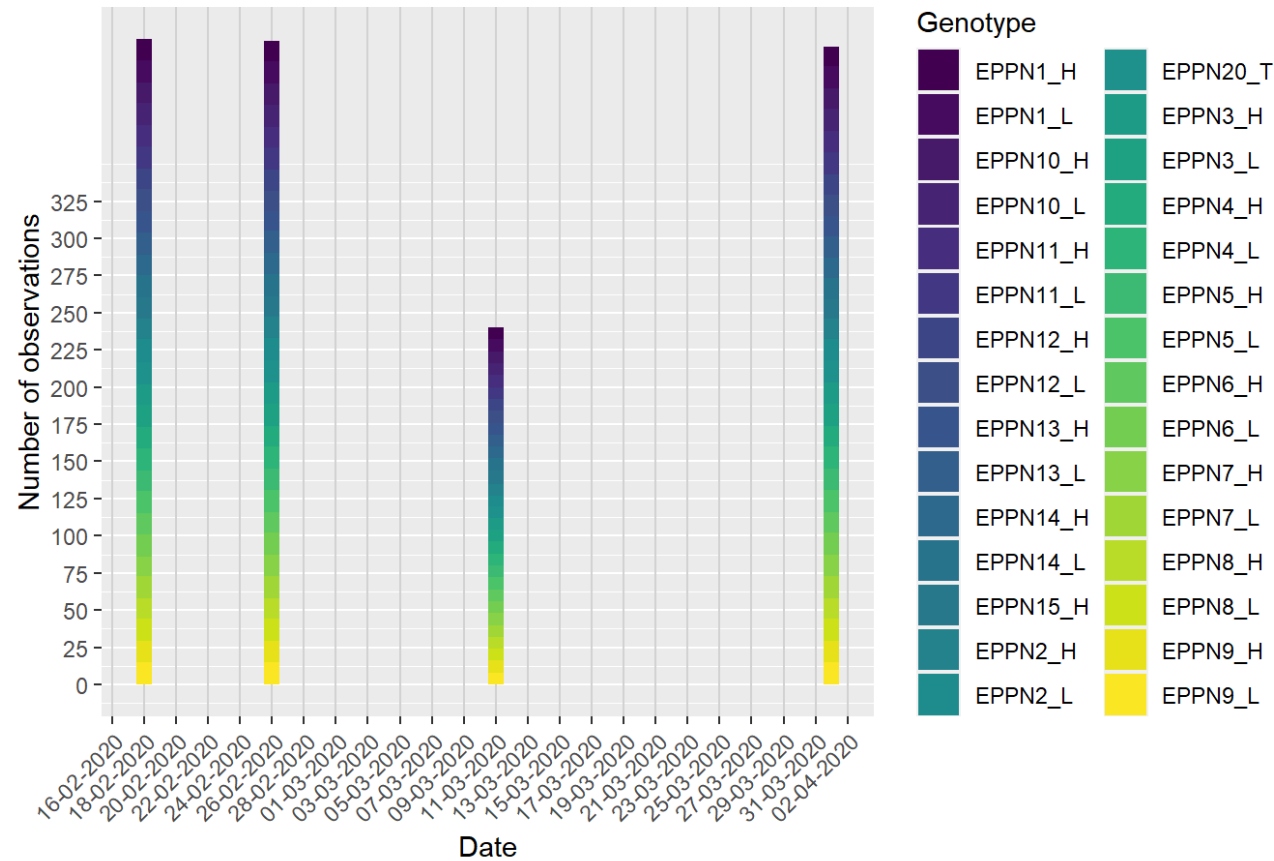
h2

Observations per day for Leaf\_number



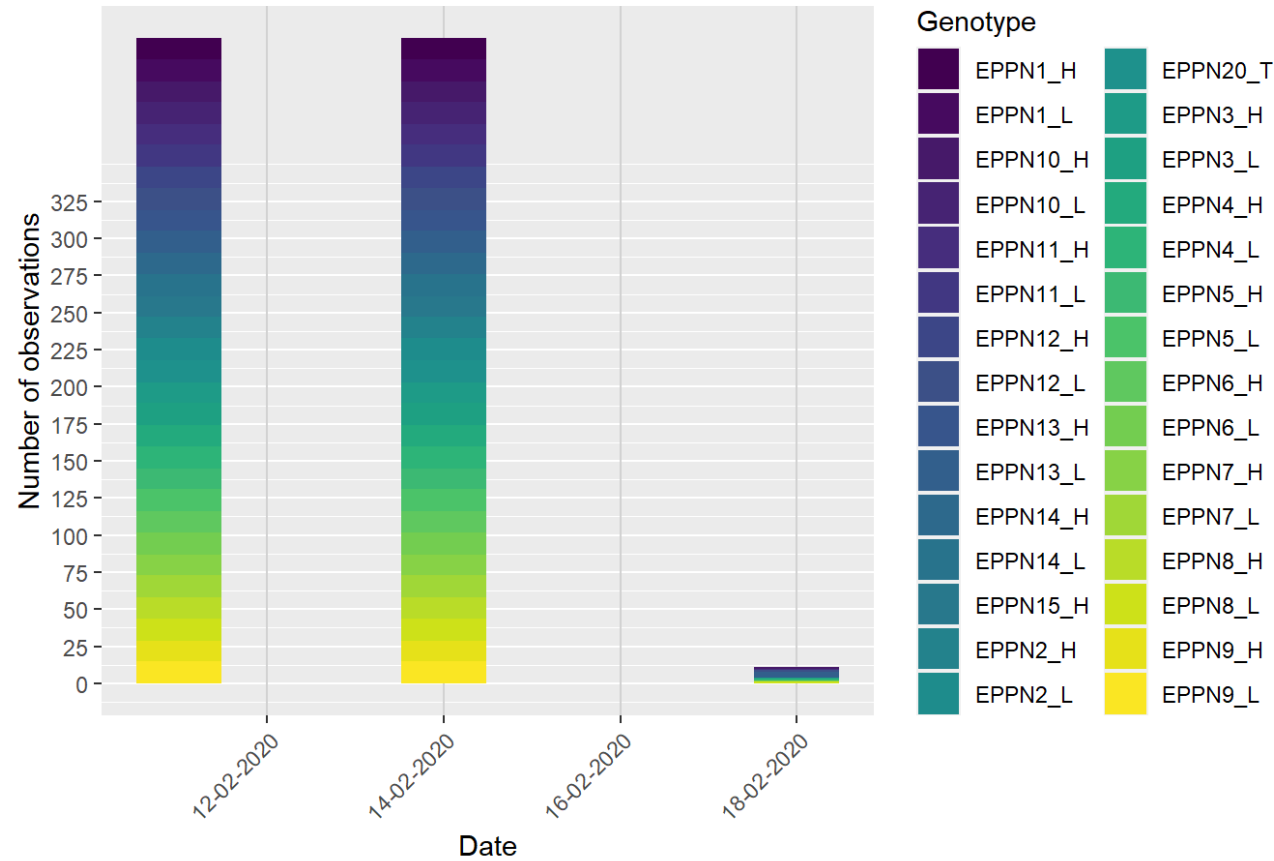
h3

Observations per day for Ligulated\_leaf\_number



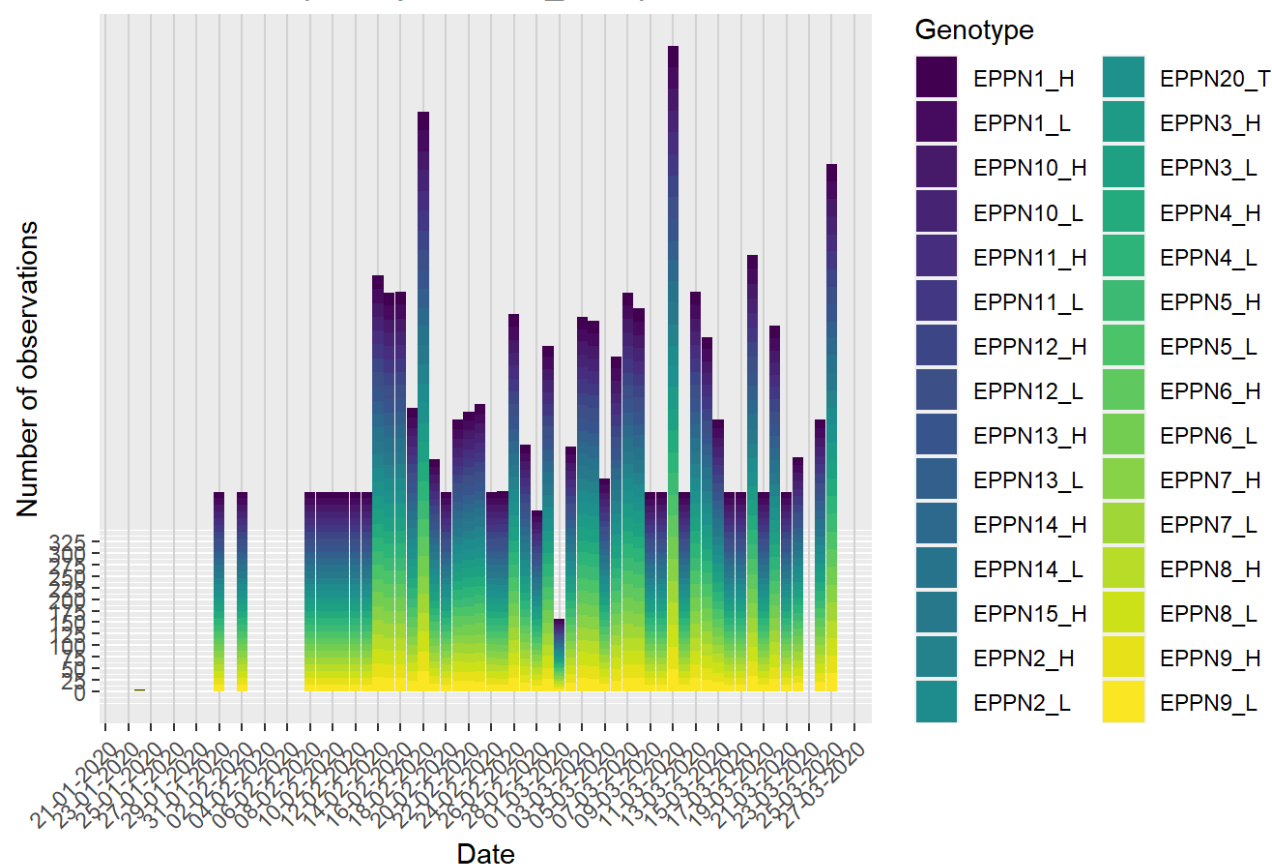
h4

Observations per day for Plant\_emergence



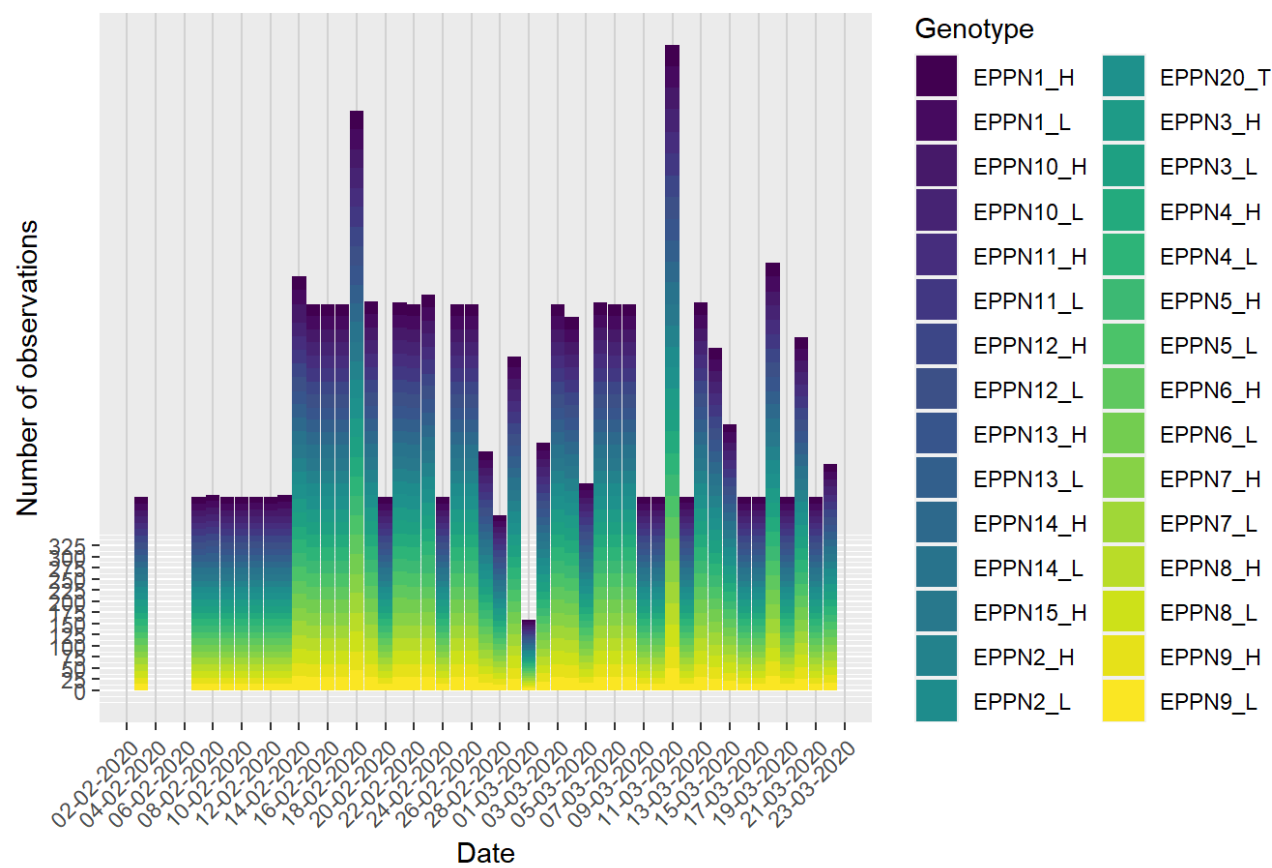
h5

Observations per day for Plant\_transpiration



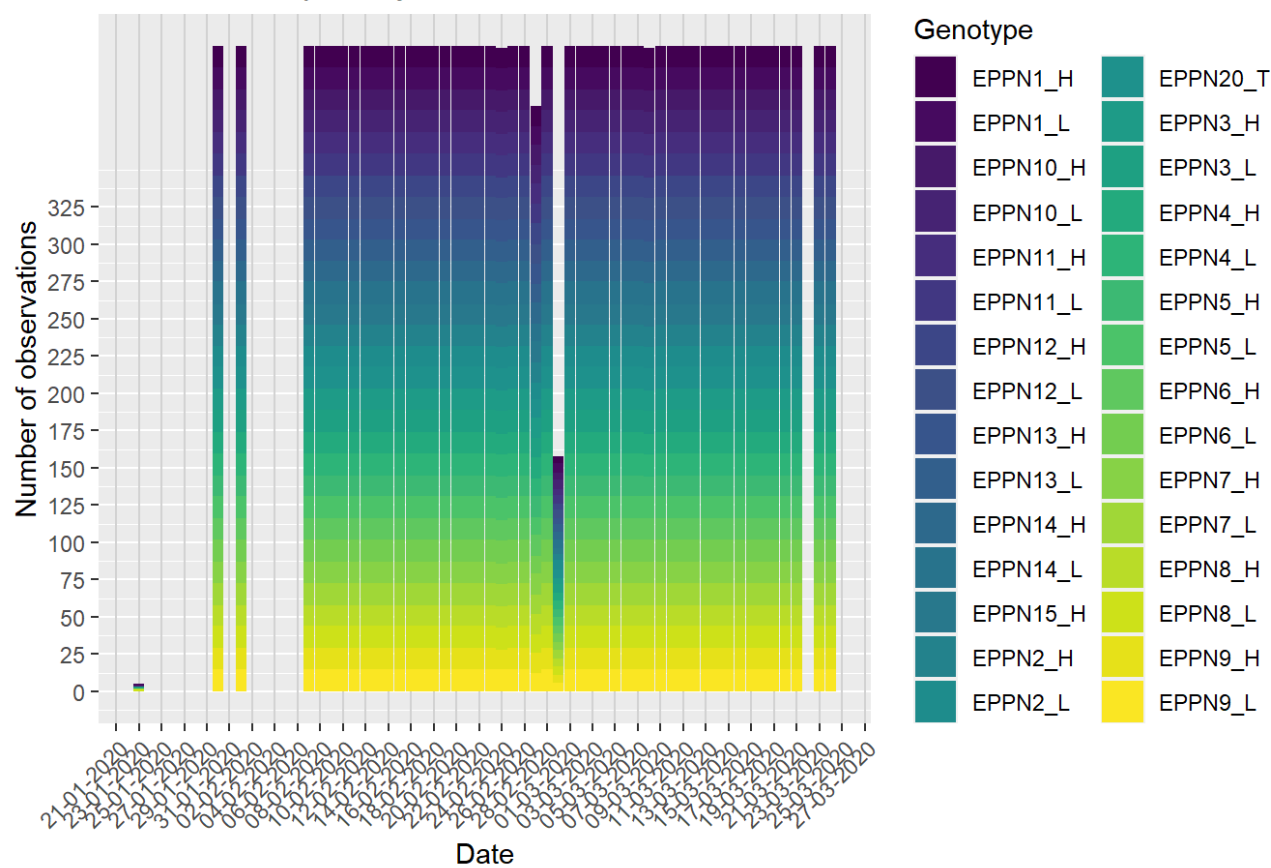
h6

Observations per day for Soil\_water\_potential



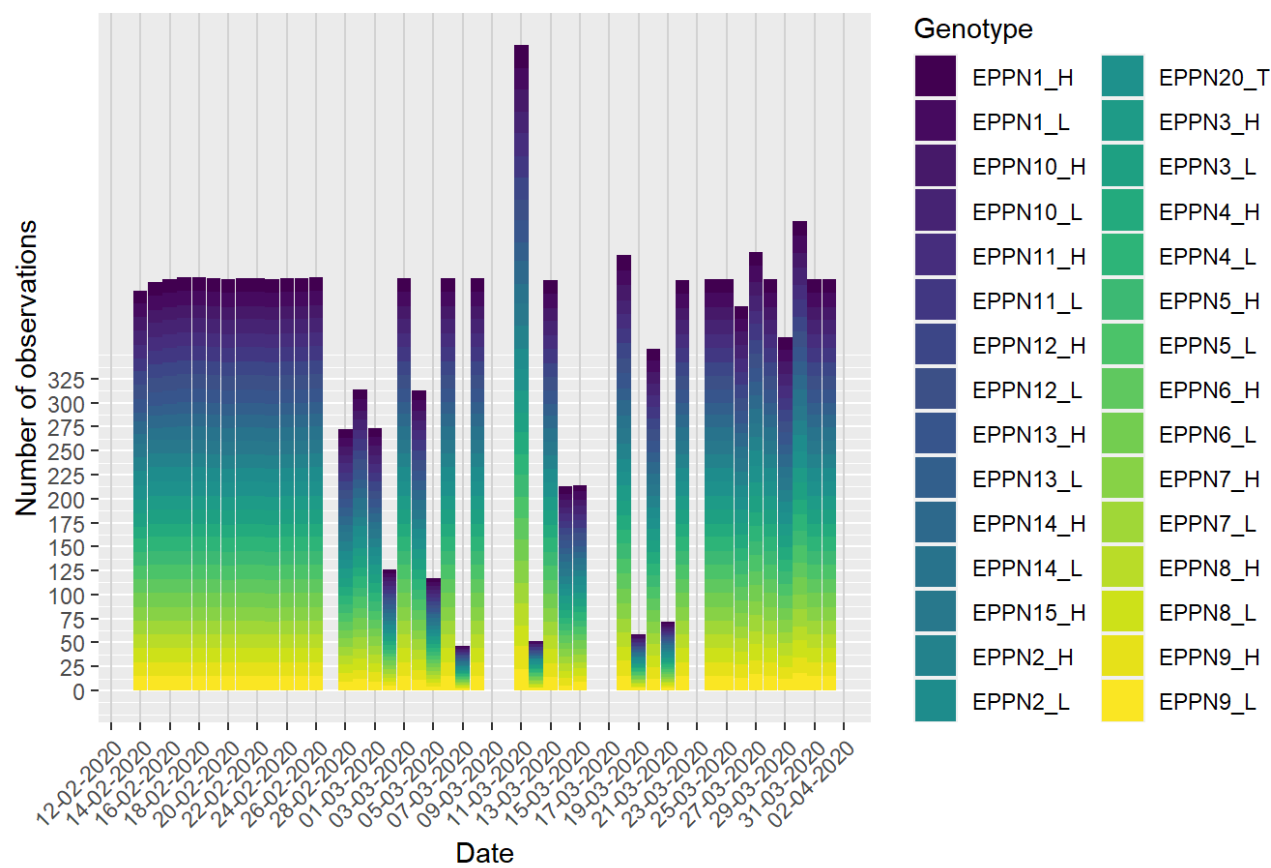
h7

Observations per day for Water



h8

Observations per day for S\_timeseries

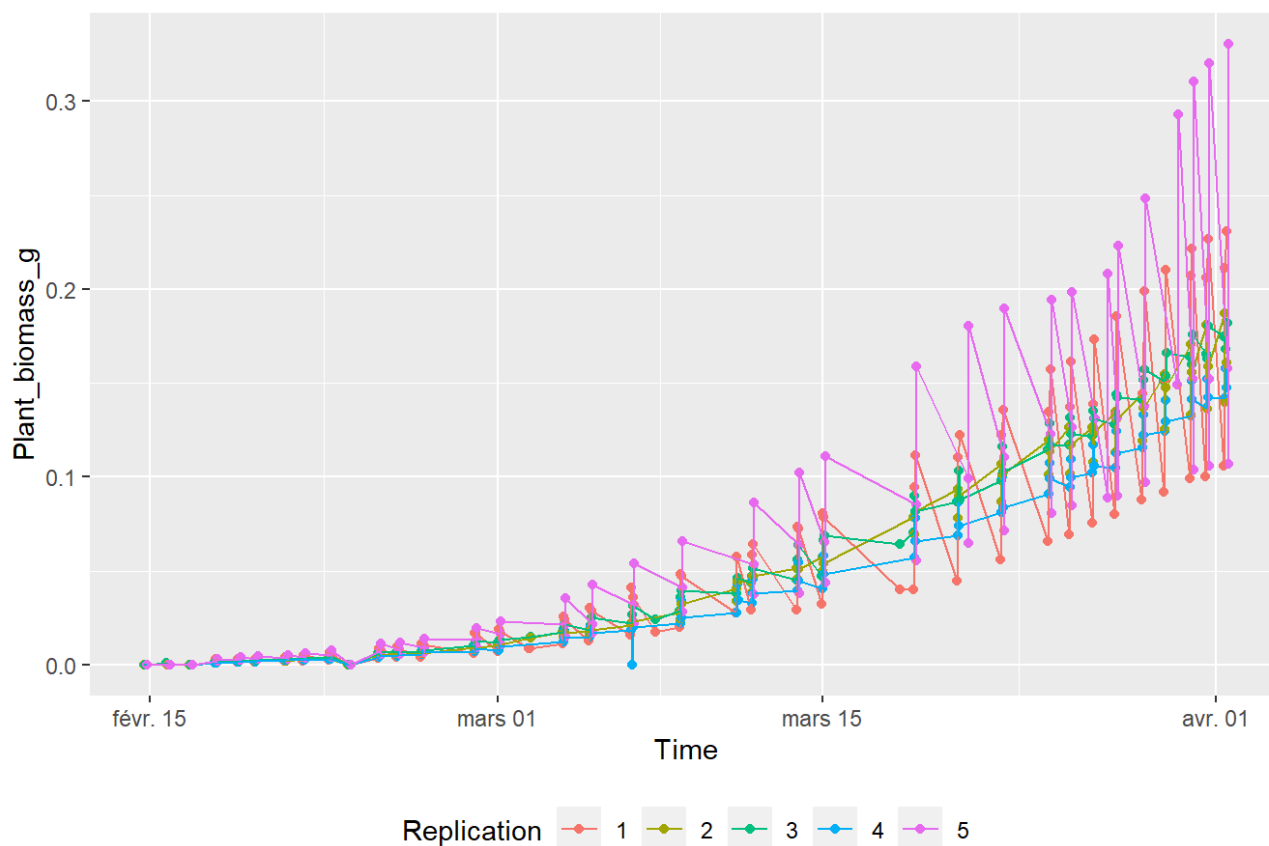


# A. Exploration of the timeseries dataframe

## Scatter plots by Genotype

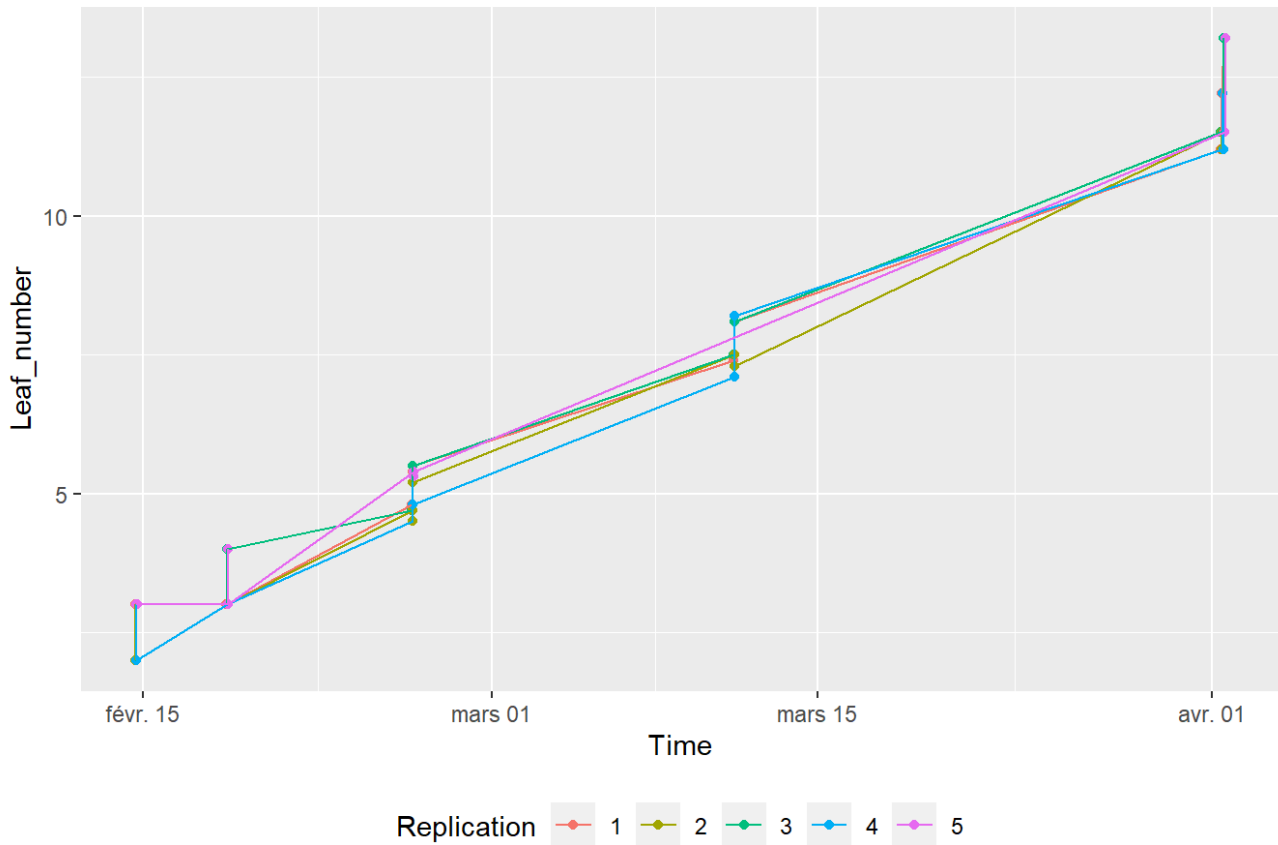
```
plot_scatter_by_genotype(timeseries, variables_t[1], "EPPN20_T")
```

Scatterplot of Plant\_biomass\_g for Genotype EPPN20\_T



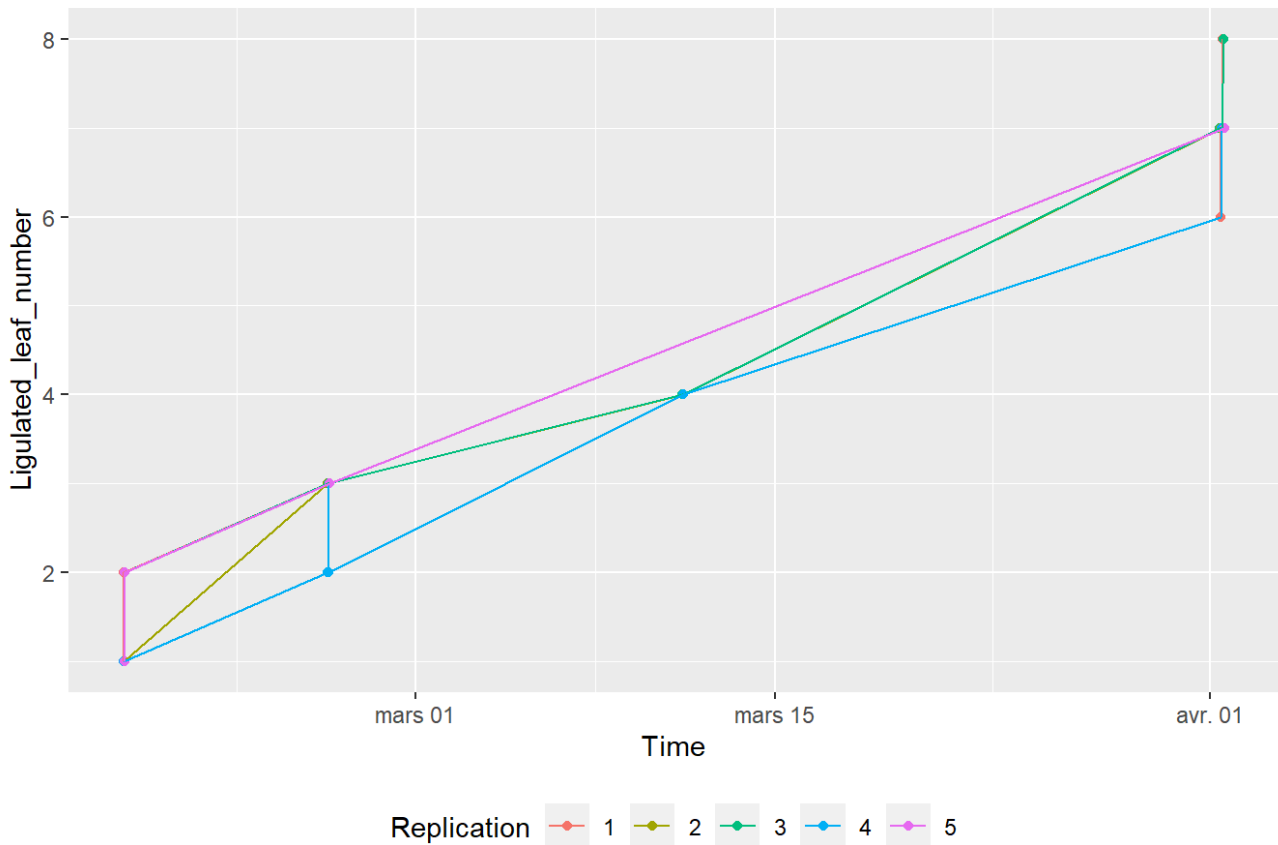
```
plot_scatter_by_genotype(timeseries_Leaf_number, variables_t[2], "EPPN20_T")
```

Scatterplot of Leaf\_number for Genotype EPPN20\_T



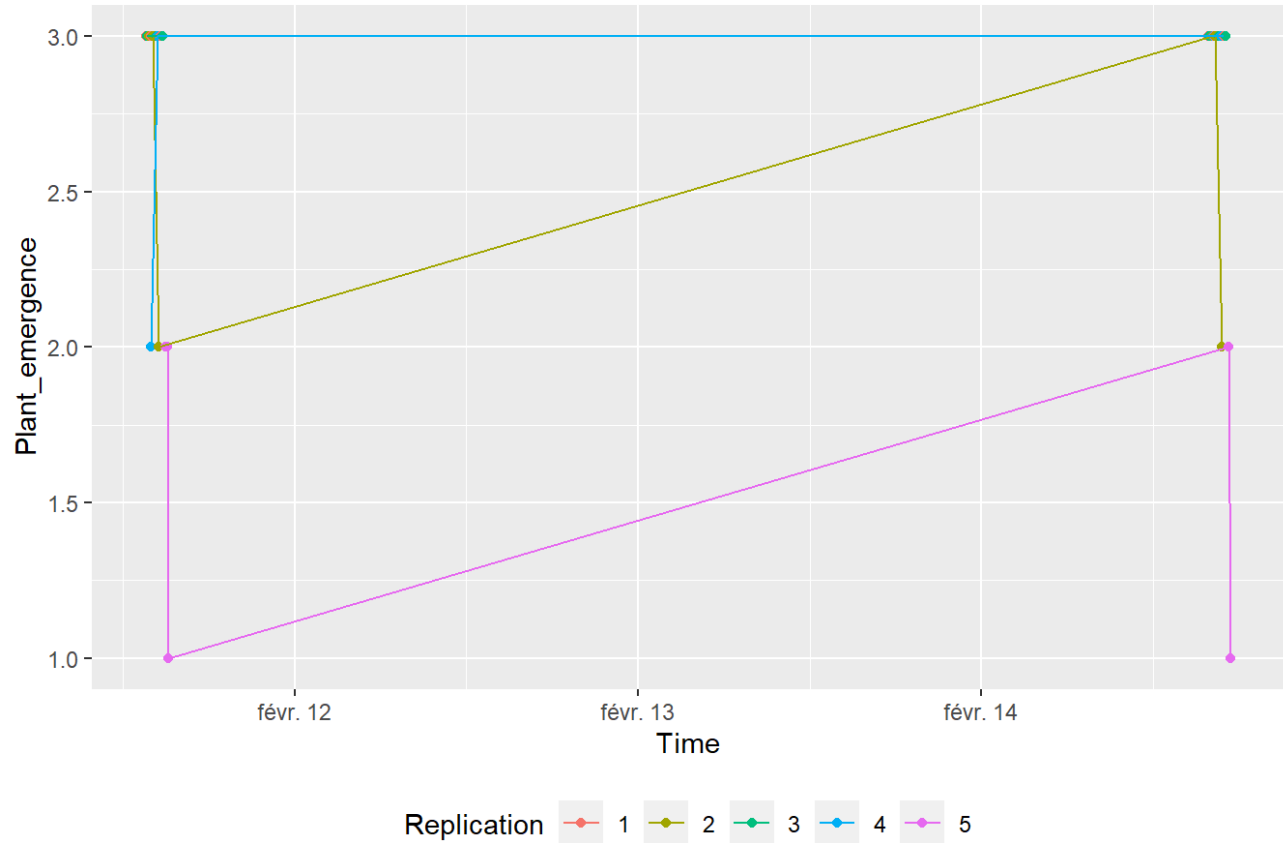
```
plot_scatter_by_genotype(timeseries_Ligulated_leaf_number, variables_t[3], "EPPN20_T")
```

Scatterplot of Ligulated\_leaf\_number for Genotype EPPN20\_T



```
plot_scatter_by_genotype(timeseries_Plant_emergence, variables_t[4], "EPPN20_T")
```

Scatterplot of Plant\_emergence for Genotype EPPN20\_T



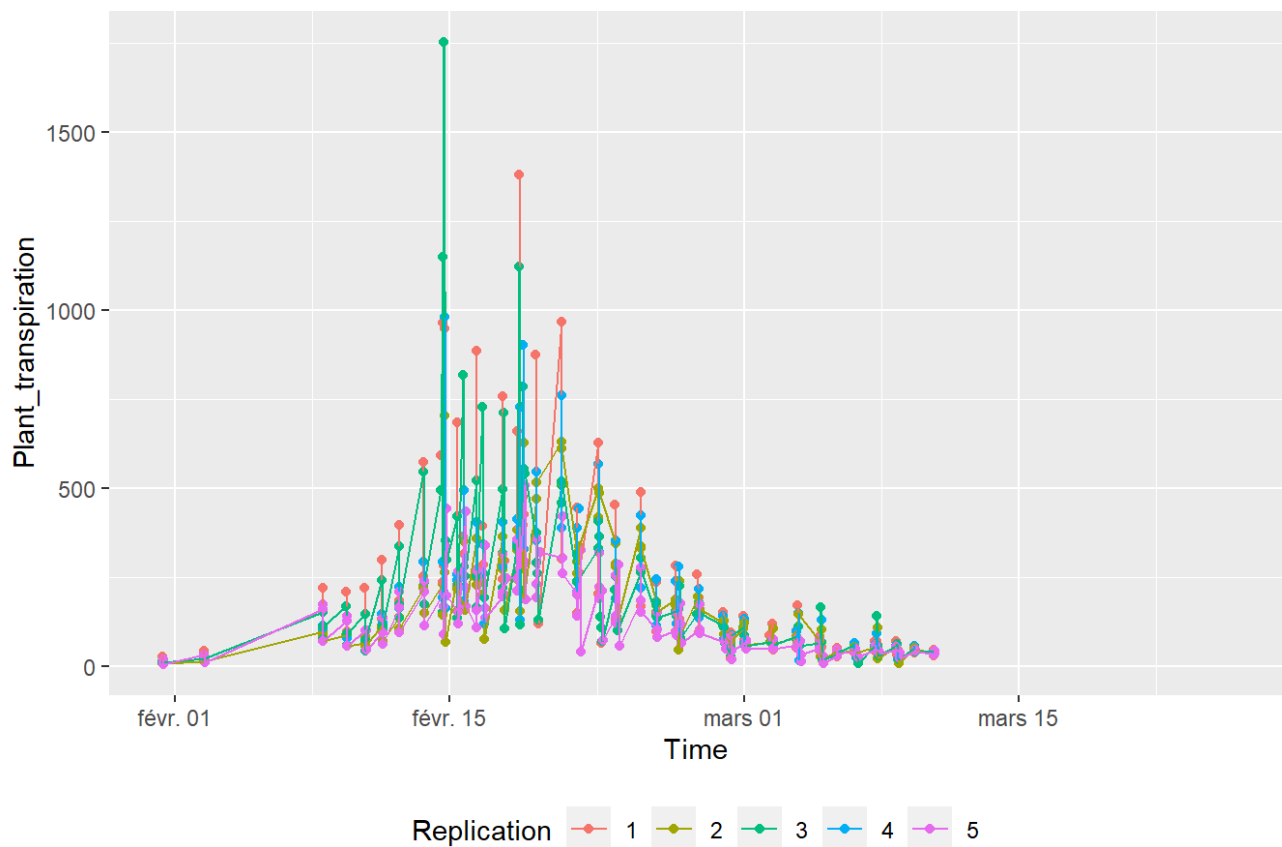
```
plot_scatter_by_genotype(timeseries_Plant_transpiration, variables_t[5], "EPPN20_T")
```

```
## Warning: Removed 433 rows containing missing values (`geom_point()`).
```

```
## Warning: Removed 337 rows containing missing values (`geom_line()`).
```

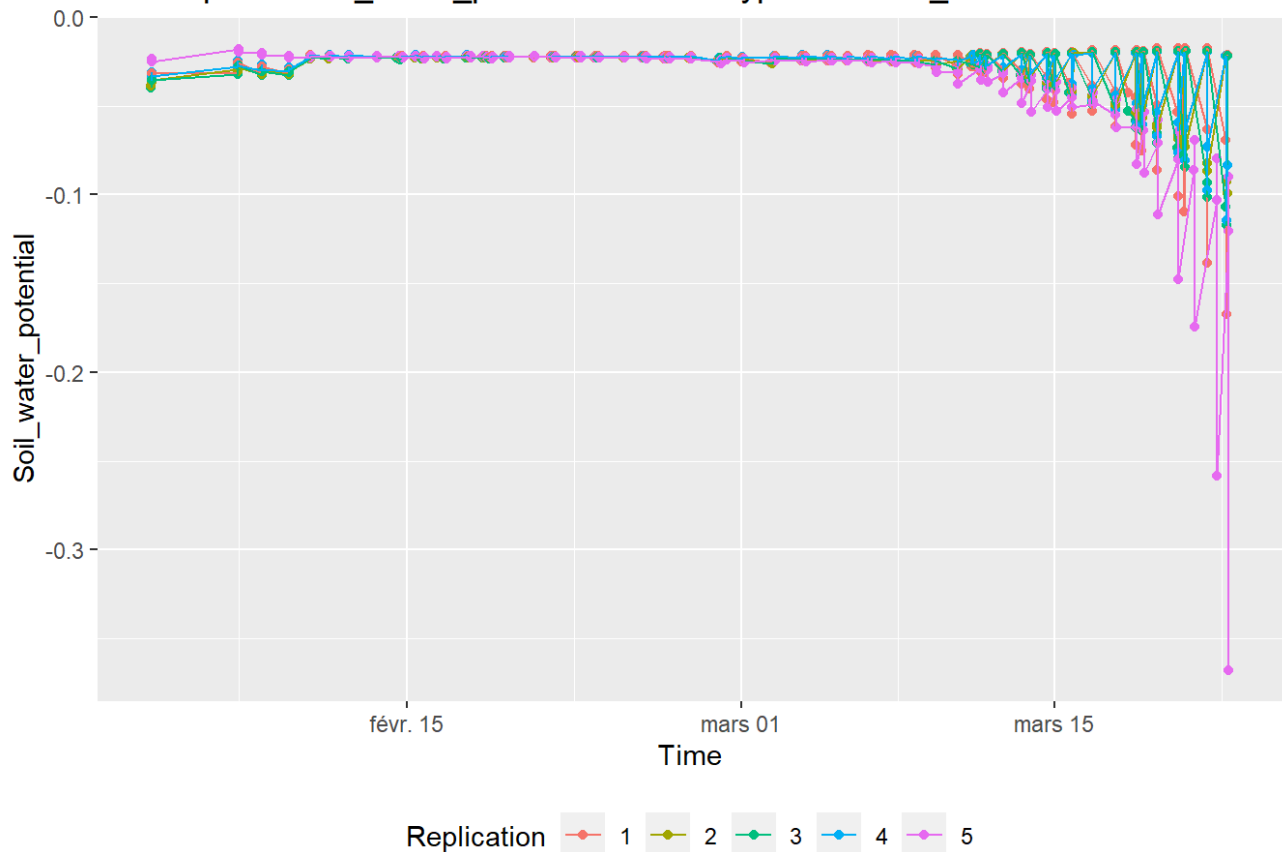


## Scatterplot of Plant\_transpiration for Genotype EPPN20\_T



```
plot_scatter_by_genotype(timeseries_Soil_water_potential, variables_t[6], "EPPN20_T")
```

## Scatterplot of Soil\_water\_potential for Genotype EPPN20\_T



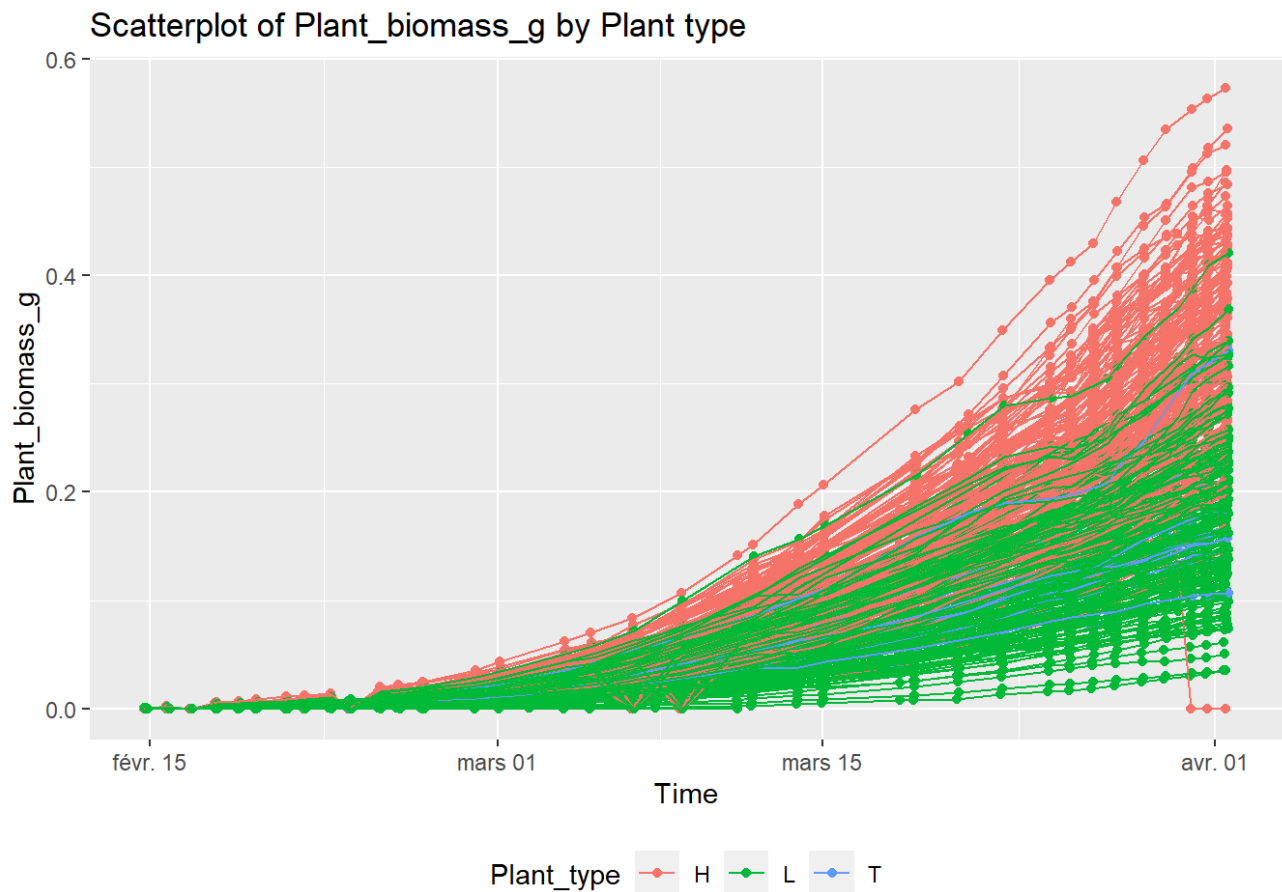
```
# Problem for water timeseries data
```

Scatterplots for all genotypes by Plant type (Hybride, Line, EPPN20\_T) with smooth line.

```
plot_scatter_with_smooth(timeseries, variables_t[1])
```

```
## Warning: Removed 1 rows containing missing values (`geom_point()`).
```

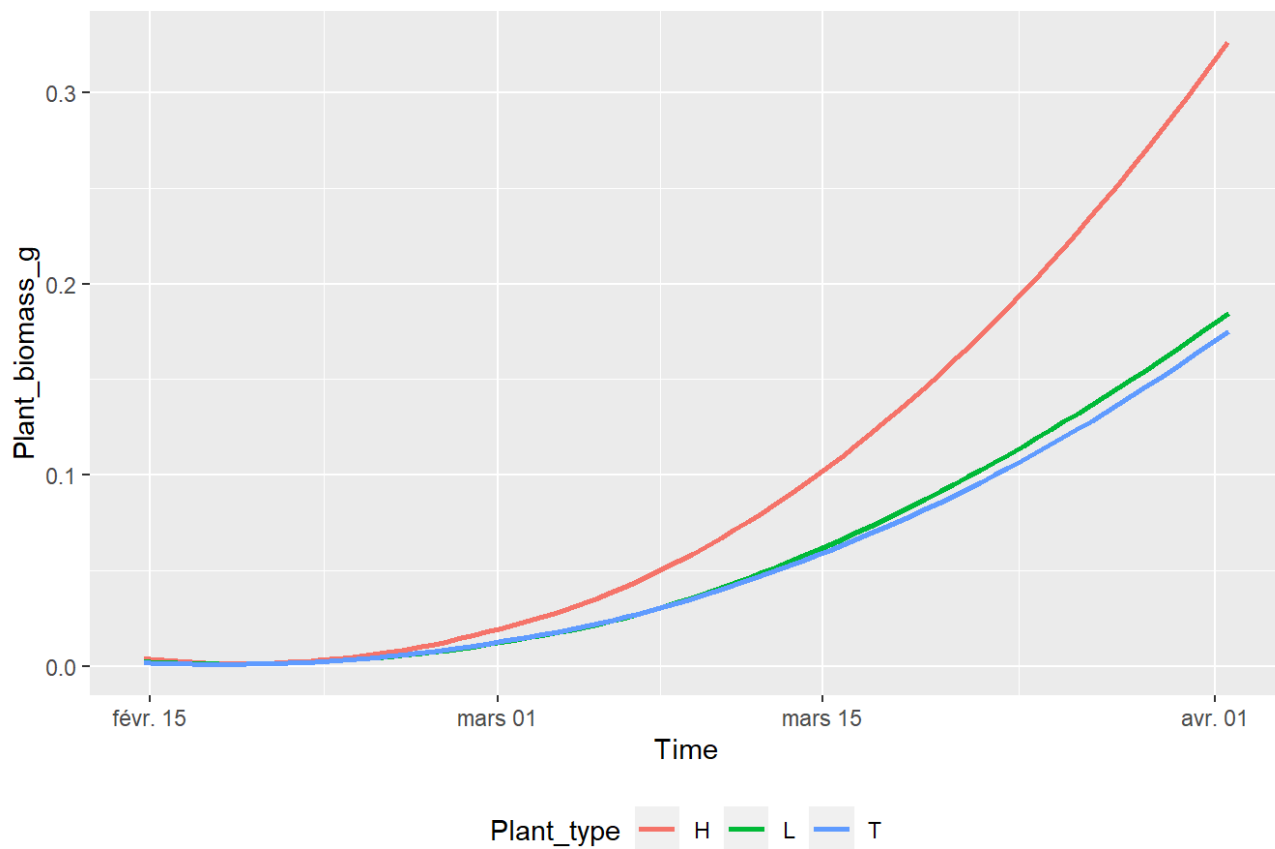
```
## Warning: Removed 1 row containing missing values (`geom_line()`).
```



```
## `geom_smooth()` using formula = 'y ~ x'
```

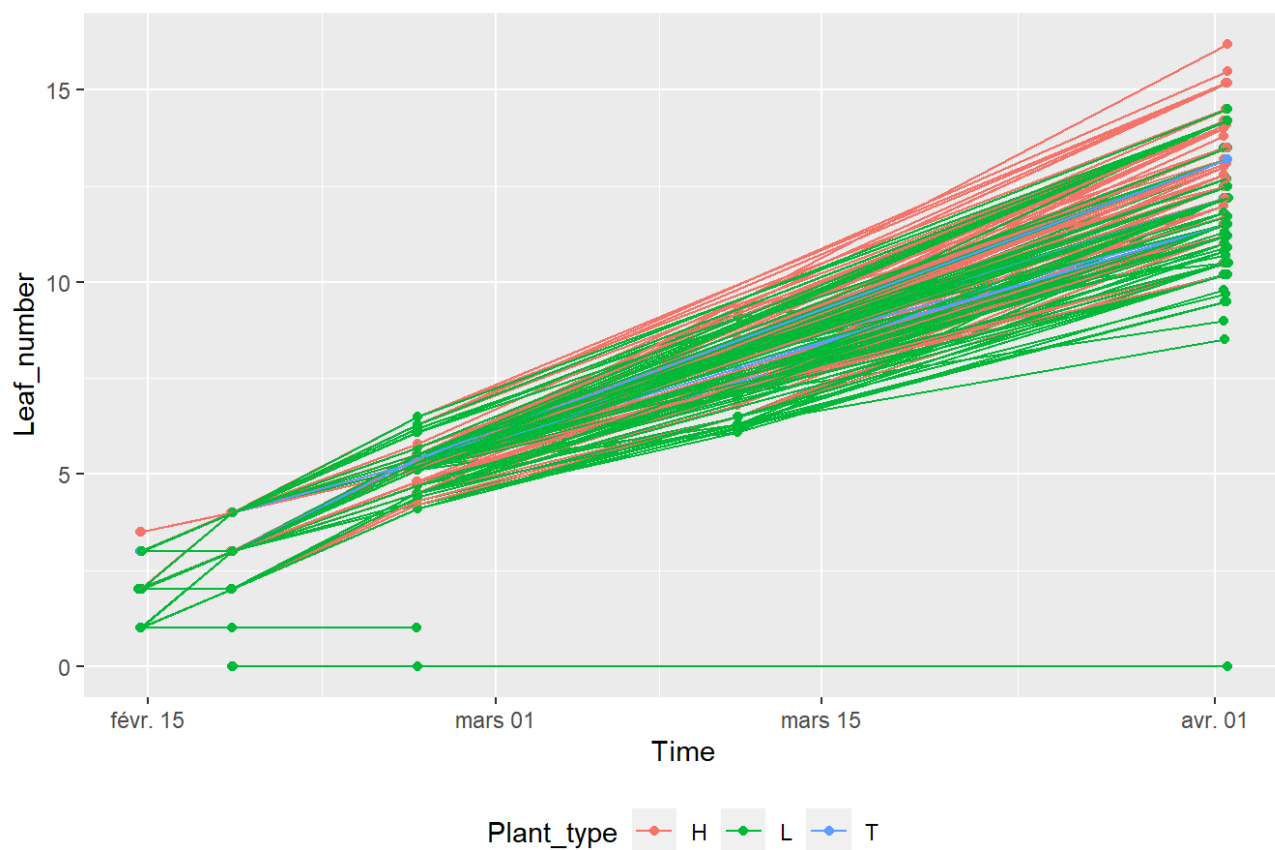
```
## Warning: Removed 1 rows containing non-finite values (`stat_smooth()`).
```

Smooth line of Plant\_biomass\_g by Plant type



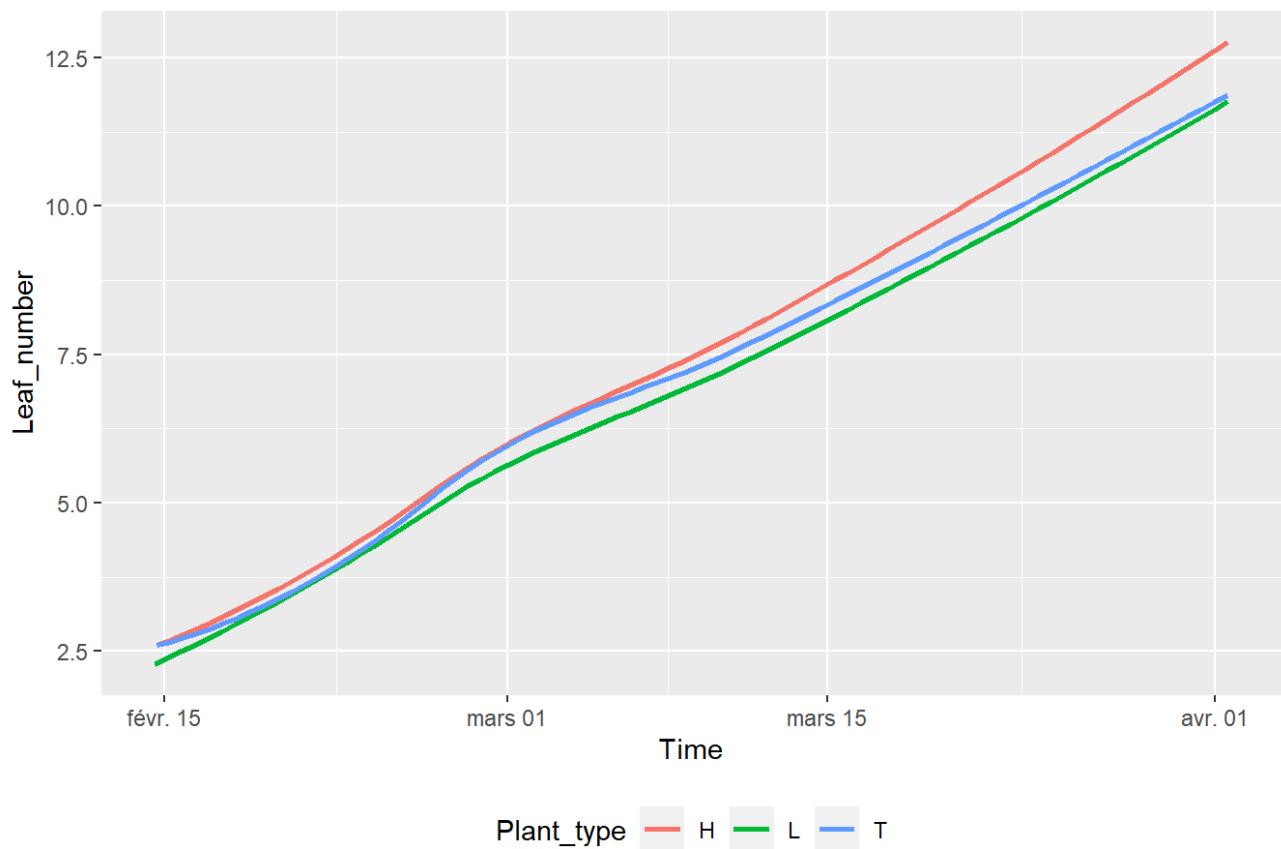
```
plot_scatter_with_smooth(timeseries_Leaf_number, variables_t[2])
```

Scatterplot of Leaf\_number by Plant type



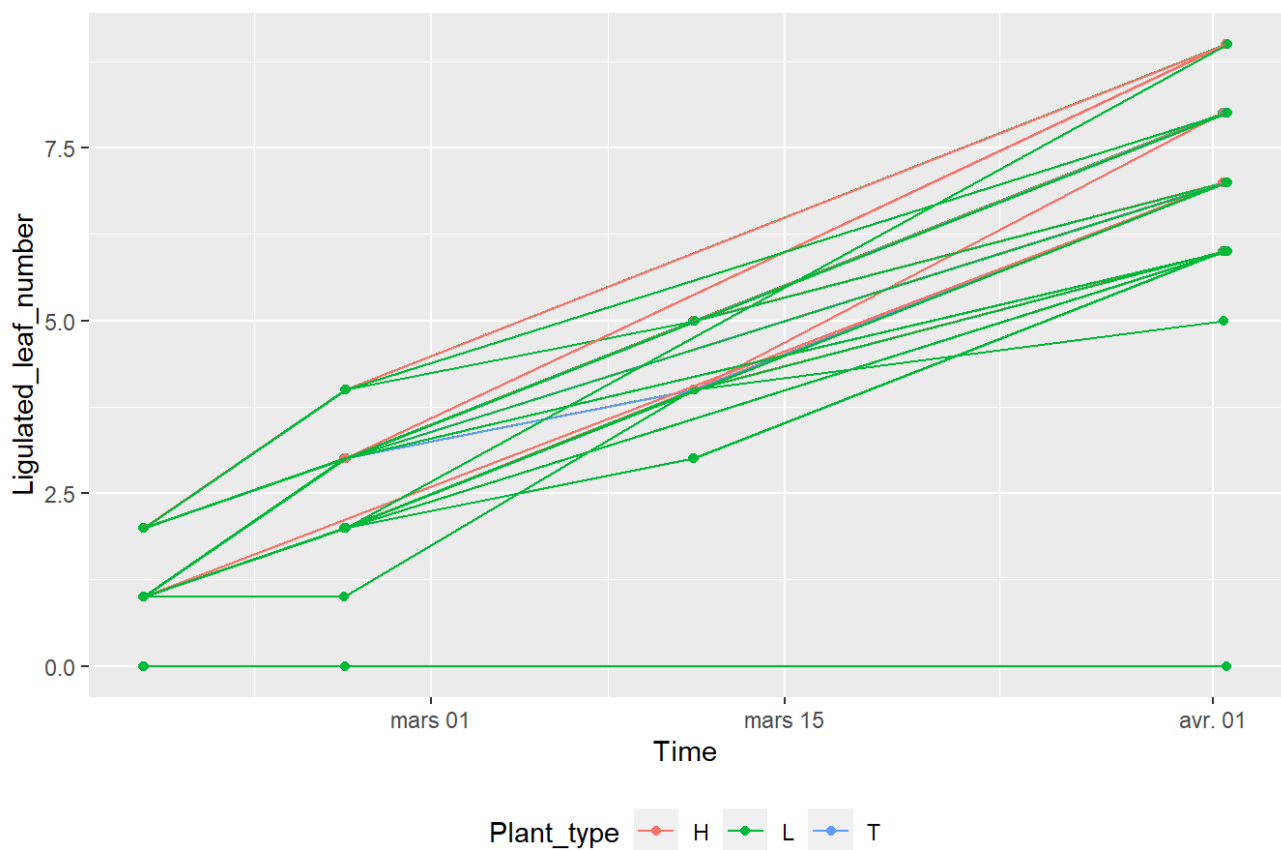
```
## `geom_smooth()` using formula = 'y ~ x'
```

Smooth line of Leaf\_number by Plant type



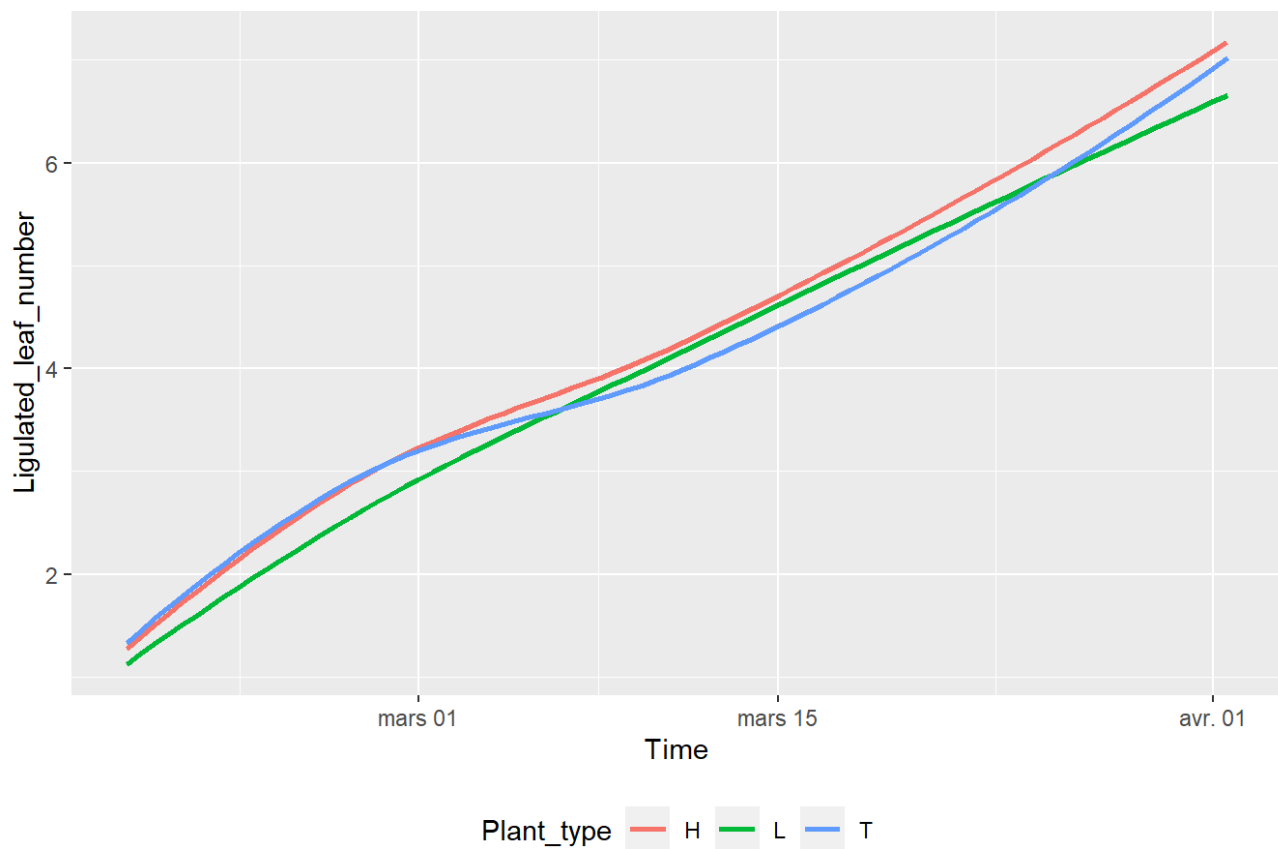
```
plot_scatter_with_smooth(timeseries_Ligulated_leaf_number, variables_t[3])
```

Scatterplot of Ligulated\_leaf\_number by Plant type



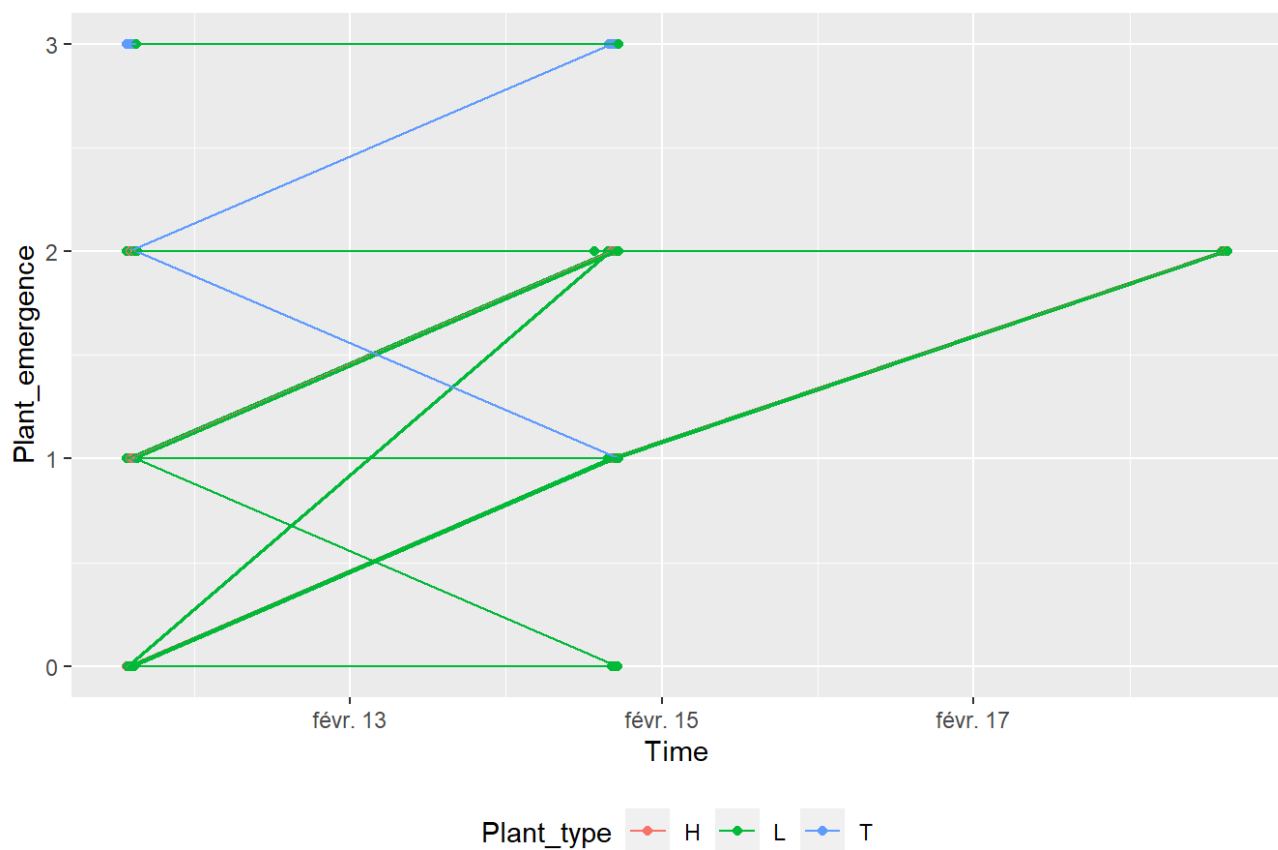
```
## `geom_smooth()` using formula = 'y ~ x'
```

Smooth line of Ligulated\_leaf\_number by Plant type



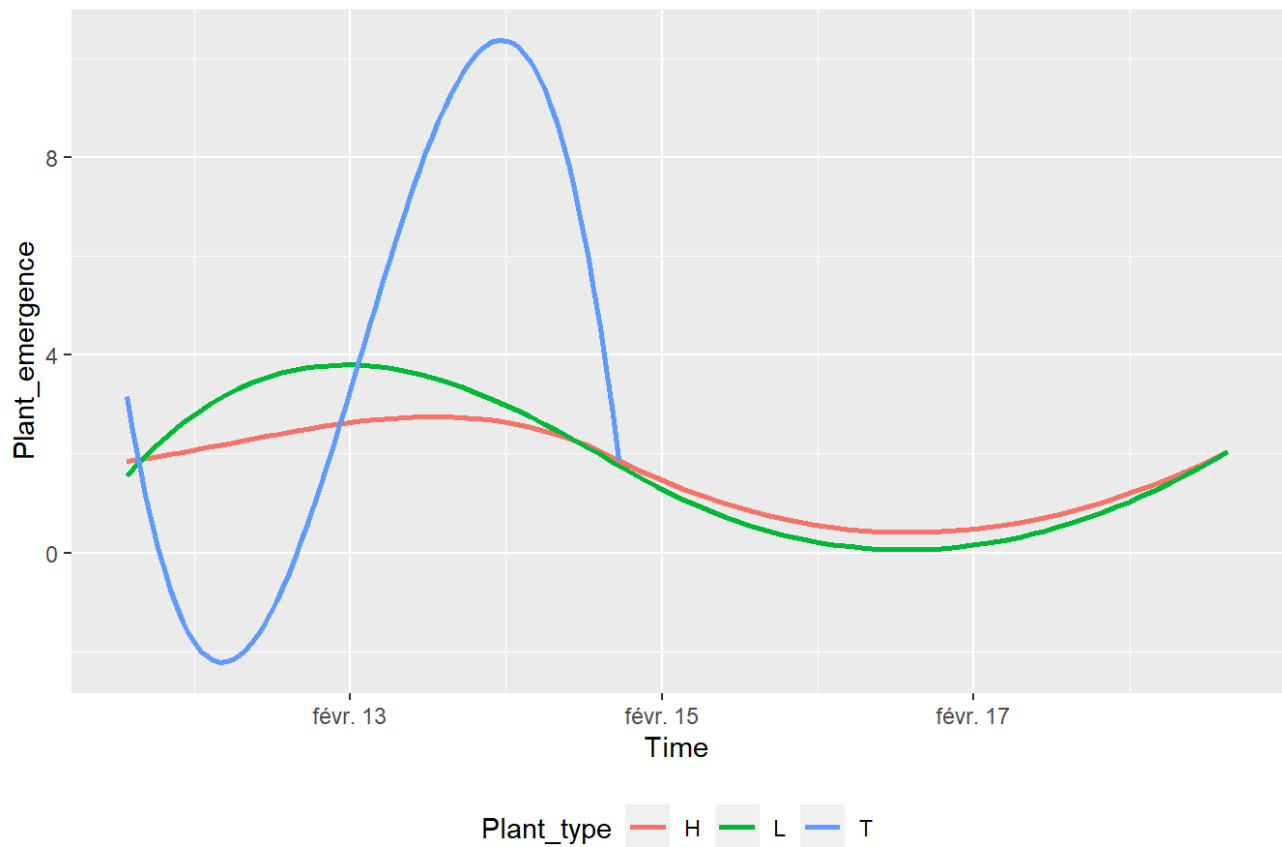
```
plot_scatter_with_smooth(timeseries_Plant_emergence, variables_t[4])
```

Scatterplot of Plant\_emergence by Plant type



```
## `geom_smooth()` using formula = 'y ~ x'
```

Smooth line of Plant\_emergence by Plant type

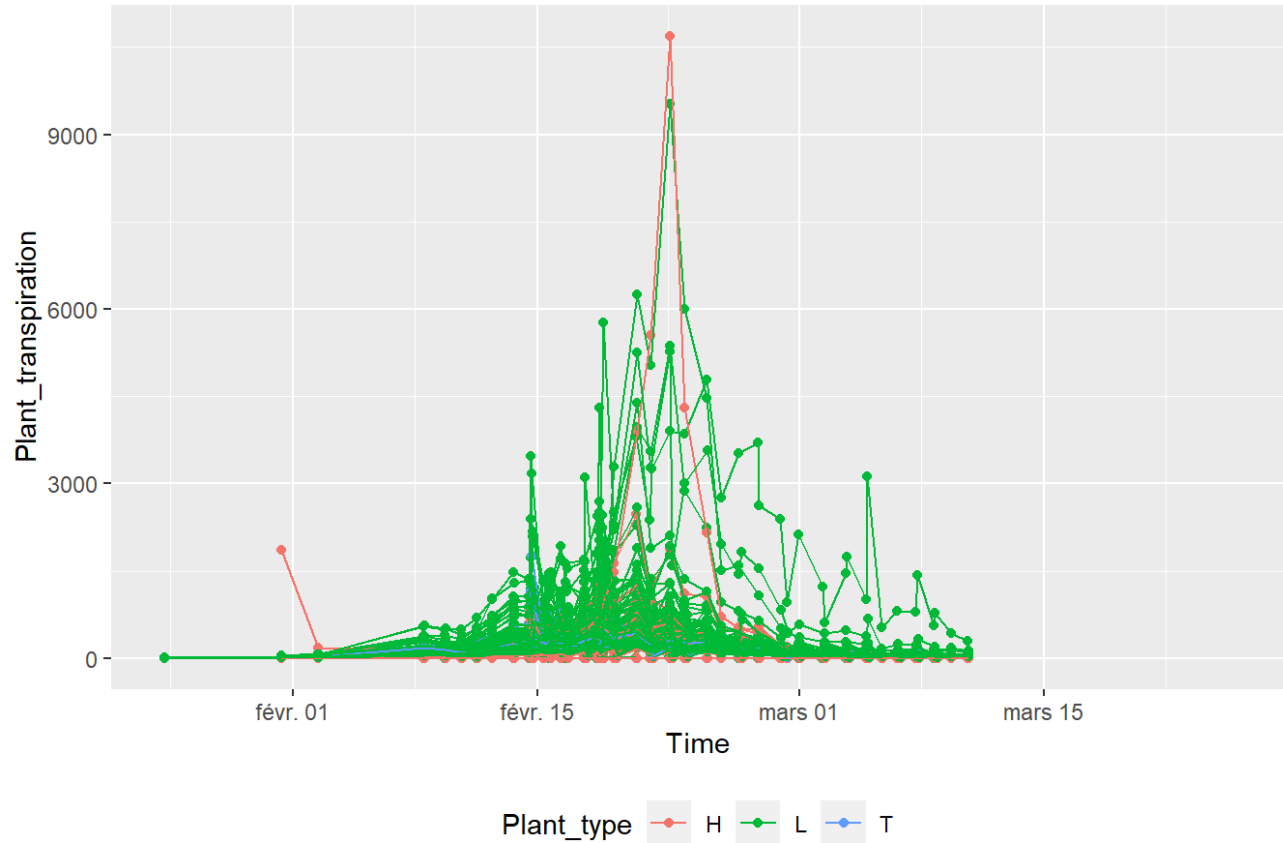


```
plot_scatter_with_smooth(timeseries_Plant_transpiration, variables_t[5])
```

```
## Warning: Removed 13341 rows containing missing values (`geom_point()`).
```

```
## Warning: Removed 13341 rows containing missing values (`geom_line()`).
```

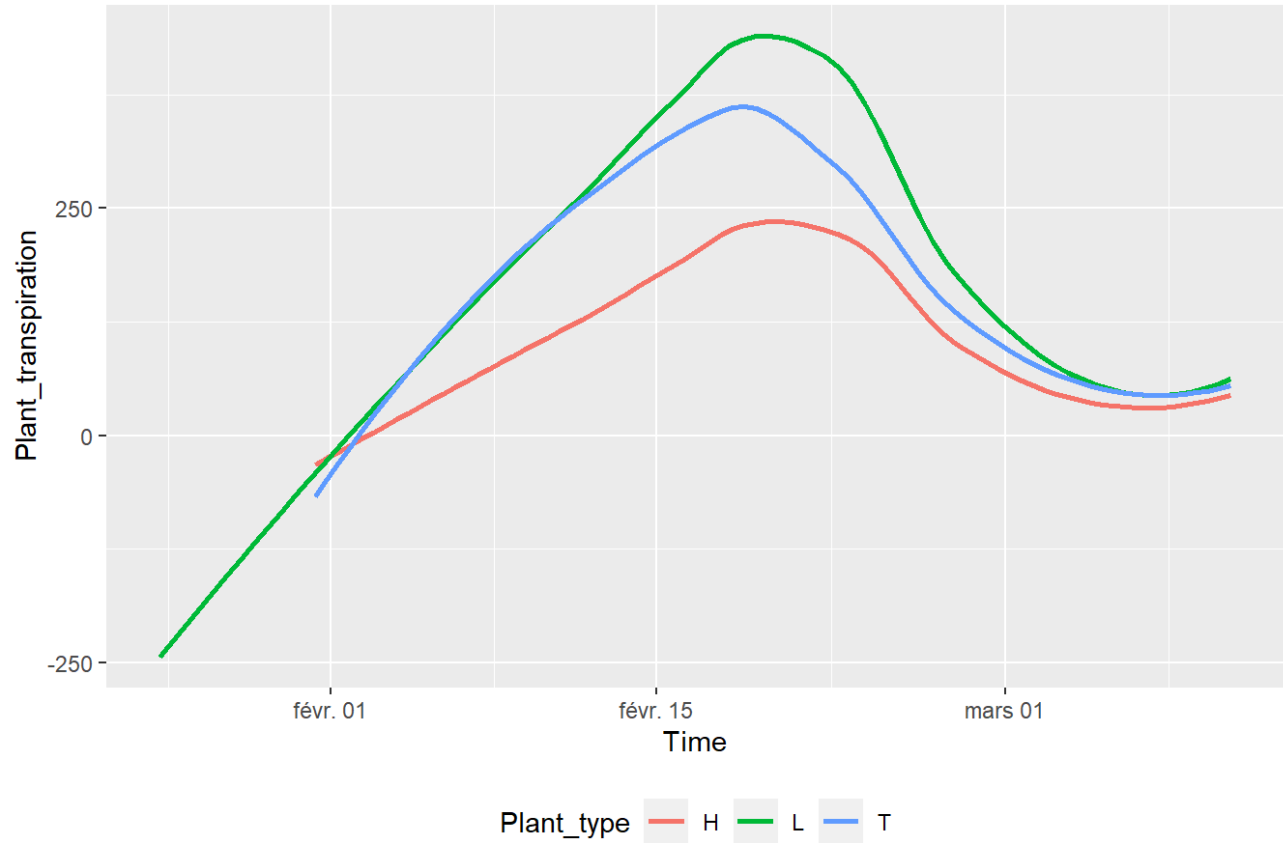
Scatterplot of Plant\_transpiration by Plant type



```
## `geom_smooth()` using formula = 'y ~ x'
```

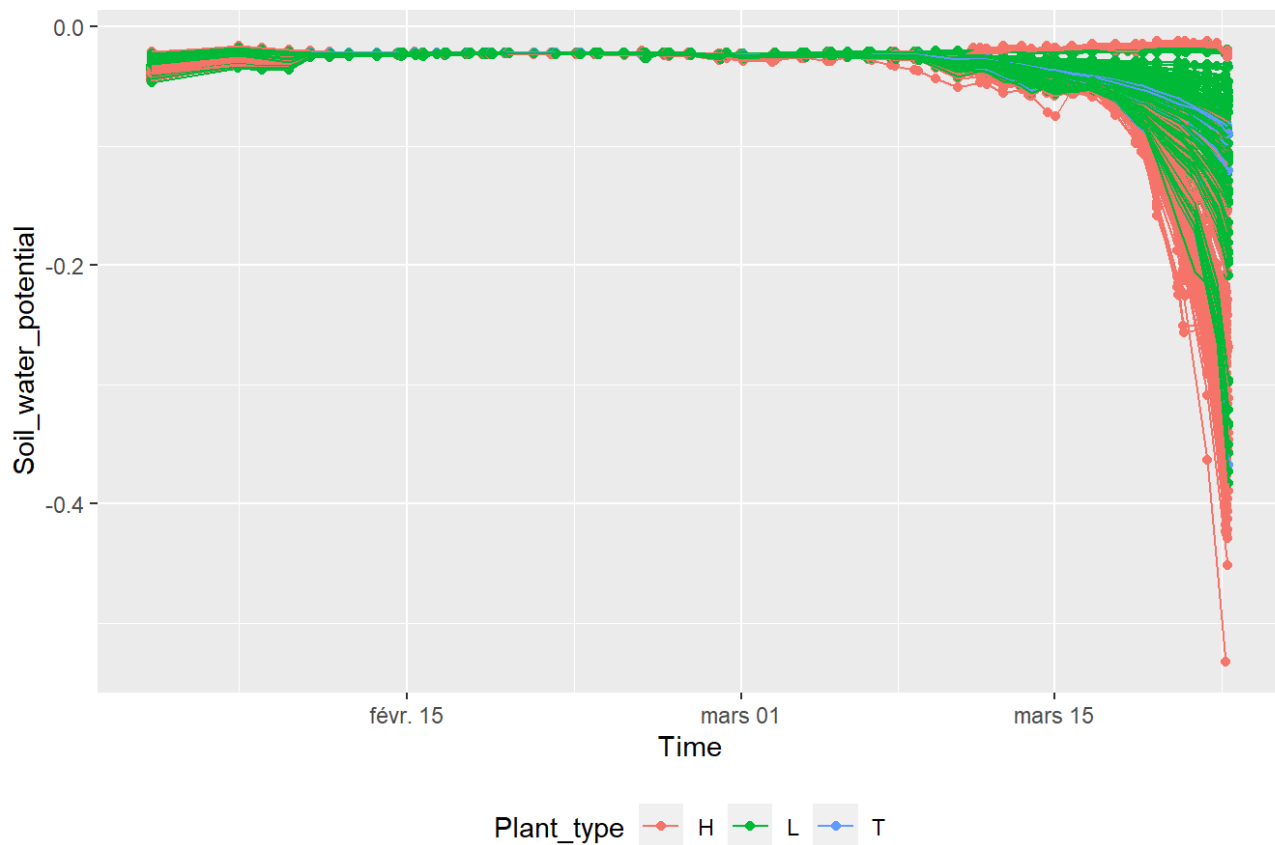
```
## Warning: Removed 13341 rows containing non-finite values (`stat_smooth()`).
```

Smooth line of Plant\_transpiration by Plant type



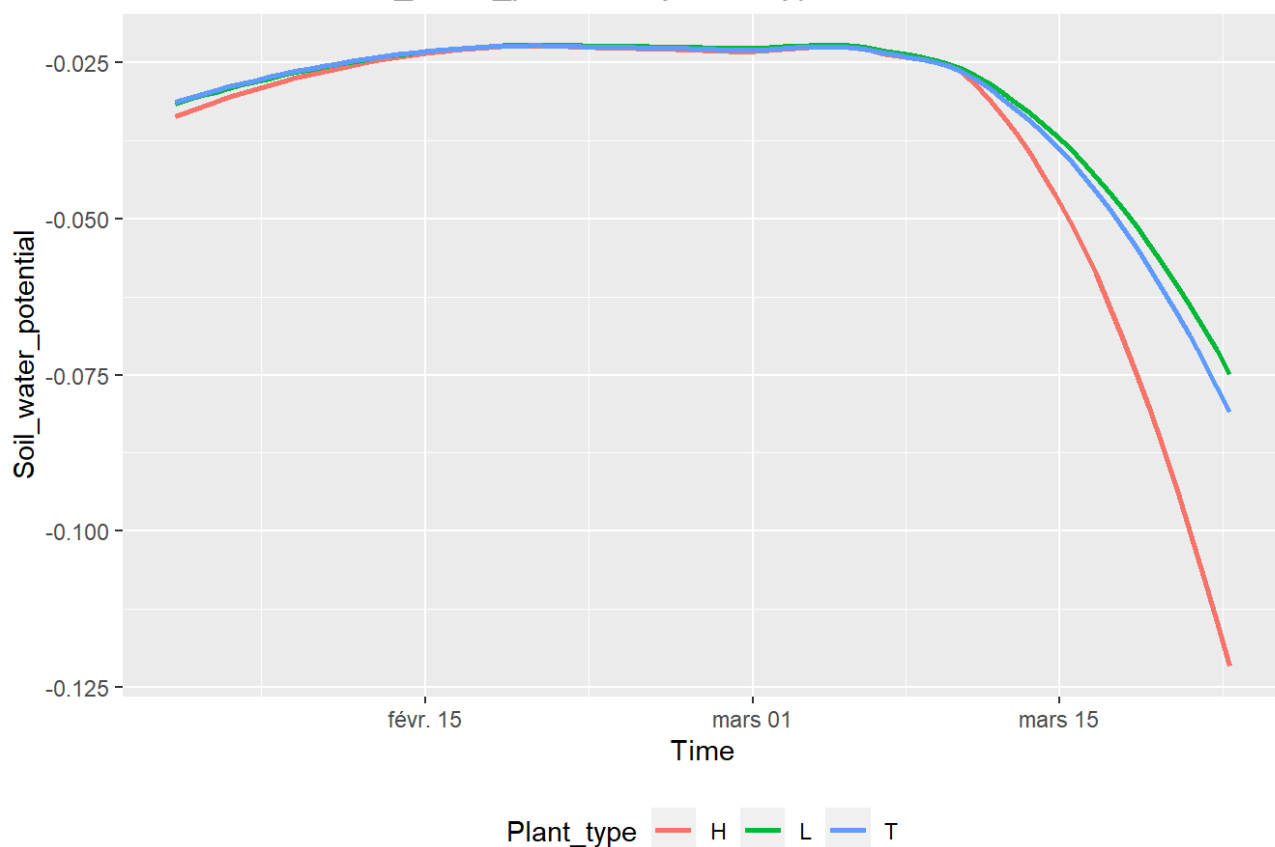
```
plot_scatter_with_smooth(timeseries_Soil_water_potential, variables_t[6])
```

### Scatterplot of Soil\_water\_potential by Plant type



```
## `geom_smooth()` using formula = 'y ~ x'
```

### Smooth line of Soil\_water\_potential by Plant type





```
# Problem for water timeseries data
```

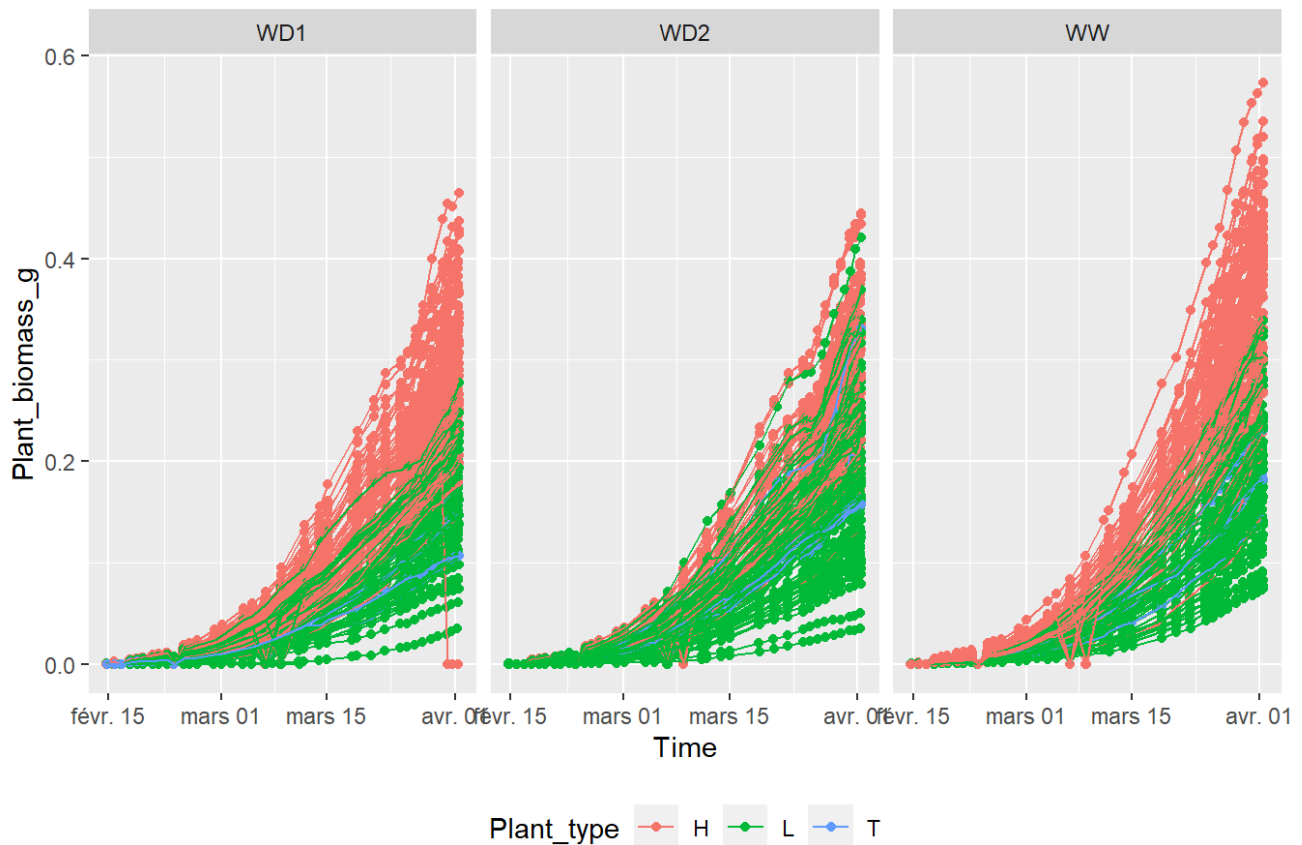
Scatter plots for all genotypes by water treatment

```
plot_scatter_with_smooth_water(timeseries, variables_t[1])
```

```
## Warning: Removed 1 rows containing missing values (`geom_point()`).
```

```
## Warning: Removed 1 row containing missing values (`geom_line()`).
```

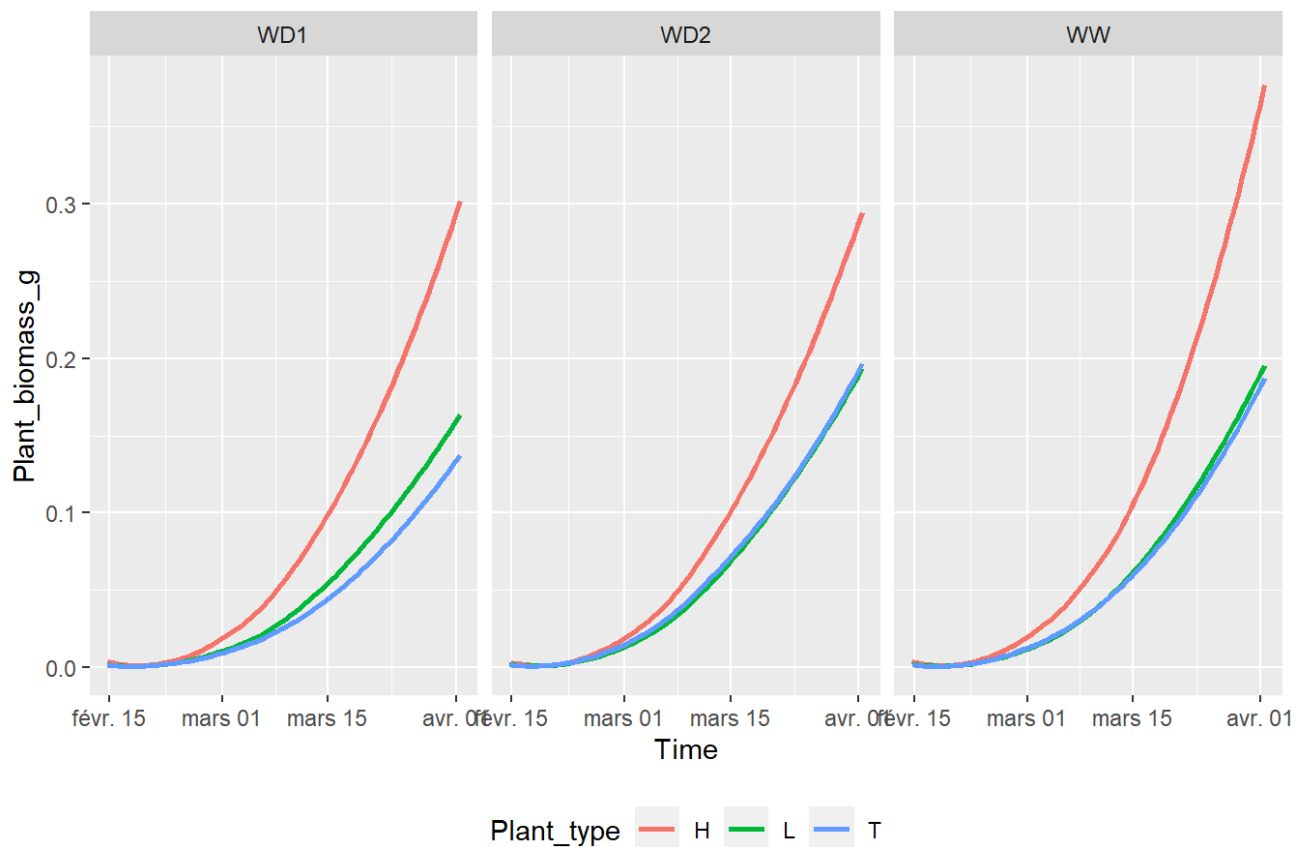
Scatterplot of Plant\_biomass\_g by Plant type and Soil



```
## `geom_smooth()` using formula = 'y ~ x'
```

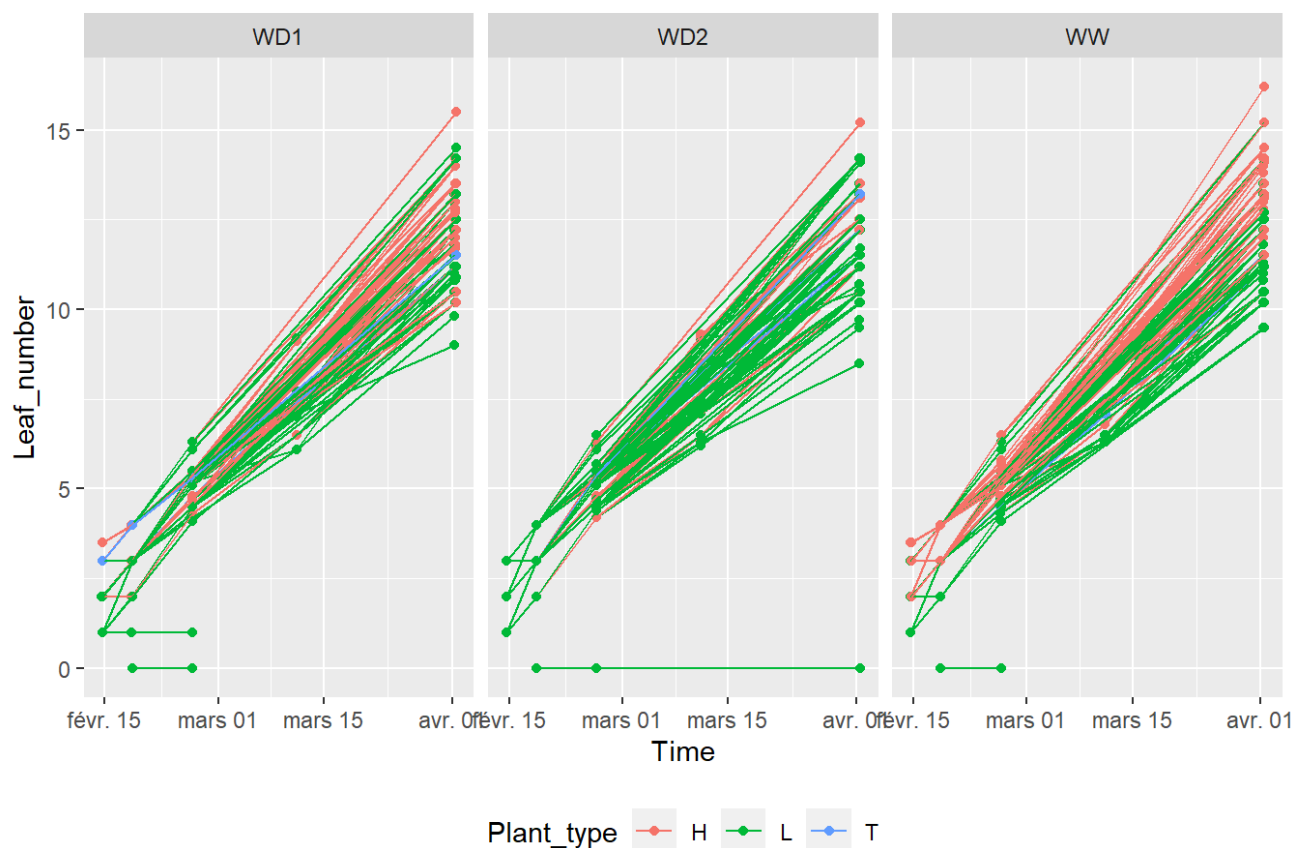
```
## Warning: Removed 1 rows containing non-finite values (`stat_smooth()`).
```

Smooth line of Plant\_biomass\_g by Plant type and Soil



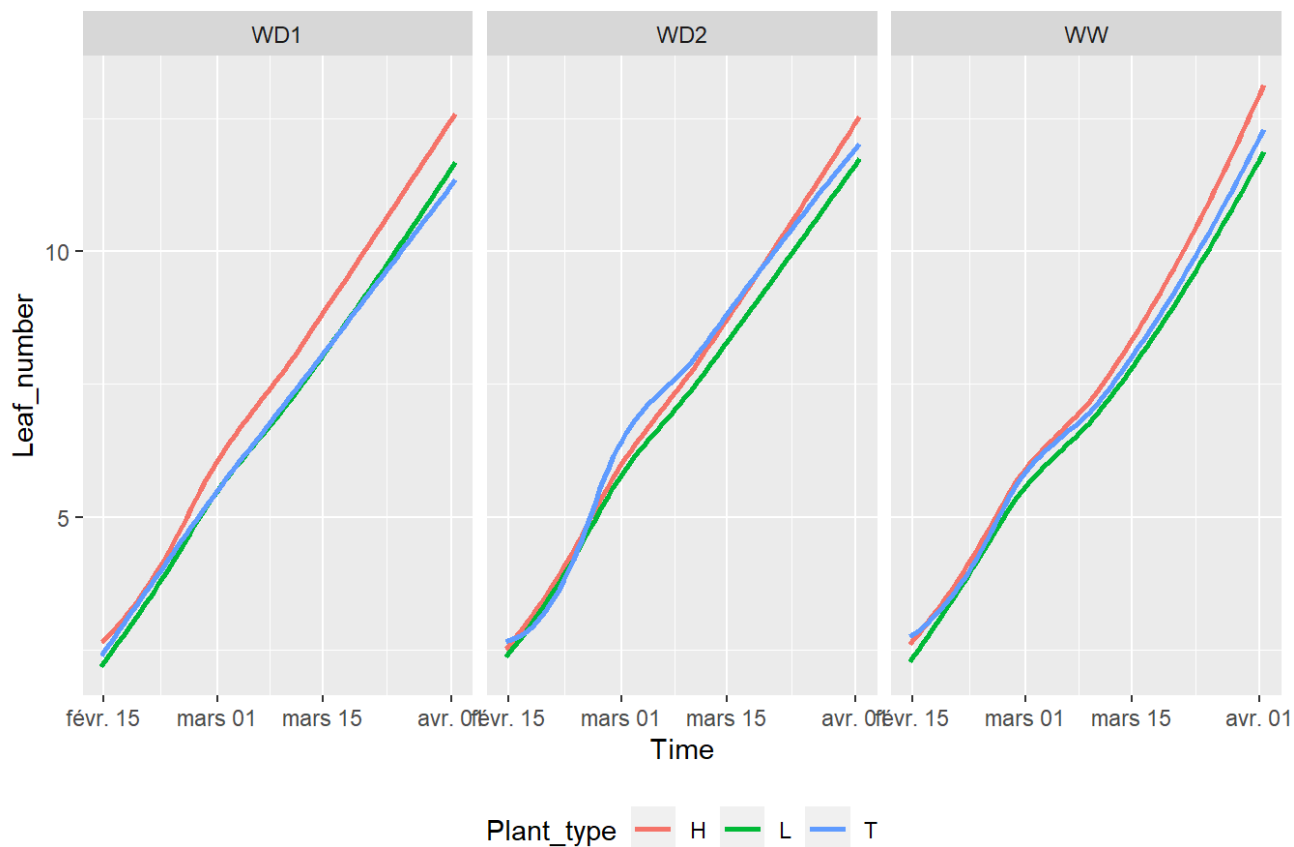
```
plot_scatter_with_smooth_water(timeseries_Leaf_number, variables_t[2])
```

Scatterplot of Leaf\_number by Plant type and Soil



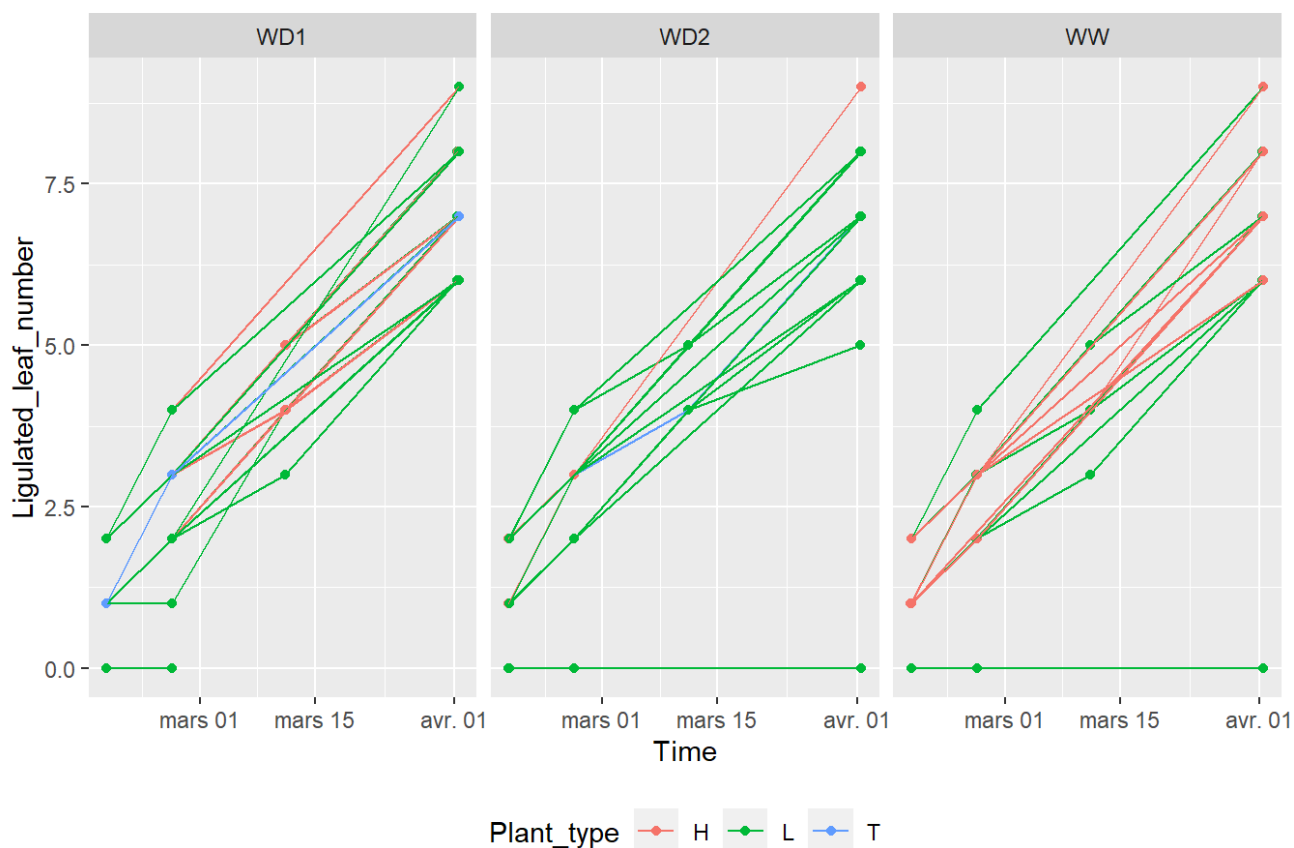
```
## `geom_smooth()` using formula = 'y ~ x'
```

## Smooth line of Leaf\_number by Plant type and Soil



```
plot_scatter_with_smooth_water(timeseries_Ligulated_leaf_number, variables_t[3])
```

## Scatterplot of Ligulated\_leaf\_number by Plant type and Soil



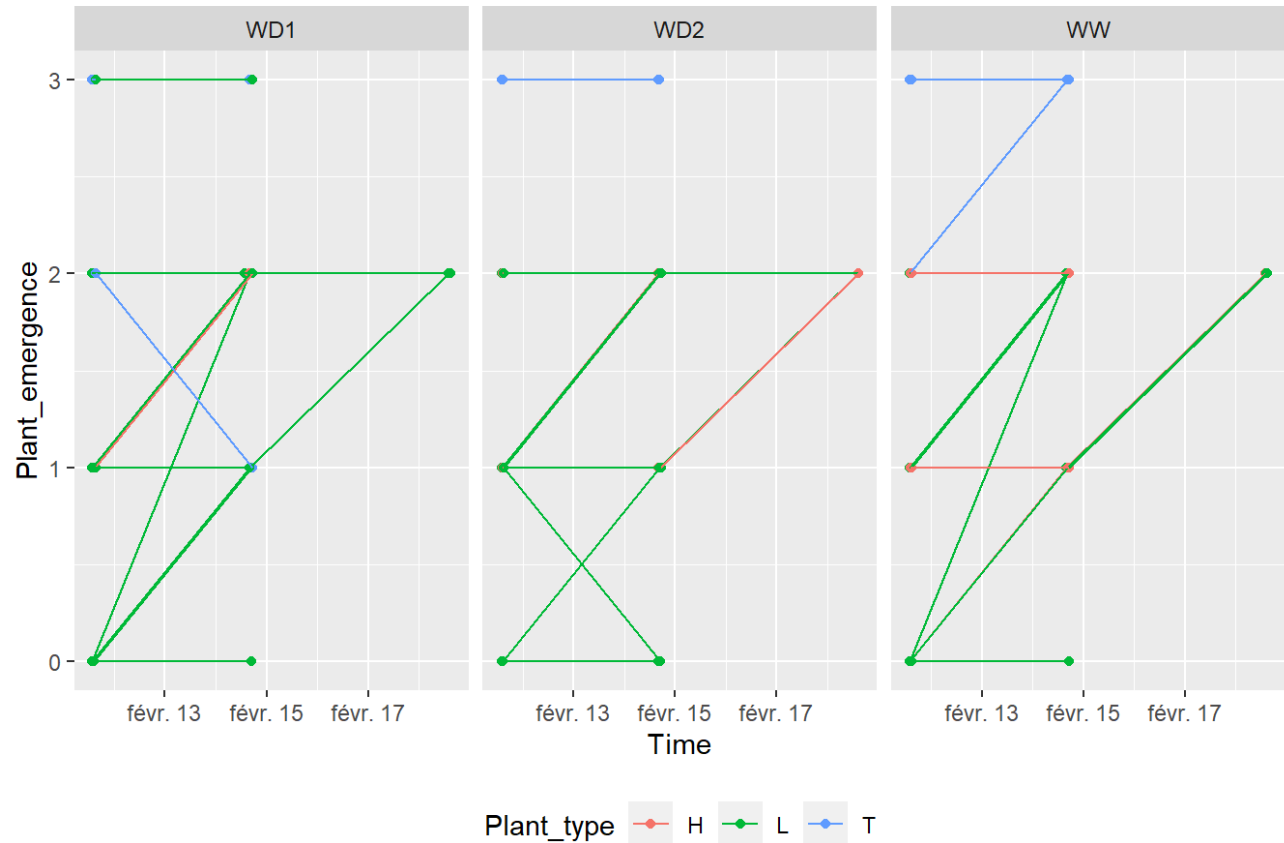
```
## `geom_smooth()` using formula = 'y ~ x'
```

Smooth line of Ligulated\_leaf\_number by Plant type and Soil



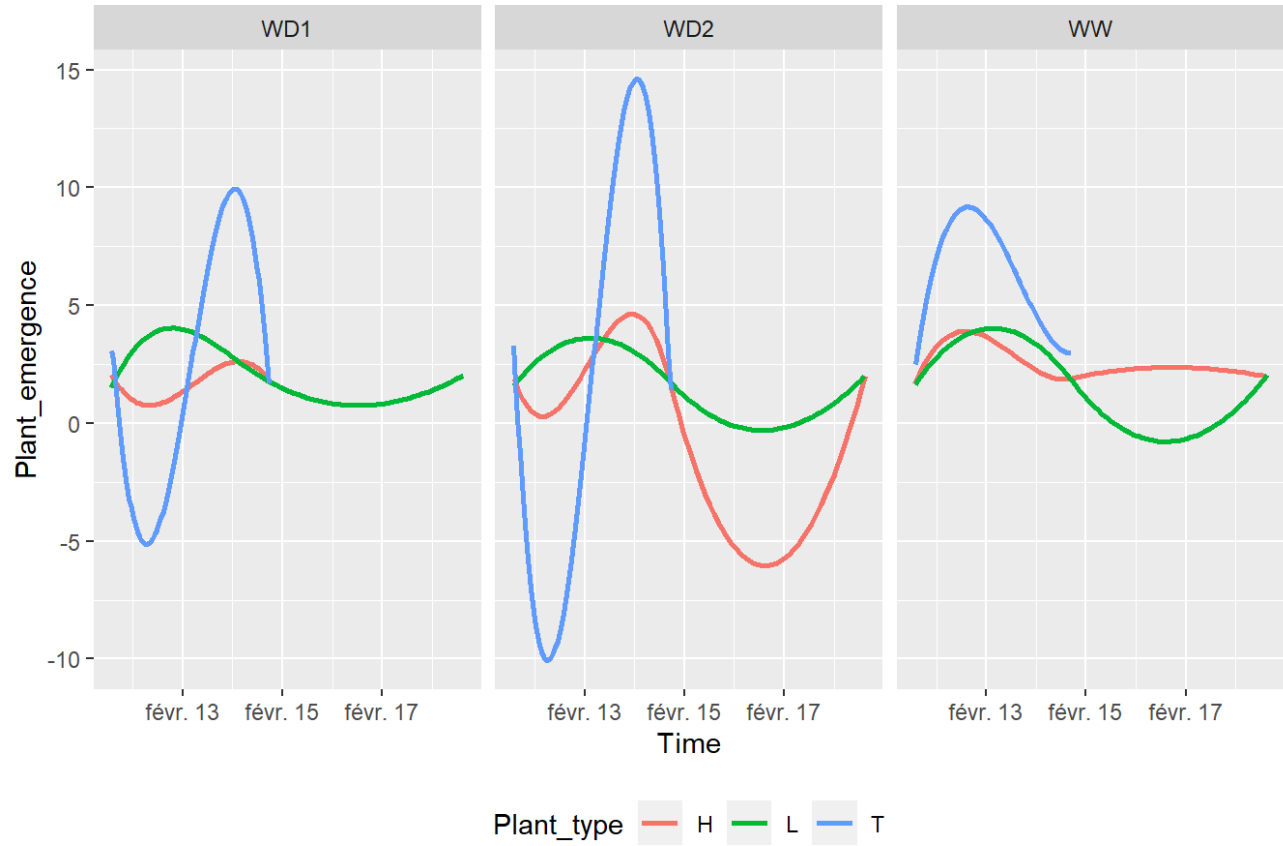
```
plot_scatter_with_smooth_water(timeseries_Plant_emergence, variables_t[4])
```

Scatterplot of Plant\_emergence by Plant type and Soil



```
## `geom_smooth()` using formula = 'y ~ x'
```

Smooth line of Plant\_emergence by Plant type and Soil

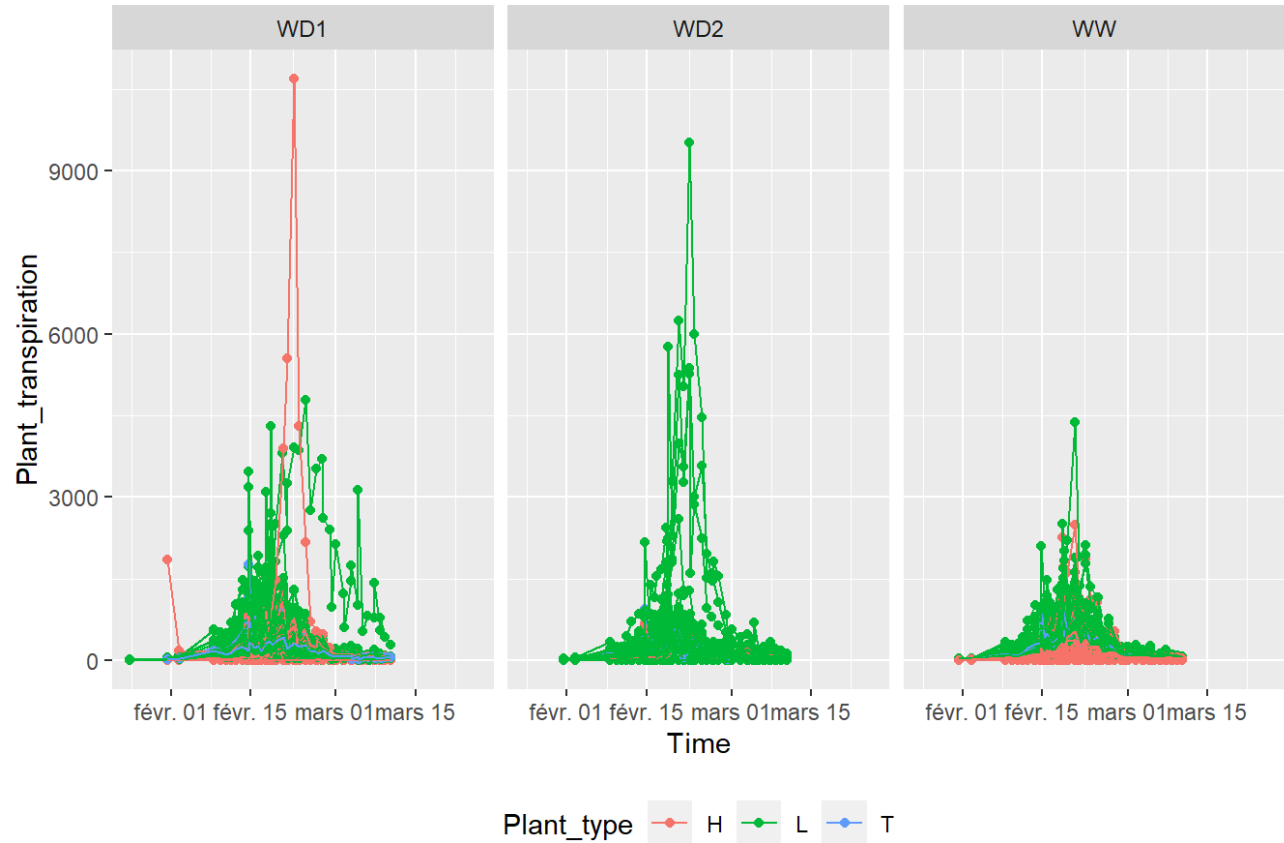


```
plot_scatter_with_smooth_water(timeseries_Plant_transpiration, variables_t[5])
```

```
## Warning: Removed 13341 rows containing missing values (`geom_point()`).
```

```
## Warning: Removed 13341 rows containing missing values (`geom_line()`).
```

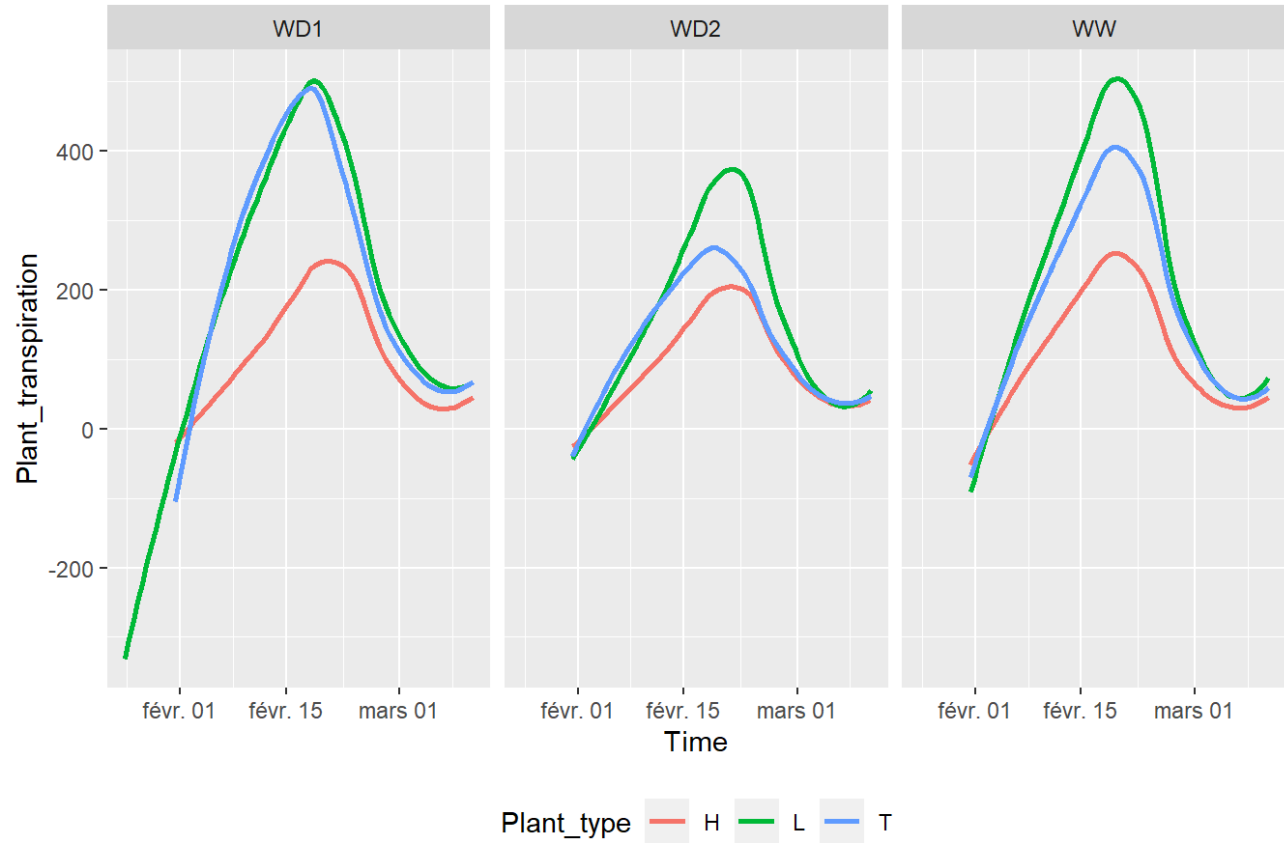
Scatterplot of Plant\_transpiration by Plant type and Soil



```
## `geom_smooth()` using formula = 'y ~ x'
```

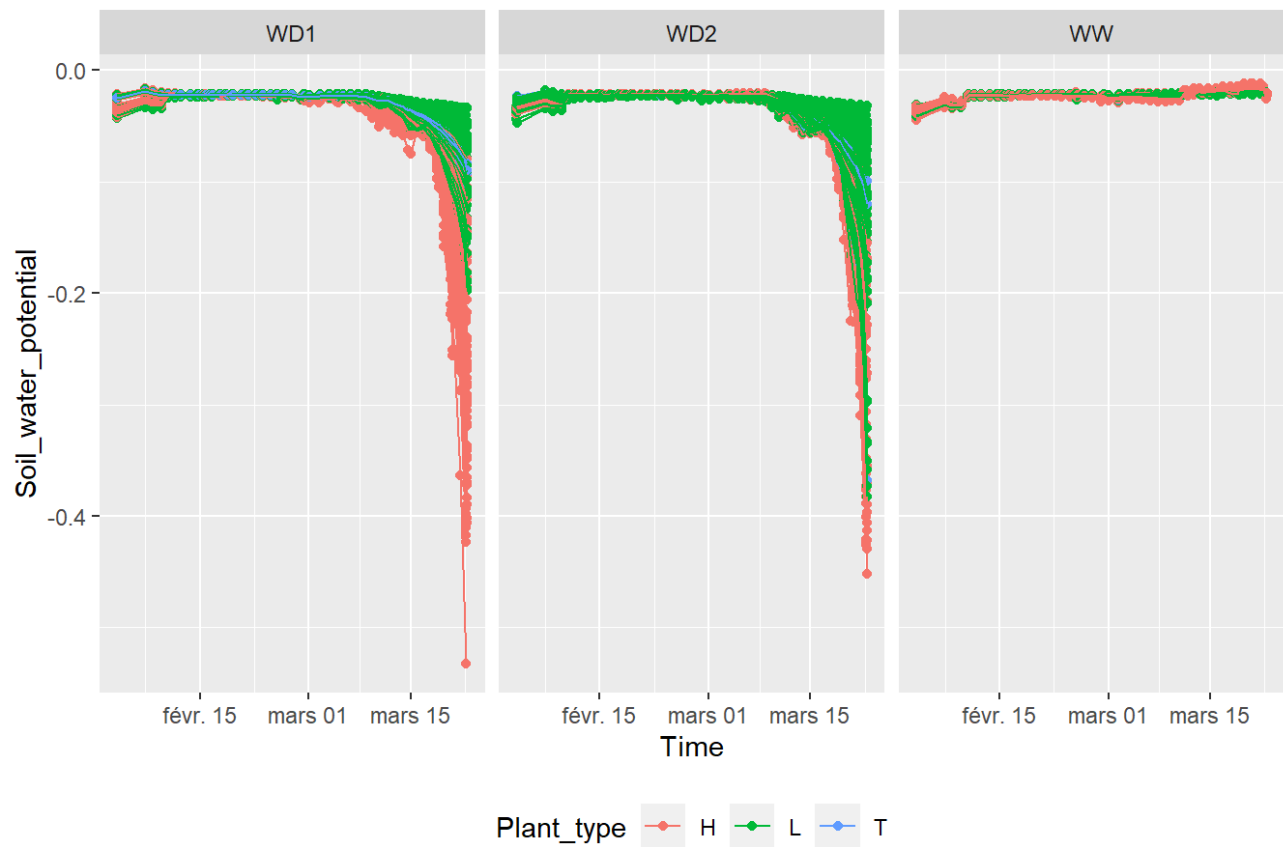
```
## Warning: Removed 13341 rows containing non-finite values (`stat_smooth()`).
```

Smooth line of Plant\_transpiration by Plant type and Soil



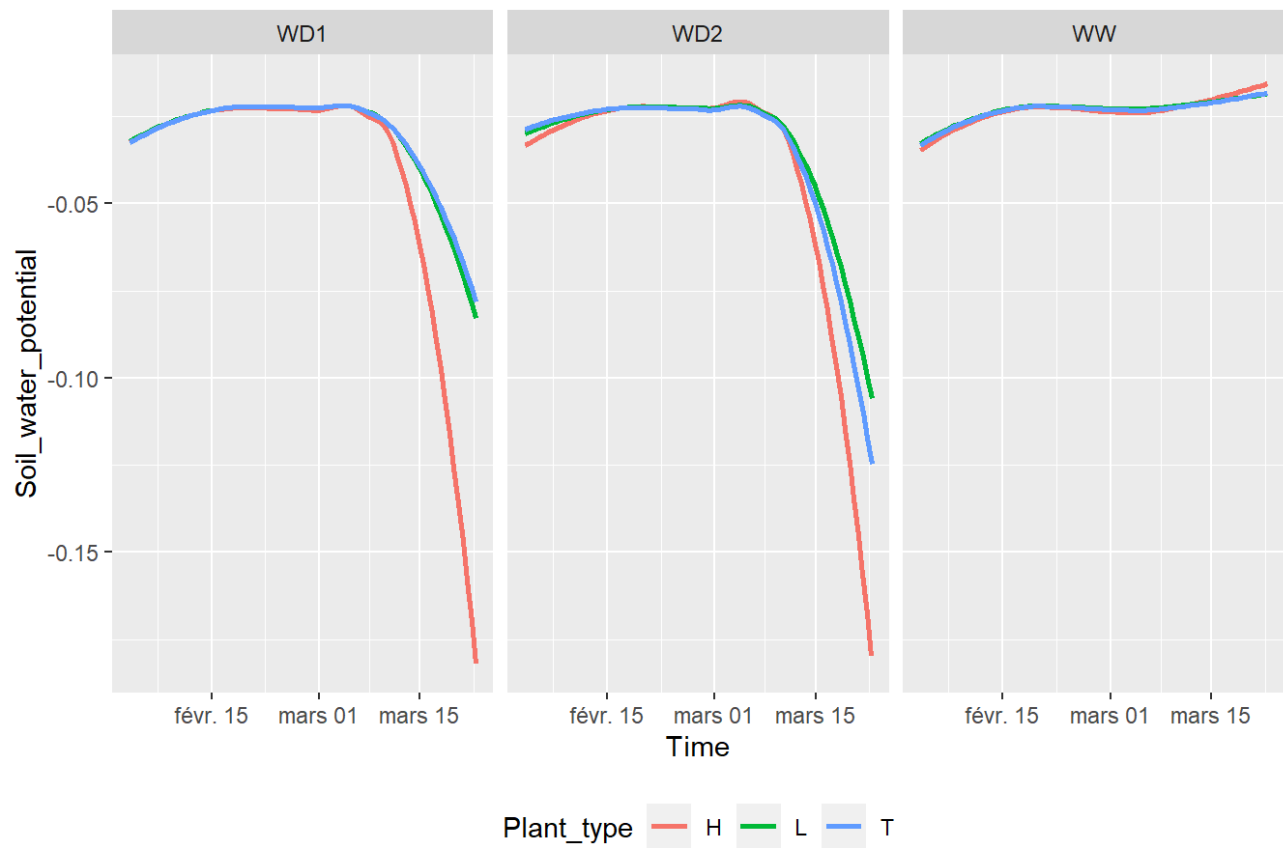
```
plot_scatter_with_smooth_water(timeseries_Soil_water_potential, variables_t[6])
```

Scatterplot of Soil\_water\_potential by Plant type and Soil



```
## `geom_smooth()`` using formula = 'y ~ x'
```

Smooth line of Soil\_water\_potential by Plant type and Soil



```
# Problem for water timeseries data
```

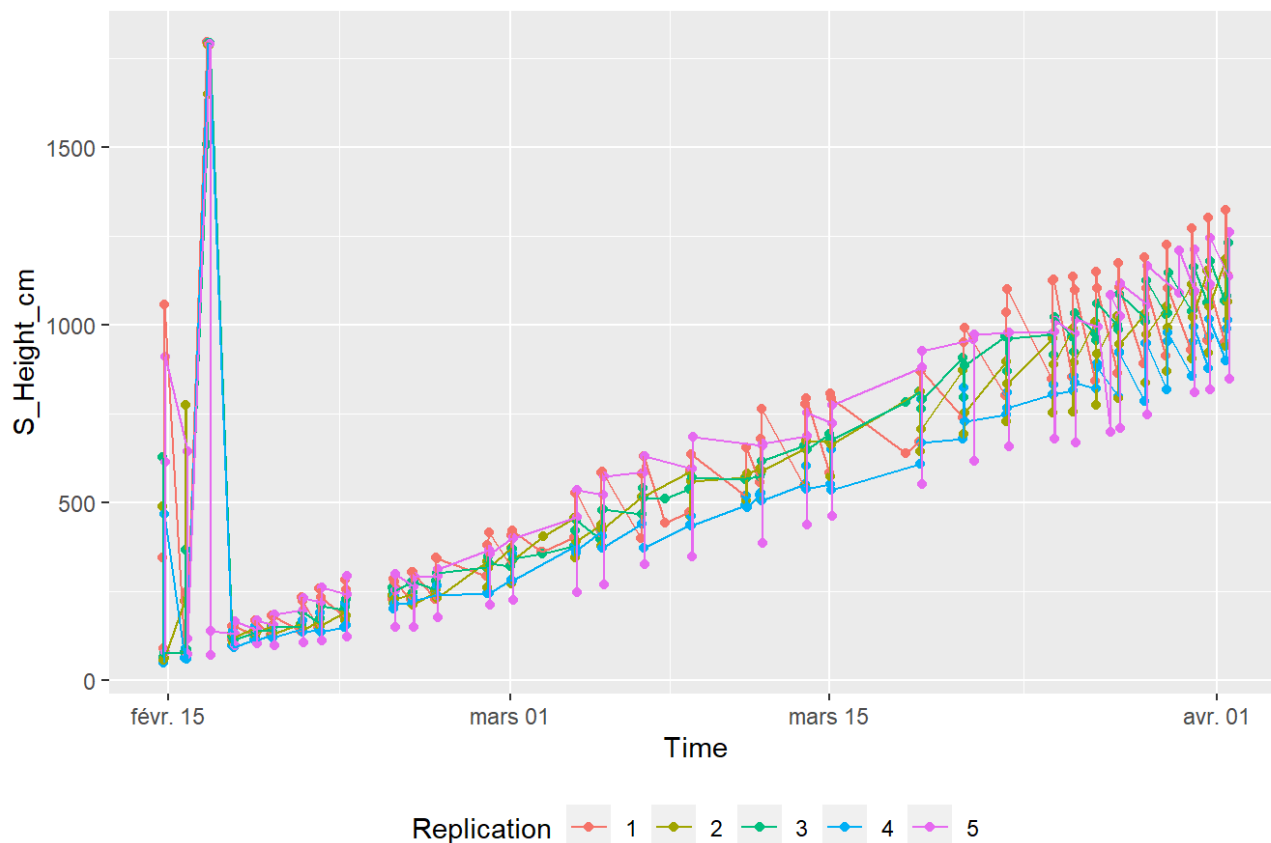
## B. Exploration of the S\_timeseries dataframe

Scatter plots by Genotype

```
plot_scatter_by_genotype(S_timeseries, variables_S, "EPPN20_T")
```

```
## Warning: Removed 17 rows containing missing values (`geom_point()`).
```

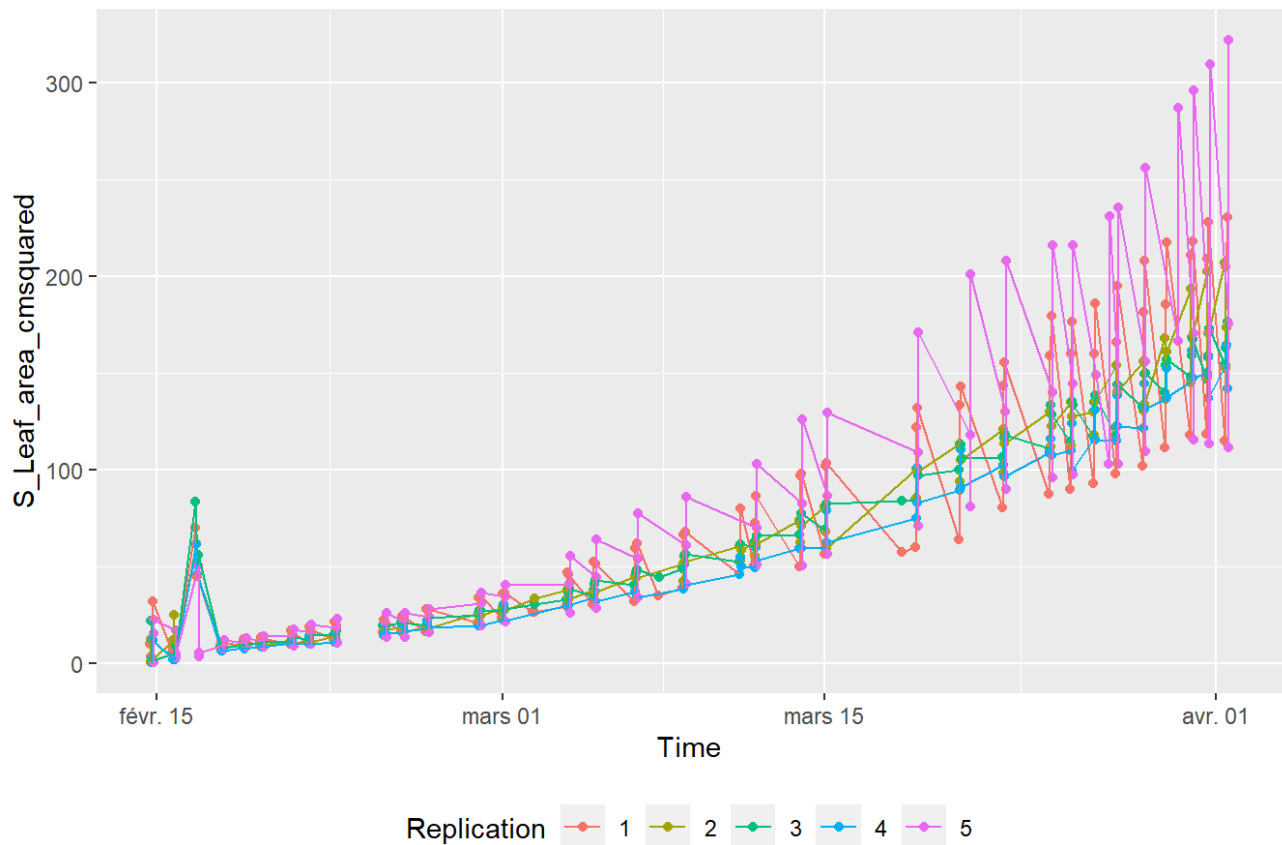
Scatterplot of S\_Height\_cm for Genotype EPPN20\_T



```
## Warning: Removed 17 rows containing missing values (`geom_point()`).
```



Scatterplot of S\_Leaf\_area\_cmsquared for Genotype EPPN20\_T



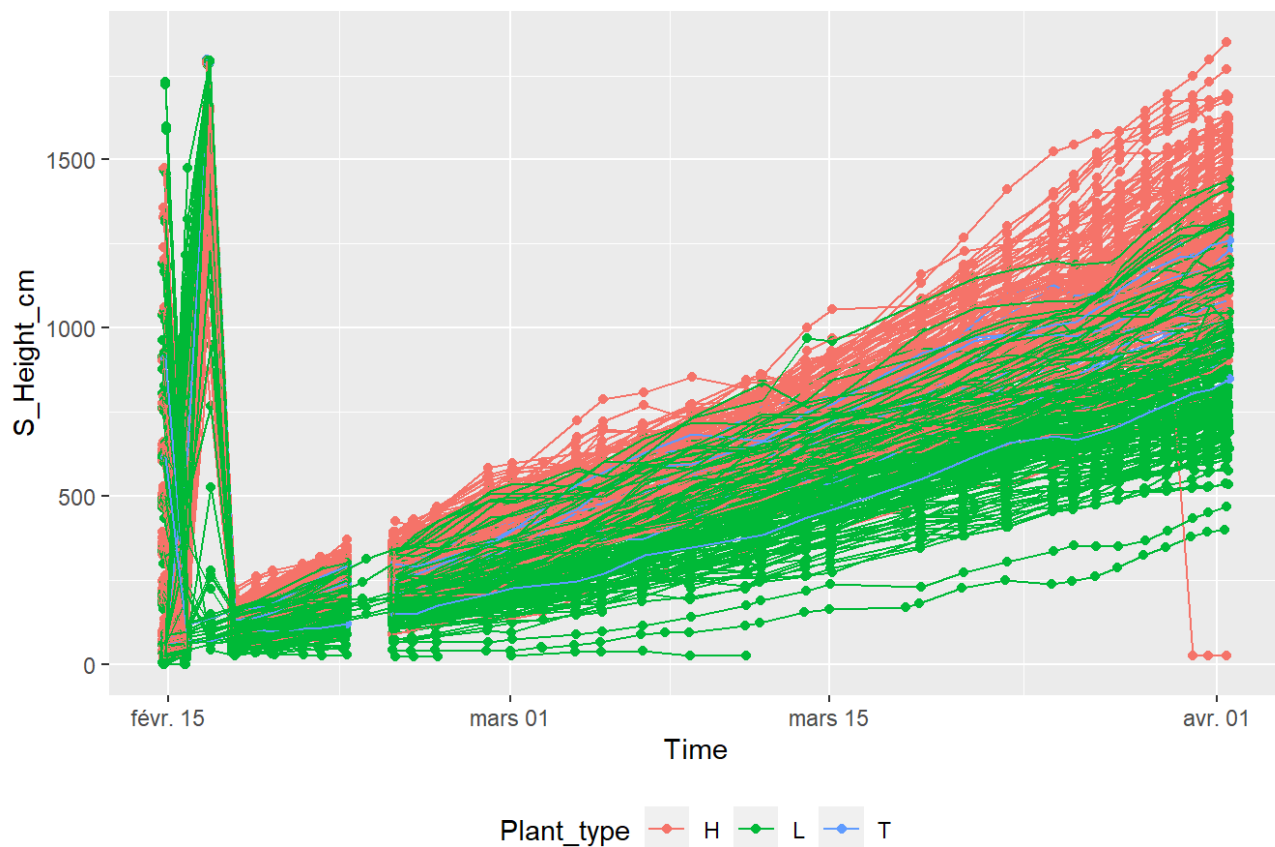
Scatterplots for all genotypes by Plant type (Hybride, Line, EPPN20\_T) with smooth line.

```
plot_scatter_with_smooth(S_timeseries, variables_S)
```

```
## Warning: Removed 491 rows containing missing values (`geom_point()`).
```

```
## Warning: Removed 1 row containing missing values (`geom_line()`).
```

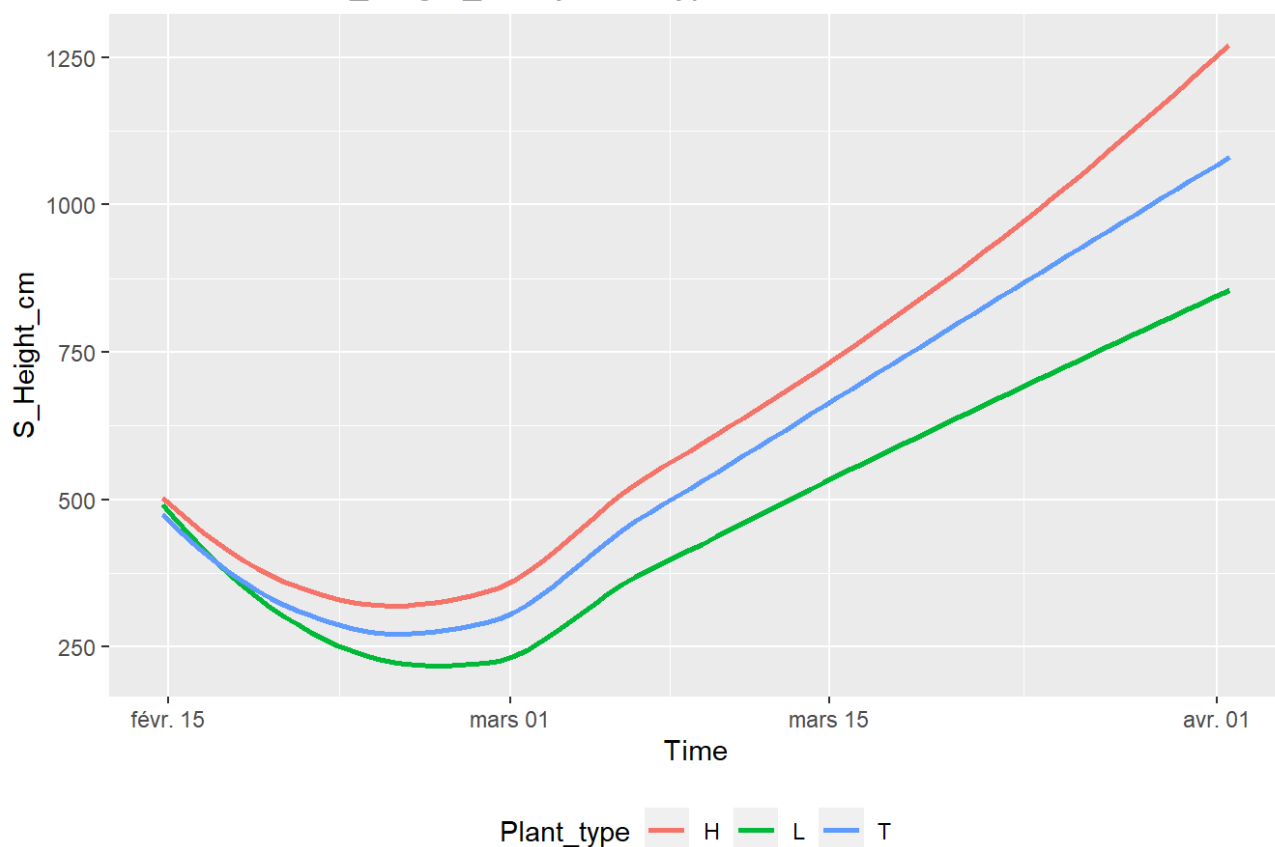
Scatterplot of S\_Height\_cm by Plant type



```
## `geom_smooth()` using formula = 'y ~ x'
```

```
## Warning: Removed 491 rows containing non-finite values (`stat_smooth()`).
```

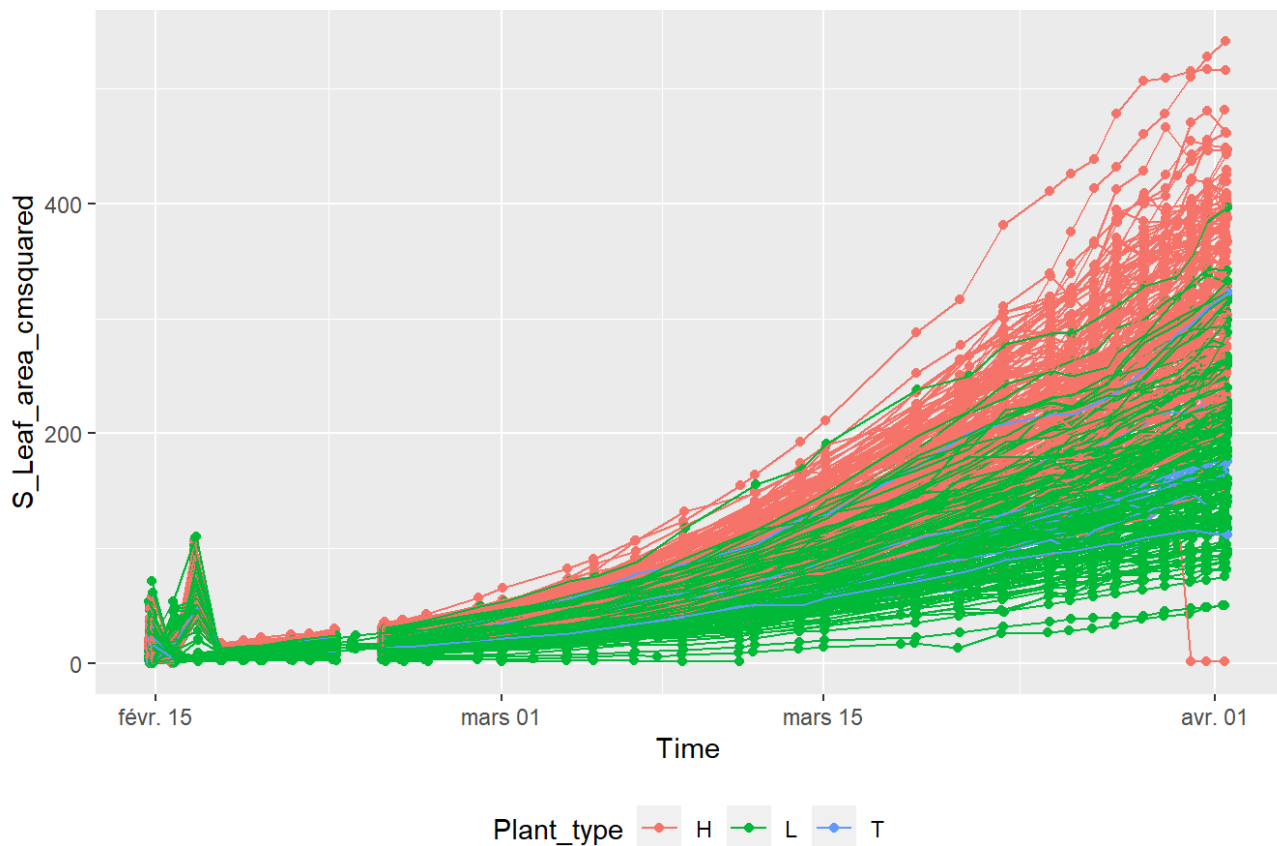
Smooth line of S\_Height\_cm by Plant type



```
## Warning: Removed 500 rows containing missing values (`geom_point()`).
```

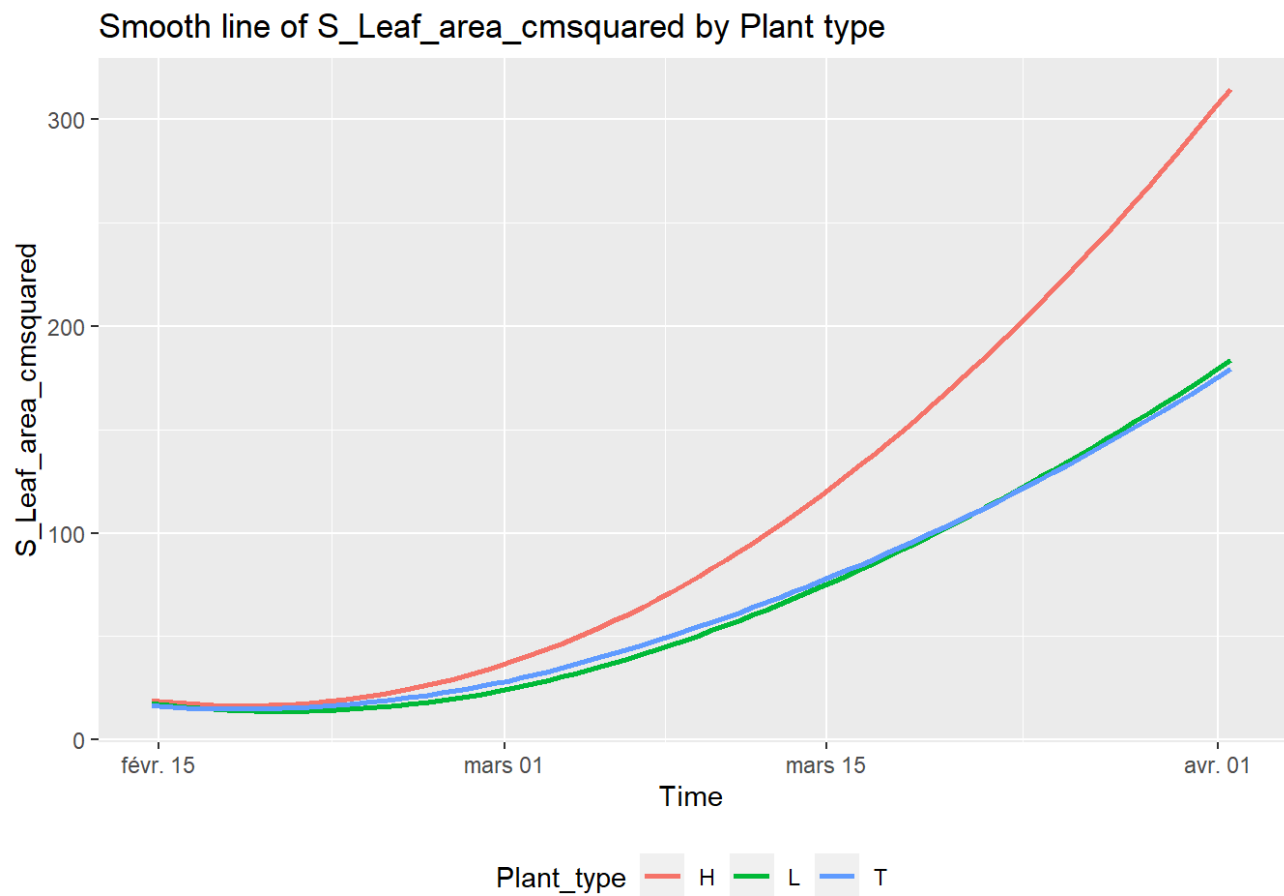
```
## Warning: Removed 10 rows containing missing values (`geom_line()`).
```

Scatterplot of S\_Leaf\_area\_cmsquared by Plant type



```
## `geom_smooth()` using formula = 'y ~ x'
```

```
## Warning: Removed 500 rows containing non-finite values (`stat_smooth()`).
```



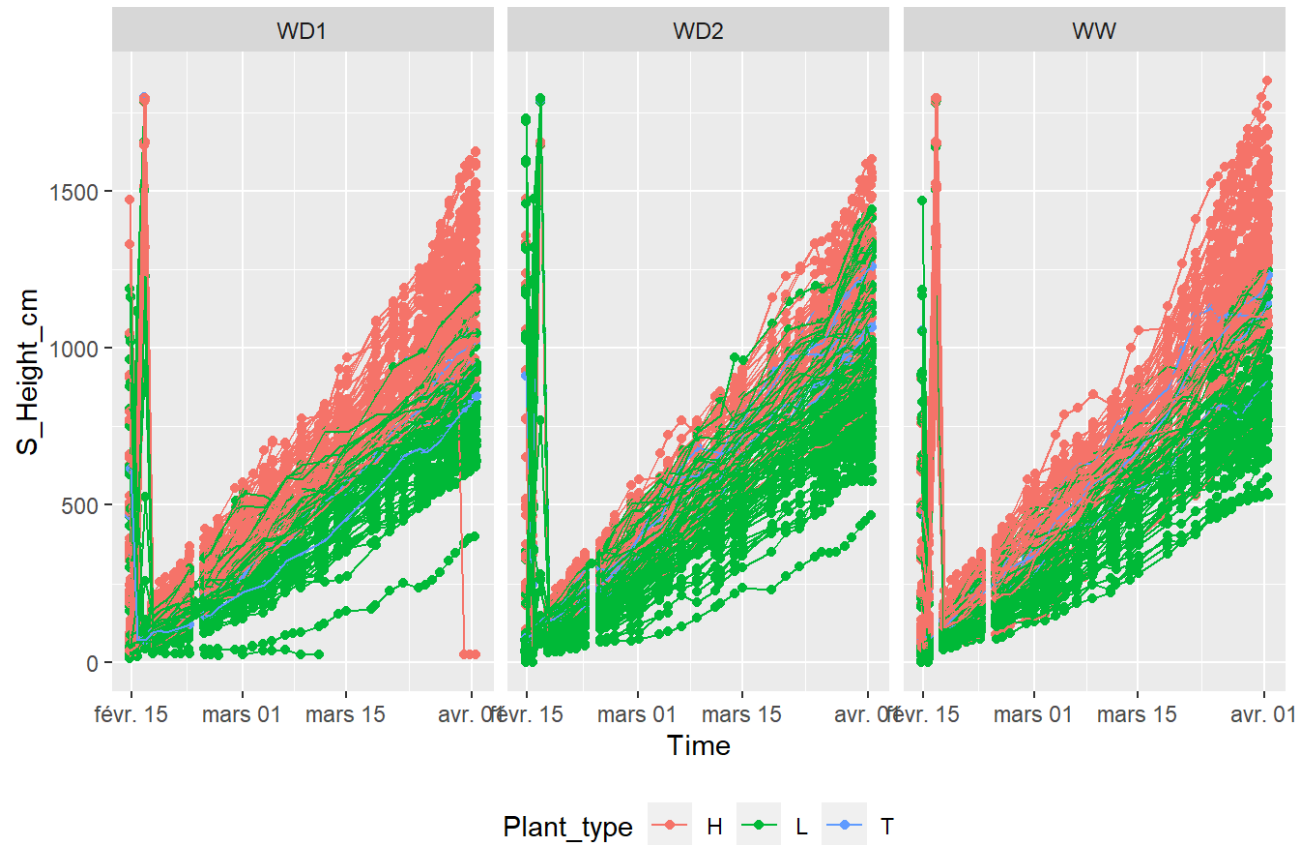
Scatter plots for all genotypes by water treatment

```
plot_scatter_with_smooth_water(S_timeseries, variables_S)
```

```
## Warning: Removed 491 rows containing missing values (`geom_point()`).
```

```
## Warning: Removed 1 row containing missing values (`geom_line()`).
```

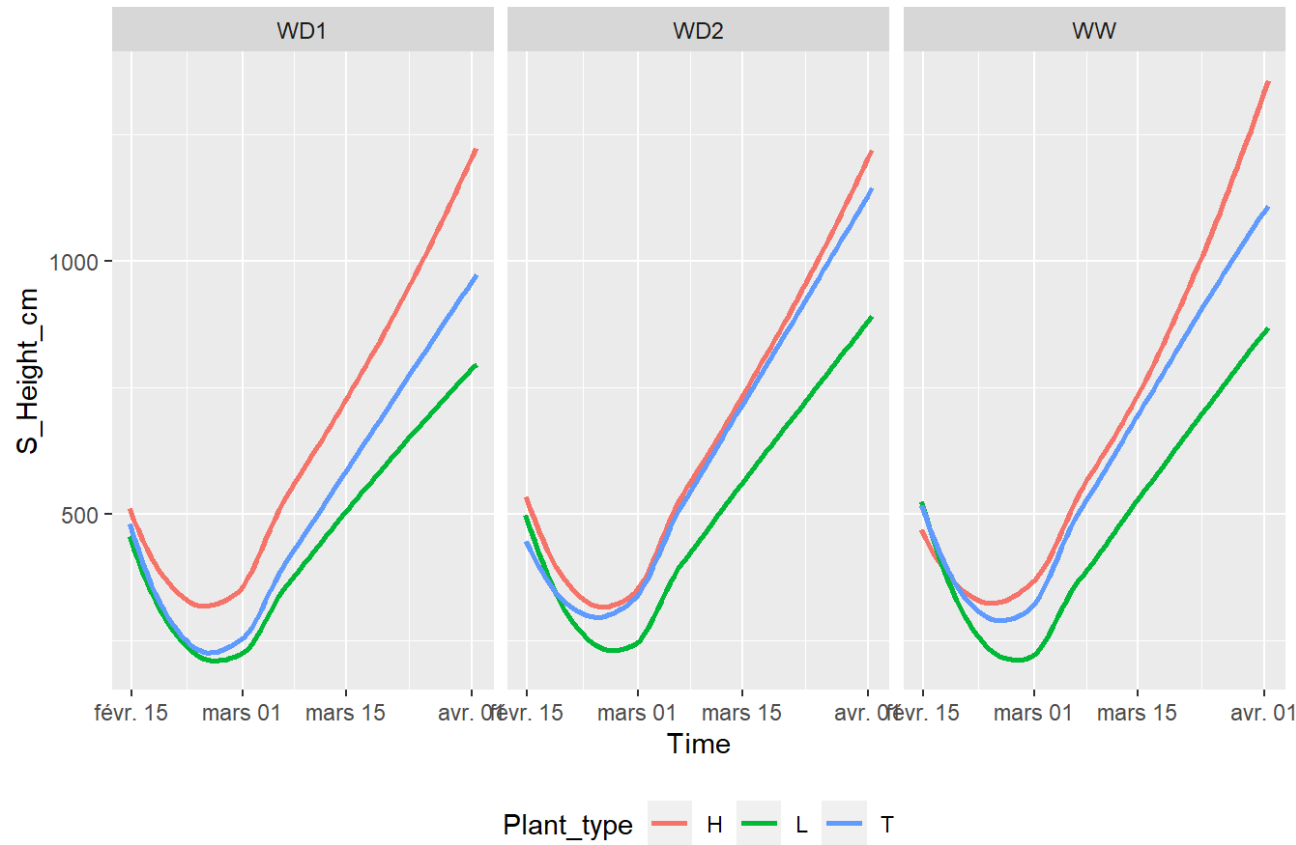
Scatterplot of S\_Height\_cm by Plant type and Soil



```
## `geom_smooth()` using formula = 'y ~ x'
```

```
## Warning: Removed 491 rows containing non-finite values (`stat_smooth()`).
```

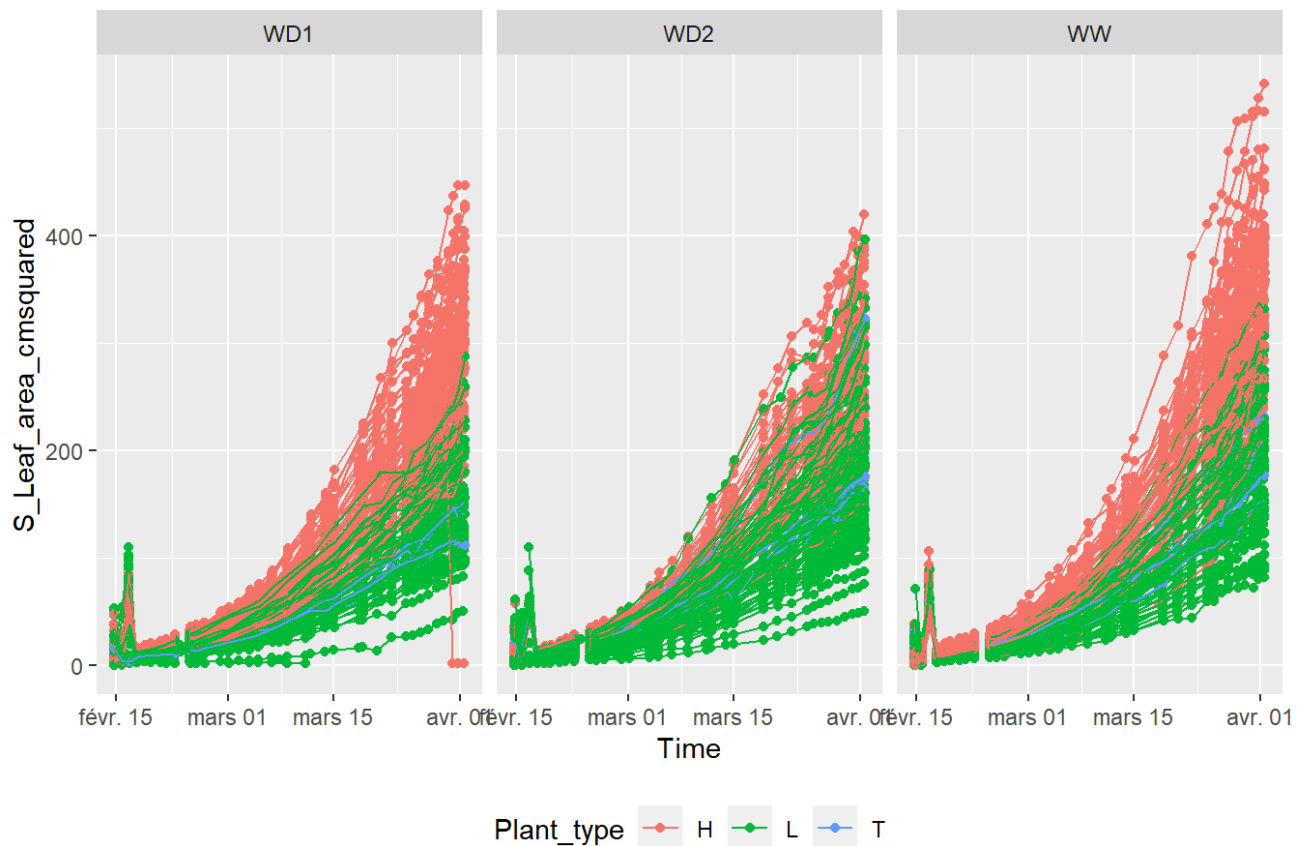
Smooth line of S\_Height\_cm by Plant type and Soil



```
## Warning: Removed 500 rows containing missing values (`geom_point()`).
```

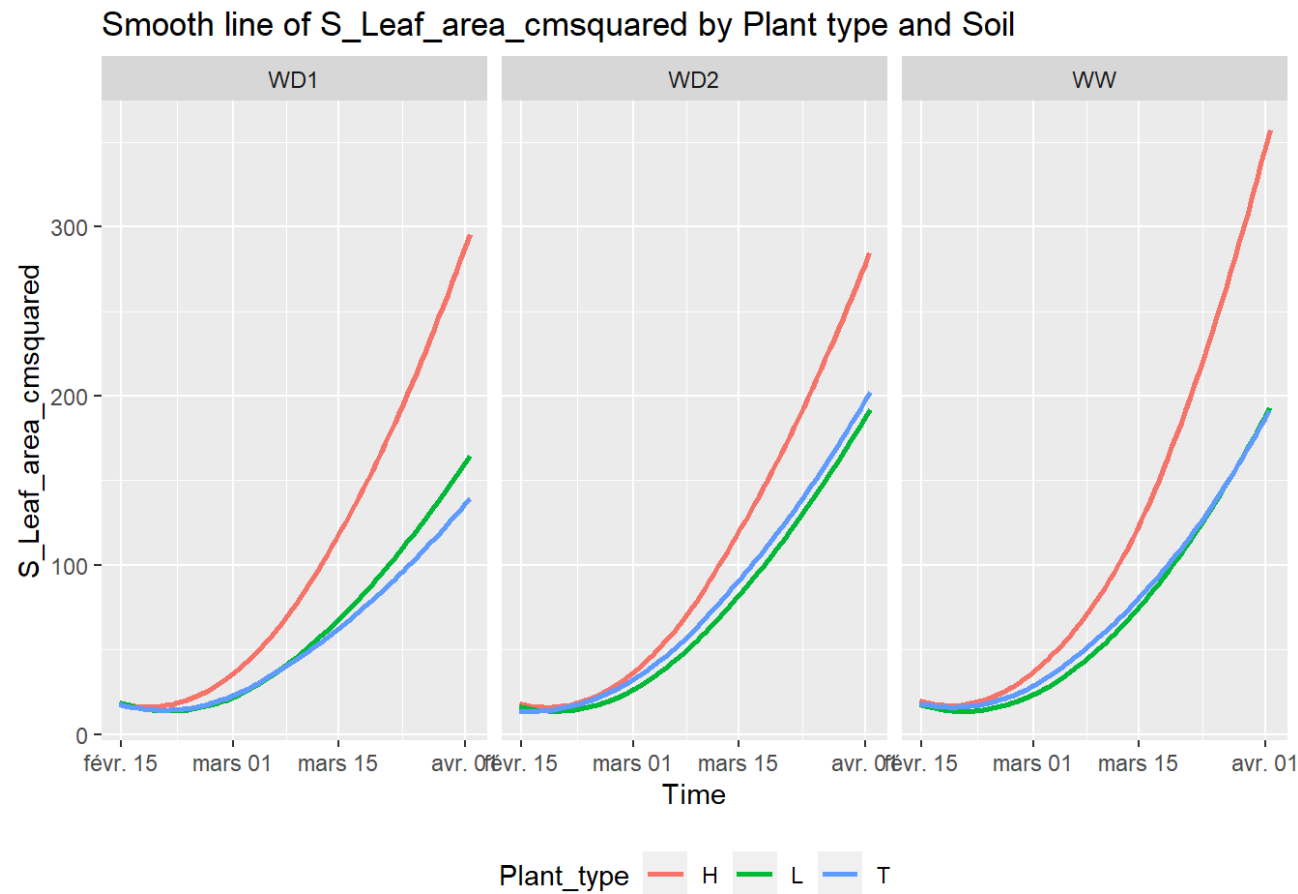
```
## Warning: Removed 10 rows containing missing values (`geom_line()`).
```

Scatterplot of S\_Leaf\_area\_cmsquared by Plant type and Soil



```
## `geom_smooth()` using formula = 'y ~ x'
```

```
## Warning: Removed 500 rows containing non-finite values (`stat_smooth()`).
```



## C. Exploration of the T\_timeseries dataframe

Scatter plots by Genotype

```
print(paste0("No data for", platform))
```

```
## [1] "No data forM3P"
```

Scatterplots for all genotypes by Plant type (Hybride, Line, EPPN20\_T) with smooth line.

```
print(paste0("No data for", platform))
```

```
## [1] "No data forM3P"
```

Scatter plots for all genotypes by water treatment

```
print(paste0("No data for", platform))
```

```
## [1] "No data forM3P"
```