SDHI Working Group
FRAC
FUNGICIDE RESISTANCE
ACTION COMMITTEE

Succinate Dehydrogenase Inhibitor (SDHI) Working Group

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Protocol of the discussions and use recommendations of the SDHI Working Group of the Fungicide Resistance Action Committee (FRAC)

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1. Monitoring results (FRAC members)

Wheat – Septoria leaf blotch (*Zymoseptoria tritici* syn. *Septoria tritici* syn. *Mycosphaerella graminicola*)
(Bayer, Syngenta, BASF, Corteva, FMC, Sumitomo, Adama)

In 2024, the disease pressure was high.
Samples from Bulgaria, Croatia, Hungary, Romania, Slovakia and Spain were sensitive.
Low frequencies of reduced sensitivity ([1]) were found in the following countries: Austria, Czech Republic, Estonia, Denmark, Latvia, Lithuania, Norway, Poland, Sweden, Switzerland and Ukraine. France and Germany show a variable picture with low frequencies in esp. Southern regions and areas with higher frequency of adapted samples in the Northern parts.
Moderate frequencies were observed in Belgium.
High frequencies were detected in Ireland, Italy, the Netherlands and the United Kingdom.

In 2024, C-N86S, which is linked with low resistance factors, still represents the majority of detected mutations.
Even though a high frequency of this and the other reported mutations (e.g. C-T79N) is expected to have a noticeable impact on field performance, SDHIs continue to significantly contribute to disease control and remain important tools for Septoria disease control in wheat-growing regions.

For information on mutations detected in the sdh, please refer to the following link.

Depending on the SDHI, the sensitivity impact of the different mutations detected so far in *Z. tritici*, can be different.
C-H152R and several double mutations, such as C-N86S+B-N225T and C-N86S+C-L85P were shown to impact the sensitivity of *Z. tritici* to SDHIs most. Evidence for fitness penalties associated with the mutation C-H152R were observed in research studies by FRAC member companies ([2],[3],[4]).
Isolates bearing the mutation C-H152R continued to be detected at overall low frequencies in various countries.

Historical background:

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[1] (depending on the testing system: mutations or adapted phenotypes)

[2] Schmitz H, Mehl A, Kerz-Moehlendick F, 2014. Punktmutationen am Zielgen der SDHI Fungizide – Relevanz für den Getreidebau? Julius-Kuehn-Archiv 447, 185.

[3] Schmitz H, Mehl A, Kleemann J, 2015. Relevance of point mutations in the target gene of SDHI fungicides for growing cereals. In: Feldmann F, Heinrich EAS, eds. Proceedings of the XVIII International Plant Protection Congress. [urn:nbn:de:0294-sp-2015-1-2], 195. Accessed 11 April 2017.

[4] Scalliet G, Bowler J, Luksch T, Kirchhofer-Allan L, Steinhauer D et al., 2012. Mutagenesis and Functional Studies with Succinate Dehydrogenase Inhibitors in the Wheat Pathogen Mycosphaerella graminicola. PLoS ONE 7(4): e35429. doi:10.1371/journal.pone.0035429

Extensive monitoring programs were carried out since **2003**. Most isolates tested in routine monitoring programs were sensitive, within the baseline. Since **2012**, few isolates with reduced sensitivity were detected in Germany, France, Ireland and the United Kingdom (SDH subunit C: T79N, W80S, N86S, SDH subunit B: N225T, T268I). The resistance factors were low and field performance was not affected.

In **2015** and **2016**, single isolates with moderate resistance factors and bearing the mutation H152R (SDH subunit C) were detected in Ireland and the United Kingdom. The mutation was detected for the first time in Italy and the Netherlands in 2016. The overall frequency of this mutation remains at a low level and has not increased at the European level.

The following new mutations with low resistance factors were reported for the first time: B-T268A, B-N225I, C-T79I, C-R151S, C-N86A. The following mutations were also reported for the first time but are not associated with any sensitivity change: C-N33T, C-N34T.

In **2017**, sensitivity data for roughly 2.500 isolates were presented from a broad range of countries. The majority of isolates was sensitive; a few showed slightly reduced sensitivity. These isolates, showing low resistance factors, were detected at higher frequency in Ireland and at low frequency in North-Germany, United Kingdom, Netherlands, New Zealand and even lower in France. Such strains were not detected in Ukraine, Poland, Slovakia, Czech Republic, Italy, Spain, Denmark, Sweden, Latvia, Lithuania, Switzerland, Croatia, Greece, Romania, Russia and Tunisia. These isolates are mainly associated to the following mutations: B-T268I/A, B-N225I, B-R265P, C-T168R, C-T79N/I, C-R151S/T/M, C-N86S/A, C-W80S, C-V166M, D-I50F, D-M114V.

Single isolates with moderate resistance factors and bearing the mutation H152R (SDH subunit C) were detected in **2017** again in Ireland and the United Kingdom and for the first time in Germany. The overall frequency of this mutation remains at a low level at the European level.

Disease pressure in **2018** was overall low. Field performance of SDHI fungicides against Septoria was good.

In **2018**, sensitivity data for more than 2.000 isolates were presented from a broad range of countries. The majority of isolates was sensitive. Compared to **2017**, the frequency of isolates showing low resistance factors increased in Northern-Germany, Ireland, the Netherlands and the United Kingdom. These isolates were detected again at low frequency in Denmark, France, Southern-Germany, Poland and for the first time in Ukraine. These isolates are mainly associated with the following mutations: B-T268I/A, B-N225I, B-R265P, C-A84F, C-P127A, C-T168R, C-T79N/I, C-R151S/T/M, C-N86S/A, C-W80S, C-V166M, D-I50F, D-M114V, D-D129G. Among the mentioned mutations, the C-T79N and C-N86S were the most frequent mutations in the last years.

All isolates from Austria, Bulgaria, Czech Republic, Hungary, Italy, Latvia, Lithuania, Slovakia, Spain, Sweden, Switzerland, Romania and Russia were sensitive.

Single isolates with moderate resistance factors and bearing the mutation H152R (SDH subunit C) were also detected in **2018** in Germany, Ireland, the Netherlands and the United Kingdom. For the first time, this mutation was detected at low frequency in a single population originating from France (Normandie). The overall frequency of this mutation in Europe remains at a low level.

The following mutations were also reported but are not associated with any sensitivity change: B-C266G, C-N33T, C-N34T, C-L184W.

For full details on historical monitoring data, please refer to the archive on the SDHI FRAC WG webpage.

Disease pressure in **2019** was overall moderate. Field performance of SDHI-fungicides against Septoria was good.

In **2019**, the majority of isolates was sensitive and the overall situation stable compared to **2018**, as was the frequency for the isolates showing low resistance factors. C-T79N and C-N86S were the most frequent mutations in this group in the last years.

All isolates from Austria, Bulgaria, Croatia, Czech Republic, Greece, Hungary, Italy, Latvia, Lithuania, Slovakia, Slovenia, Spain, Sweden, Switzerland, Tuerkiye, Romania, Russia and Ukraine were sensitive.

A mostly sensitive situation was monitored in France with a low frequency of isolates with low resistance factors at few sites.

As in previous years, isolates bearing the mutation C-H152R continued to be detected at overall low frequencies in **2019** in Germany, Ireland, the Netherlands and the United Kingdom.

Single strains carrying double mutations associated with C-N86S and C-T79N were reported for the first time. The impact on sensitivity ranges from low to high depending on the combination. The fitness of these isolates and impact on product performance is still under investigation.

Disease pressure in **2020** was low to moderate with very dry conditions in some countries. Field performance of SDHI-fungicides when applied according to manufacturers' recommendations against Septoria was good.

All isolates from Bulgaria, Croatia, Czech Republic, Denmark, Hungary, Norway, Slovakia, Spain, Tuerkiye, Romania, Russia and Ukraine were sensitive.

As in **2019**, the majority of isolates in **2020** was sensitive in Europe with the exception of Ireland and the United Kingdom. C-T79N and C-N86S were the most frequent mutations with low resistance factor in the last years.

As in previous years, isolates bearing the mutation C-H152R continued to be detected at overall low frequencies in **2020** in Ireland and the United Kingdom. In Switzerland, France, Italy, the Netherlands and Germany, this mutation was detected at low frequencies in single locations only.

Low frequencies of reduced sensitivity ([5]) were found in the following countries: Austria, Switzerland, Sweden, France, Italy, Lithuania, Latvia, Poland, Belgium.

Low frequencies were found in Germany with a more widespread distribution.

Moderate frequencies were detected in Ireland, the United Kingdom and the Netherlands.

Outside of Europe, an overall sensitive situation was found in New Zealand in monitoring programs from **2016** to **2019** with the exception of a single population in a single trial location.

Disease pressure in **2021** was moderate with a later onset in some wheat-growing regions of Europe. Field performance of SDHI-fungicides when applied according to manufacturers' recommendations against Septoria was good.

The overall sensitivity levels were observed to be stable compared to **2020**.

All isolates from Bulgaria, Croatia, Estonia, Norway, Romania, Russia, Slovakia, Tuerkiye and Ukraine were sensitive.

As in the previous 3 years, the majority of isolates was sensitive in Europe with the exception of Ireland and the United Kingdom. C-T79N and C-N86S were the most frequent mutations with low resistance factor in the last years.

Low frequencies of reduced sensitivity ([8]) were found in the following countries: Austria, Czech Republic, Denmark, Hungary, Italy, Lithuania, Latvia, Poland, Spain, Sweden and Switzerland.

Low to moderate frequencies were found in Belgium, Northern coastal France and Northern Germany while in other parts of Germany and France, the frequency of adapted isolates is low.

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[5] (depending on the testing system: mutations or adapted phenotypes)

Moderate to high frequencies were detected in Ireland, the Netherlands (limited data set) and the United Kingdom.

As in previous years, isolates bearing the mutation C-H152R continued to be detected at overall low frequencies in **2021** in Ireland and the United Kingdom. In Belgium, France (Northern coastal regions), Northern Germany, Italy, the Netherlands, Poland, Sweden and Switzerland, this mutation was detected at low frequencies in single locations only.

Disease pressure in **2022** was variable ranging from low to moderate, depending on the wheat-growing regions of Europe.

All isolates from Bulgaria, Croatia, Hungary, Romania, Russia, Slovakia, Tuerkiye and Ukraine were sensitive.

In **2022**, C-T79N and C-N86S, which are linked with low resistance factors, still represent the majority of detected mutations and show an increase in frequency.

Even though a high frequency of these mutations is expected to have a noticeable impact on field performance, SDHIs continue to significantly contribute to disease control and remain important tools for Septoria disease control in wheat-growing regions.

Low frequencies of reduced sensitivity ([6]) were found in the following countries: Austria, Czech Republic, Estonia, Denmark, Latvia, Lithuania, Norway, Spain, Sweden and Switzerland.

Low to moderate frequencies were found in Belgium, France, Germany and Poland.

High frequencies were detected in Ireland, Italy, the Netherlands and the United Kingdom.

In **2023**, the disease pressure was moderate to high following a mild winter with lower levels in the North due to dry conditions.

Samples from Bulgaria, Croatia, Romania, Slovakia and Spain were sensitive.

Low frequencies of reduced sensitivity ([9]) were found in the following countries: Austria, Czech Republic, Estonia, Denmark, Hungary, Latvia, Lithuania, Norway, Russia, Sweden and Ukraine. France and Germany show a variable picture with low frequencies in esp. Southern regions and areas with higher frequency of adapted samples in the Northern parts.

Moderate frequencies were observed in Belgium, the Netherlands, Poland and Switzerland.

High frequencies were detected in Ireland, Italy and the United Kingdom.

In **2023**, C-N86S, which is linked with low resistance factors, represents the majority of detected mutation and shows an increase in frequency.

Even though a high frequency of this and the other reported mutations (e.g. C-T79N) is expected to have a noticeable impact on field performance, SDHIs continue to significantly contribute to disease control and remain important tools for Septoria disease control in wheat-growing regions.

Isolates bearing the mutation C-H152R continued to be detected at overall low frequencies in Germany, the Netherlands, Ireland, Italy and the United Kingdom.

Wheat – Brown rust (*Puccinia triticina* syn. *Puccinia recondita*)

(Syngenta, Bayer, FMC, Sumitomo, BASF)

Extensive monitoring programs were carried out since **2005**.

Disease pressure in **2024** was moderate to high, depending on the region.

Isolates carrying the mutation C-I87F, showing variable resistance factors depending on the compound, were detected with increasing frequencies in samples from France, Germany and the United Kingdom.

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[6] (depending on the testing system: mutations or adapted phenotypes)

Single mutants have been detected in samples originating from Hungary, Slovakia, Belgium, the Netherlands, Denmark, Romania and Poland.
No mutants were detected in samples originating from Italy and Sweden.
The following mutations were detected in single isolates: C-N89K and C-L28F.

Historic background:
Samples from the following countries were tested in **2018**: Belgium, Denmark, France, Germany, Hungary, Sweden and the United Kingdom. All tested isolates were sensitive, within the baseline.
One single isolate, showing a low resistance factor (~5) has been identified in Pas de Calais, France and was genetically characterized without any detection of a mutation in sdh subunits B, C and D.
In **2019**, samples were analyzed from Belgium, Czech Republic, France, Germany, Italy, Poland, Slovakia and the United Kingdom and showed full sensitivity.
In **2020**, samples originating from France, Poland, Denmark, Germany, Hungary and the United Kingdom showed full sensitivity.
In **2021**, samples originating from Belgium, Denmark, Estonia, Germany, Hungary, Italy, Latvia, Romania, Poland and the United Kingdom showed high sensitivity.
Beside this, isolates carrying the mutation C-I87F were detected showing low resistance factors with no impact on field efficacy, originating from France and the United Kingdom.
In **2022**, samples originating from Denmark, Estonia, Hungary, Italy, Latvia, Lithuania, Romania, Poland and Spain showed high sensitivity.
Isolates carrying the mutation C-I87F, showing low resistance factors, were detected in samples from Belgium, France, Germany and the United Kingdom.
Field efficacy was not impacted.
Disease pressure in **2023** was ranging from low to moderate, linked with a late onset of the disease.
In **2023**, samples originating from Belgium, Bulgaria, Czech Republic, Denmark and Romania showed high sensitivity.
Single cases of adapted isolates were detected in Hungary, Italy and Poland.
Isolates carrying the mutation C-I87F, showing low resistance factors, were detected with increasing frequencies in samples from France, Germany and the United Kingdom.

Brown rust on rye (*Puccinia recondita* fsp. *secalis*)
(Syngenta)

2024 samples from Belgium, France, Lithuania and the Netherlands showed full sensitivity. Single populations originating from Germany and the United Kingdom showed reduced sensitivity with C-I87F being detected in part of the samples from Germany.

Wheat – Yellow rust (*Puccinia striiformis*)
(Bayer, Sumitomo, Syngenta, FMC)

In vivo analyses of **2024** samples showed variable sensitivities in France and Germany, depending on the tested compound. Populations showing variable sensitivities carried the mutation C-I87V.
Full sensitivity was observed in samples originating from Bulgaria, Croatia, Denmark, the Netherlands, Poland, Spain and the United Kingdom.

Historic background:
In **2019**, samples from Belgium, Denmark, Germany, Latvia, Sweden and the United Kingdom were tested and showed full sensitivity, within the baseline.
2020 samples originating from Belgium, Denmark, Germany, France, Italy, Poland, Portugal, Spain and the United Kingdom showed full sensitivity.
Samples analyzed in **2021** from Belgium, Czech Republic, Germany, France, Italy, the Netherlands, Poland, Romania, Spain and the United Kingdom showed full sensitivity.
Samples analyzed in **2022** from Germany, France, Italy, the Netherlands, Poland, Romania, Spain and the United Kingdom showed full sensitivity.
Samples analyzed in **2023** from Bulgaria, Czech Republic, Croatia, Germany, Hungary, France, the Netherlands, Poland, Romania, Slovakia, Spain and the United Kingdom showed full sensitivity.

Wheat – Snow mold (*Microdochium* spp.)

(Syngenta)

2024 Samples from Germany and Italy showed full sensitivity.

Historical background:
Monitoring programs carried out in **2015** showed full sensitivity of isolates from Germany, France, Italy, Slovakia and the United Kingdom, confirming the results from **2014**.
Data from **2016** and **2017** from Belgium, Germany, Denmark, Finland, France, Italy, Lithuania, Latvia, Poland, Russia, Sweden, Ukraine and the United Kingdom showed a fully sensitive situation.
Disease pressure in **2018** was very low. Isolates from France, Hungary, Italy, Poland and Spain were fully sensitive.
In **2019**, Isolates from Belgium, Germany, Hungary, the Netherlands, Ukraine and the United Kingdom were fully sensitive. Single resistant isolates bearing the mutation B-H253Q were detected in Italy and characterized as *M. nivale* var. *majus*. However, SDHI-containing products were still effective.
2020 Samples from the United Kingdom showed full sensitivity.
2021 Samples from Belgium, Bulgaria, Czech Republic, France, Germany, Italy, Romania, Russia, Spain, Ukraine and the United Kingdom showed full sensitivity.
2023 Samples from Hungary, Italy and Romania showed full sensitivity.

Wheat – Powdery mildew (*Blumeria graminis*)

(BASF, Syngenta)

Full sensitivity was observed in samples in **2024** originating from Czech Republic, Denmark, Germany, France, Hungary, Ireland, Poland, Sweden and the United Kingdom.

Historical background:
Monitoring programs carried out in **2017** confirmed the results from previous years and showed full sensitivity of isolates originating from the United Kingdom, France, Belgium, Germany and Denmark, Czech Republic.
In **2018**, full sensitivity was found in Belgium, Denmark, France, Germany and the United Kingdom.
In **2019**, full sensitivity was found in Czech Republic, Poland and the United Kingdom.

In **2020**, samples from Denmark, France, Germany and the United Kingdom showed full sensitivity.
In **2021**, samples from Bulgaria, Estonia, France, Germany, Greece, Hungary, Italy, Latvia, Lithuania, Poland, and the United Kingdom showed full sensitivity.
In **2022**, samples from the Czech Republic, Denmark, France, Germany, Hungary, Italy, Latvia, Lithuania, Poland and the United Kingdom were fully sensitive.
No monitoring was carried out in **2023**.

Wheat – Tan spot (*Pyrenophora tritici-repentis*)
(Sumitomo, Syngenta)

No monitoring was carried out in **2023** and **2024.**
2021 samples showed full sensitivity in the following countries: Hungary, Slovakia and Sweden.
In **2020**, samples from Belgium, Czech Republic, Germany, Hungary, Poland, Romania and Sweden showed full sensitivity.
2019 samples from Finland, Latvia and the United Kingdom showed full sensitivity.

Wheat – Sharp eye spot (*Rhizoctonia* spp.)
(Syngenta)

2020 samples from Germany and Spain showed full sensitivity.
2019 samples from Germany and the United Kingdom were fully sensitive.

Wheat – Glume blotch (*Phaeosphaeria nodorum* syn. *Stagonospora nodorum*)
(Syngenta)

Single isolates from **2019** to **2021,** originating from Czech Republic, Germany, Hungary, Latvia, and Sweden were analyzed and showed full sensitivity.

Wheat – smut (*Ustilago* spp.)
(Syngenta)

2024 samples originating from Austria, Bulgaria, Czech Republic, Estonia, France, Germany, Hungary, Lithuania and Poland were fully sensitive.
2020 and **2021** samples from Bulgaria, Germany, Italy, Poland, Romania, Spain and Sweden showed full sensitivity.

Wheat – eye spot, Oculimacula yallundae
(BASF, Syngenta)

Full sensitivity was observed in **2020, 2021, 2023** and **2024** samples from Czech Republic, Germany, France, Latvia, Lithuania, Poland, Romania and the United Kingdom.

Head blight on wheat – Fusarium spp. (*F.graminearum, F.asiaticum, F.sporotrichoides*)

(Syngenta)

Samples originating from Italy, Germany and the United Kingdom, representing F.poae, F.graminearum, *F.sporotrichoides* from **2024** showed high sensitivity. A monitoring program in China on *F. graminearum* and *F. asiaticum*, carried out in **2022**, resulted in full sensitivity.

Barley – Net blotch (*Pyrenophora teres*)

(BASF, Bayer, Sumitomo, Syngenta)

In **2024**, a heterogeneous sensitivity situation was found in Austria, Bulgaria, Croatia, Czech Republic, Denmark, Hungary, Latvia, Lithuania, Romania, Slovakia, Sweden, Poland and Ukraine.

Moderate to high frequencies were observed in France, Germany, Italy, Spain, Belgium, the Netherlands, Ireland and the United Kingdom.
Among the mutations with decreased sensitivity, C-G79R, C-H134R, C-N75S and C-S135R are the most frequently detected mutations.
For information on mutations detected in the sdh, please refer to the following link.

Historical background:
Extensive monitoring programs were carried out since **2003**. Until **2011**, all tested isolates were sensitive, within the baseline. In **2012**, the sensitivity of 2 isolates from North-Germany was outside of the baseline range. A target site mutation was identified in the SDH-B subunit at position 277 (B-H277Y).
In **2013** and **2014**, more isolates were detected with reduced sensitivity, carrying different mutations (**link** to mutations table) in Germany, France, Italy and the United Kingdom. The predominant mutation was C-G79R. The resistance factors were low for B-H277Y, D-D124E, D-D145G and moderate for C-G79R, C-H134R, C-S135R, C-N75S, C-R64K, D-H134R, C-K49E.
The mutation D-G138V was detected for the first time in **2015** and found to be associated to very low resistance factors.
The sensitivity situation in **2016** was similar to **2015**: The frequency of mutations was low in the Czech Republic, Denmark, Italy, Poland, Southern France, Southern Germany and the United Kingdom. Moderate frequencies were observed in Northern Germany and Northern France. Among the mutations with moderately decreased sensitivity, C-G79R and C-H134R are the most frequently detected mutations. While in France, C-G79R is the predominating mutation, in Germany C-H134R is observed to be the more frequent mutation.
No mutations were detected in Bulgaria, Estonia, Finland, Hungary, Ireland, Latvia, Lithuania, Romania, Russia, Slovakia, Spain, Sweden and the Ukraine (in **2016**).

In **2017**, control of net blotch, esp. in areas in France, was difficult and potentially related to e.g. the high disease pressure, low varietal diversity, coupled with the break-down of variety-resistance (variety ETINCEL, reference: https://www.arvalis-infos.fr/_plugins/WMS_BO_Gallery/page/getElementStream.jspz?id=46981&prop=file) at significant cultivation areas and higher frequencies of mutated strains.
In **2017**, the frequency of mutations or insensitive isolates was low in the Czech Republic, Denmark, Greece (trial site), Italy, Lithuania, Poland, Sweden and the Ukraine. Moderate

frequencies were observed in Germany and the United Kingdom but moderate to high in France. Among the mutations with moderately decreased sensitivity, C-G79R and C-H134R are the most frequently detected mutations. In France, C-G79R is the predominating mutation. In the United Kingdom, C-H134R is the more frequent mutation. Whereas in Germany, both mutations are found at similar levels.

No mutations or reduced sensitivity were detected in Bulgaria, Estonia, Finland, Hungary, Ireland, Latvia, Romania, Russia, Slovakia and Spain.

Disease pressure was generally low in **2018**. Thus, the field performance of SDHI-containing fungicides against net blotch is hard to evaluate.

In **2018**, the frequency of mutations was comparable to the previous season.

The frequency of insensitive isolates was low in the Czech Republic, Denmark, Hungary, Italy, Poland, Sweden and Ukraine. Moderate to high frequencies were observed in Belgium, France, Germany, Ireland, the Netherlands and the United Kingdom. Among the mutations with moderately decreased sensitivity, C-G79R, C-H134R and C-S135R are the most frequently detected mutations.

No mutations or reduced sensitivity were detected in Bulgaria, Finland, Latvia, Romania, Russia, Slovakia and Spain.

In **2019**, the frequency of mutations was similar to the previous season.

The frequency of insensitive isolates was low in Bulgaria, Czech Republic, Denmark, Greece, Hungary, Italy, Poland, Spain, Sweden, Switzerland and Ukraine. Moderate to high frequencies were observed in Austria, Belgium, France, Germany, Ireland, the Netherlands and the United Kingdom. Among the mutations with moderately decreased sensitivity, C-G79R, C-H134R and C-S135R are the most frequently detected mutations.

No mutations or reduced sensitivity were detected in Hungary, Latvia, Lithuania, Romania, Russia and Slovakia.

In **2020**, the frequency of mutations was similar to the previous season.

No mutations or reduced sensitivity were detected in Bulgaria, Romania, Russia and Slovakia.

The frequency of mutations or reduced sensitivity was low in Czech Republic, Denmark, Hungary, Italy, Latvia, Lithuania, Spain, Sweden, Switzerland and Ukraine.

Moderate to high frequencies were observed in Austria, Belgium, France, Germany, Ireland, Poland, the Netherlands and the United Kingdom. Among the mutations with moderately decreased sensitivity, C-G79R, C-H134R and C-S135R are the most frequently detected mutations.

Disease pressure in **2021** was moderate.

In **2021**, the frequency of mutations was similar to the previous season.

No mutations or reduced sensitivity were detected in Bulgaria, Finland, Greece, Latvia, Russia and Slovakia.

The frequency of mutations or reduced sensitivity was low in Czech Republic, Denmark, Hungary, Italy, Lithuania, Spain, Sweden and Switzerland.

Moderate frequencies were detected in Poland, Romania and Ukraine.

Moderate to high frequencies were observed in Austria, Belgium, France, Germany, Ireland, the Netherlands and the United Kingdom.

Among the mutations with moderately decreased sensitivity, C-G79R, C-H134R, C-N75S and C-S135R are the most frequently detected mutations while the mutation B-H277Y was observed to decrease since 2016.

For information on mutations detected in the sdh, please refer to the following link.

Disease pressure in **2022** was variable, ranging from low to moderate depending on the barley-growing regions of Europe.

In **2022**, the frequency of mutations increased compared to the previous season and is at a high level in North-Western Europe.No mutations or reduced sensitivity were detected in Russia.

The frequency of mutations or reduced sensitivity was low in Bulgaria, Czech Republic, Denmark, Hungary, Latvia, Lithuania, Romania, Slovakia, Sweden, Switzerland and Ukraine.
Moderate frequencies were detected in Italy, Poland and Spain.
Moderate to high frequencies were observed in France, Germany, Ireland and the United Kingdom.
Disease pressure in **2023** was low to moderate depending on the barley-growing regions of Europe.
In **2023**, the frequency of mutations increased compared to the previous season and is at a high level in North-Western Europe.
No mutations or reduced sensitivity were detected in Latvia and Russia.
The frequency of mutations or reduced sensitivity was low in Bulgaria, Czech Republic, Denmark, Finland, Italy, Romania, Slovakia, Sweden, Switzerland and Ukraine.
Moderate frequencies were detected in Austria, Greece, Hungary, Lithuania, the Netherlands, Poland and Spain.
Variable frequencies, ranging from moderate to high, were observed in France, Germany, Ireland and the United Kingdom.
Among the mutations with moderately decreased sensitivity, C-G79R, C-H134R, C-N75S and C-S135R are the most frequently detected mutations while the mutation B-H277Y was observed to further decrease since 2016.

For information on mutations detected in the sdh, please refer to the following link.

Barley – Scald (*Rhynchosporium secalis* syn. *Rhynchosporium commune*)
(BASF, Sumitomo, Syngenta, FMC)

In **2024**, full sensitivity was observed for the following countries: Germany, France, Hungary, Ireland, Slovakia, Romania and the United Kingdom. Single isolates showing slightly decreased sensitivity were observed and the mutation sdh C-N85S was detected again in samples originating from Spain and for the first time in Czech Republic.

Historical background:
Monitoring programs were carried out since **2003**.
In **2017**, isolates were tested from France, the United Kingdom, Germany, Denmark, Spain, Latvia, Italy, Czech Republic and Poland and were sensitive, within the baseline.
In **2018**, isolates coming from Denmark, France, Germany, Ireland, Poland and the United Kingdom showed full sensitivity.
In **2019**, isolates coming from Belgium, France, Germany, Ireland, Poland and the United Kingdom showed full sensitivity.
2020 samples originating from France, Germany, Hungary, Ireland, Italy, Latvia, the Netherlands, Poland, Slovakia, Spain, Ukraine, the United Kingdom showed full sensitivity.
In **2021**, high sensitivity was observed for the following countries: Czech Republic, Denmark, Germany, France, Hungary, Ireland, Italy, Poland, Spain and the United Kingdom.
Single isolates showing slightly decreased sensitivity with no reported reduction in field efficacy were detected. In some isolates, the mutation sdh C-N85S was detected.
In **2022**, high sensitivity was observed for the following countries: Czech Republic, Germany, France, Ireland, Italy, Poland and the United Kingdom.

Single isolates showing slightly decreased sensitivity were observed and the mutation sdh C-N85S was detected in samples originating from Spain.
In **2023**, full sensitivity was observed for the following countries: Denmark, Germany, France, Hungary, the Netherlands and Romania. Single isolates showing slightly decreased sensitivity were observed and the mutation sdh C-N85S was detected again in samples originating from Spain.

Barley - Ramularia leaf spot (*Ramularia collo-cygni*)

(BASF, Bayer, Syngenta)

In **2024**, moderate to high frequencies of mutations were observed in Austria, Bulgaria, Czech Republic, Croatia, Denmark, France, Germany, Hungary, Ireland, Italy, Lithuania, the Netherlands, Poland, Sweden, Slovenia, Spain, Switzerland and the United Kingdom.
The mutation C-N87S, linked to lower resistance factors, was detected at high frequencies and is still dominating in most monitored geographies.
Significantly decreased sensitivity is mainly associated with the mutations C-G91R, C-H146R/L, C-G171D or C-H153R.
Overall, SDHIs continue to contribute to Ramularia disease control.

Historical background:
In **2014**, single isolates with slightly decreased sensitivity were detected in France and Germany. Retesting of **2014** isolates showed full sensitivity. Isolates sampled in **2014** from the Czech Republic were sensitive, within the baseline.
In **2015**, extensive monitoring in Germany showed particularly in trial-sites for the first time occurrence of strains with strongly decreased dose-response in bioassays, carrying the mutation C-H146R or C-H153R. Another mutation, C-N87S, which was found to be associated with low resistance factors, was found in Germany, Ireland and Slovenia in single isolates. No mutations were detected in Austria and Croatia.
In **2016**, no mutations were detected in Sweden, Denmark, Estonia, Slovakia, France and Greece.
Samples carrying the mutations C-H146R or C-H153R, associated with significantly decreased sensitivity, were detected in Germany, Ireland, the Netherlands and the UK. Observations in trial sites confirmed the results from **2015**. A decreased dose response was observed in field trial sites in Germany and the United Kingdom with high proportions of SDHIs in spray programs. Samples taken from the untreated plots at the same sites showed baseline level sensitivity.
In **2017** (disease pressure moderate), reported data show no mutations in Finland, Norway, Spain and Greece. Low frequency had been found in Estonia, Latvia, Italy, Austria, Switzerland, Czech Republic, Denmark and Sweden. A heterogeneous situation, ranging from low to high (frequency of mutations and sensitivity), was observed in Germany, France, United Kingdom, Ireland and Netherlands.
Disease pressure was low in **2018**. No mutations were found in Czech Republic, Finland, Italy, Latvia, Norway, Romania, Russia, Spain, Sweden and Switzerland.
Low frequency has been found in Austria, France, Hungary, Poland and the Ukraine.
A heterogeneous situation, ranging from low to high (frequency of mutations and sensitivity), was observed in Belgium, Germany, Denmark, the United Kingdom, Ireland and the Netherlands.

Significantly decreased sensitivity is mainly associated with the mutations C-G91R, C-H146R/L, C-G171D or C-H153R. Additionally, a mutation linked to lower resistance factors (C-N87S) was detected.

Data from **2019** showed no mutations in Austria, Italy, Latvia, Norway, Spain, Slovenia, Slovakia and Switzerland.

Low frequency has been found in Austria, Hungary, Poland, Sweden and Ukraine.

A heterogeneous situation, ranging from low to high (frequency of mutations and sensitivity), was observed in Belgium, Germany and the Netherlands.

Moderate to high frequencies of mutations were detected in Denmark, France, Ireland and the United Kingdom.

Data from **2020** showed no mutations in Czech Republic and Slovakia.

Low frequency has been found in Hungary, Italy, Spain and Switzerland.

A heterogeneous situation, ranging from low to high (frequency of mutations and sensitivity), was observed in Germany, Denmark, France, Lithuania, Sweden and the United Kingdom.

Moderate to high frequencies of mutations were detected in Ireland.

Significantly decreased sensitivity is mainly associated with the mutations C-G91R, C-H146R/L, C-G171D or C-H153R. Additionally, mutations linked to lower resistance factors (C-N87S, B-T267I, B-N224T) were detected.

Data from **2021** showed no mutations in Italy.

Low frequency has been found in Austria, Czech Republic, Croatia, Denmark, Sweden and Spain.

A heterogeneous situation, ranging from low to high (frequency of mutations and sensitivity), was observed in France, Germany, Ireland, the Netherlands and the United Kingdom.

Significantly decreased sensitivity is mainly associated with the mutations C-G91R, C-H146R/L, C-G171D or C-H153R. Additionally, mutations linked to lower resistance factors (C-N87S, B-T267I, B-N224T) were detected.

Overall, the previously dominating C-H146R mutation is observed to decrease while C-N87S is increasing.

In **2022**, a low frequency of SDHI-adaptations has been found in Italy and Spain.

Moderate to high frequencies of mutations were observed in Austria, Denmark, France, Germany, Ireland, the Netherlands, Poland, Sweden, Switzerland and the United Kingdom.

Significantly decreased sensitivity is mainly associated with the mutations C-G91R, C-H146R/L, C-G171D or C-H153R. Additionally, mutations linked to lower resistance factors (C-N87S, B-T267I, B-N224T) were detected.

The previously mentioned increase of C-N87S is further continuing. Overall, SDHIs continue to contribute to Ramularia disease control.

In **2023**, a low frequency of SDHI-adaptations has been found in Romania and Spain.

Moderate to high frequencies of mutations were observed in Croatia, Denmark, Germany, Hungary, Ireland, Italy, the Netherlands, Poland, Slovenia, Switzerland and the United Kingdom.

A variable frequency of mutations was recorded for France, ranging from low (South) to high (North).

The mutation C-N87S, linked to lower resistance factors, was detected at high frequencies and is dominating in most monitored geographies.

Significantly decreased sensitivity is mainly associated with the mutations C-G91R, C-H146R/L, C-G171D or C-H153R.

Overall, SDHIs continue to contribute to Ramularia disease control.

Barley – Rust (*Puccinia hordei*)

(Bayer, Sumitomo, Syngenta)

In **2024**, samples from Belgium, Bulgaria, Denmark, France, Germany, Lithuania, Poland, Sweden and the United Kingdom were analyzed. Single isolates, carrying the mutation C-I87F were detected in Belgium, France, Germany and the United Kingdom with no change in field efficacy being reported. In the remaining countries, full sensitivity was reported.

Historical background:
Monitoring programs were carried out since **2006**. All isolates tested until **2014** were sensitive, within the baseline. No monitoring was carried out in **2015, 2016** and **2017**.
In **2018**, few isolates with a low resistance factor have been identified for the first time in France and the United Kingdom. All isolates originating from Denmark, Germany and Sweden were fully sensitive.
2019 samples from France and the United Kingdom showed a similar sensitivity pattern as observed in **2018** with some isolates showing low resistance factors (no impact on field efficacy reported).
High sensitivity was observed in **2020** and **2021** samples originating from Bulgaria, Denmark, France, Germany, Hungary, Italy, Poland, Romania, Spain and the United Kingdom.
Single isolates carrying the mutation C-I87F were detected showing low resistance factors with no impact on field efficacy, originating from France and the United Kingdom.
In **2022**, samples from France, Germany and Hungary were analyzed with full sensitivity shown in Germany and France. Single isolates, carrying the mutation C-I87F were detected in France, showing low resistance factors with no impact on field efficacy.
In **2023**, samples from Belgium, Bulgaria, Denmark, France, Germany, Hungary, Italy, the Netherlands, Poland, Romania, Sweden and the United Kingdom were analyzed. Single isolates, carrying the mutation C-I87F were detected in France, Germany and the Netherlands, showing low resistance factors with no impact on field efficacy. In the remaining countries, full sensitivity was reported.

Barley – smut (*Ustilago* spp.)

(Syngenta)

No monitoring was carried out in **2024**.

Historical background:
Samples collected in **2018** from the Czech Republic, Denmark, Ireland, Italy, Poland, Sweden and the United Kingdom were fully sensitive.
A monitoring program was carried out in **2019** including samples from Belgium, Bulgaria, Czech Republic, Denmark, France, Germany, Italy, the Netherlands, Poland, Romania, Slovakia, Spain, Sweden, Switzerland and the United Kingdom. All isolates showed full sensitivity.
Monitoring in **2020** was carried out using samples from Belgium, Czech Republic, Denmark, Germany, Ireland, Latvia, Poland, Romania, Slovakia, Sweden, Switzerland and the United Kingdom. The samples showed full sensitivity.

Full sensitivity was observed in **2021** samples originating from Austria, Bulgaria, Denmark, France, Germany, Hungary, Italy, Lithuania, Latvia, Poland, Romania, Slovakia, Spain, Sweden, Switzerland and the United Kingdom.
Samples originating from Austria, Bulgaria, Czech Republic, Estonia, France, Germany, Hungary, Lithuania, Poland, Romania and the United Kingdom showed full sensitivity in **2022** monitoring programs.
Samples originating from Austria, Bulgaria, Czech Republic, France, Germany, Hungary, Italy, Lithuania, Poland, Romania and the United Kingdom showed full sensitivity in **2023** monitoring programs.

Barley – Powdery mildew (*Blumeria graminis*)

(Sumitomo, Syngenta)

No monitoring was carried out in **2023** and **2024**.

2019 monitoring programs included samples from Czech Republic, France, Germany and the United Kingdom and showed full sensitivity.
No monitoring results are available from **2020**.
Full sensitivity was reported in **2021** from Bulgaria, France, Germany, Hungary, Italy, Poland, Romania and the United Kingdom.
In **2022** samples originating from Estonia, France, Germany, Hungary and Italy, full sensitivity was reported.

Barley – Yellow Stripe (*Helminthosporium gramineum*)

(Syngenta)

A limited monitoring program in **2024** (Lithuania and Sweden) showed full sensitivity.

In limited monitoring programs in **2020** and **2021**, samples originating from Germany, Poland and Sweden were analyzed and showed full sensitivity.
In **2022**, samples originating from Germany, Hungary, Poland, Sweden and the United Kingdom showed full sensitivity.
In **2023**, samples originating from Finland, France, Hungary, Italy, Poland and the United Kingdom showed full sensitivity.

1.2. Grape diseases

Grape grey mold (*Botrytis cinerea*)

(Bayer, BASF)

In **2024**, monitoring was carried out in Italy and Germany. Results show mostly sensitive strains in Italy and high frequency of mutations in Germany with more severe mutations remaining at a low level.

Historical background:
Extensive monitoring programs were carried out since **2003**.
In **2012**, few isolates with resistance to SDHIs were detected in France and Germany.

An increasing frequency was observed in Germany in **2013**. No new mutations have been identified in **2014** and the percentage of less sensitive isolates remained stable compared to **2013**.
In **2015**, resistant isolates were detected in Germany, France, Italy, Portugal and Chile at low frequency.
In **2016**, samples were tested coming from Spain, France, Germany, Austria, Hungary, Italy and Greece. New mutations were detected at the following positions: C-P80H and C-P80L in single isolates in Germany and France. The resistance factor of these mutations was very low. Depending on the regions, the overall frequency of mutation B-H272Y, /R and B-N230I remains at a moderate to high level in Chile and Germany, resp. The mutation B-P225H /L /F remains overall at a low level. In France, low levels of resistance were found.
In **2017**, monitoring in France, Germany and Italy resulted in overall low frequencies of the C-P225. mutations. The C-P225F and C-N230I-mutations were found to be slightly increased in Germany.
In **2018**, monitoring in Germany and Italy resulted in overall low frequencies of the C-P225F mutations. C-N230I, C-P80H mutations were found to be increased to moderate levels in Germany. Compared to **2016**, the sensitivity of samples from Chile decreased slightly.
No monitoring results are available for **2020**.
In **2019, 2020** and **2021**, monitoring was carried out in France, Italy and Germany. Results show mostly sensitive strains in Italy, slightly increasing frequencies of strains with reduced sensitivity in France and high frequency of mutations in Germany with more severe mutations remaining at a low level.
In **2022**, monitoring was carried out in Italy and Germany. Results show mostly sensitive strains in Italy and high frequency of mutations in Germany with more severe mutations remaining at a low level.
In **2023**, monitoring was carried out in France, Italy and Germany. Results show mostly sensitive strains in France and Italy; and high frequency of mutations in Germany with more severe mutations remaining at a low level.

Grape powdery mildew (*Erysiphe necator*)
(BASF, Bayer, Syngenta)

In **2024**, monitoring programs applying bioassays, were carried out in Austria, Switzerland, France, Germany, Greece, Hungary, Italy, Portugal, Romania, Slovakia, Spain and Türkiye.
Low numbers of slightly SDHI-adapted isolates were detected in Austria, Hungary, Italy, Romania, and Slovakia. A higher number of those adapted isolates were found in France and Germany.
A few highly adapted strains were detected in France and Türkiye. An overall sensitive situation was found in Portugal, Greece, Switzerland and Spain.
Mutation analysis is still ongoing.

Historical background:
Extensive monitoring programs were carried out since **2003**. All isolates tested were sensitive, within the baseline (Austria, France, Germany, Hungary, Portugal, Spain, Switzerland). Single strains carrying a mutation (SDH subunit C-G169D) with moderate resistance factors were detected in single fields in Italy (retrospective investigations from **2014** samples, no detection in **2015**), Slovenia and Greece (both from **2015** samples), resp.

In **2016**, the mutation B-H242R was detected in Czech Republic, Slovakia and in Hungary and at very low levels in France. The mutation C-G169D was not detected in **2016** studies. Full sensitivity was observed in Greece, Portugal, Germany, Italy, Spain and Austria.

In **2017**, the mutation B-H242R or strains with the B-H242R phenotype were detected at heterogenous levels in Hungary, Slovakia and Slovenia. Low levels were found in single samples in France and in Italy in only one sample from the South.

Full sensitivity was observed in Portugal, Germany, Spain and Greece.

The mutation C-G169D/S or its phenotype was not detected in **2017** studies.

In **2018**, the mutation B-H242R was detected at heterogenous levels in Hungary and Greece.

The mutation C-G169D was detected in **2018** in Ukraine in single commercial sites.

Full sensitivity was observed in Croatia, France, Germany, Italy, Portugal and Spain.

Bioassays carried out in **2019** showed full sensitivity in Austria, Croatia, Germany, Italy, Portugal, Slovenia and Spain. Mutation analyses showed the mutation B-H242R at low levels in France, Tuerkiye and Ukraine. The mutation C-G169D was detected in **2019** in Tuerkiye in single commercial sites. The mutation B-I244V was detected in a single sample originating from Ukraine.

Bioassays carried out in **2020** showed full sensitivity in Austria, Croatia, Italy, Portugal and Spain. Single sites with insensitive isolates were detected in Hungary, France and Germany.

Bioassays carried out in **2021** showed full sensitivity in Austria, Croatia, Italy, Portugal, Spain and Switzerland. Single sites with insensitive isolates were again detected in Hungary, France and Germany.

Mutation analyses in **2020** and **2021** showed the presence of the following mutants: B-H242R, B-I244V, C-G169D/S and C-A83V. Also, double mutants with B-H242R+C-G169S and B-I244V+C-G169S were found in single locations.

C-G169D was found in Greece at high frequency. Moderate frequencies were found in Hungary and Tuerkiye; low frequencies in Austria and single cases in Italy and Germany.

B-H242R was found at moderate frequency in Austria and Hungary and low frequency in Germany, France, Italy and Tuerkiye.

B-I244V and C-G169S were found at moderate frequencies in Germany.

In **2022**, monitoring programs applying bioassays were carried out in Austria, Croatia, Czech Republic, France, Germany, Greece, Hungary, Italy, Portugal, Romania, Spain and Tuerkiye.

Based on these bioassays, full sensitivity was detected in Austria, Croatia, Czech Republic and Spain.

Low frequencies of SDHI-adapted strains were detected in France, Italy, Portugal and Romania.

Low to moderate frequencies were detected in Germany, Greece, Hungary and Tuerkiye.

As in previous years, mutation analyses showed the presence of the following mutants: B-H242R, B-I244V, C-G169D/S. Also, double mutants with B-H242R+C-G169S and B-I244V+C-G169S were found in single locations. For the first time, C-A83V was detected in single isolates originating from France and Germany.

No mutations were detected in Bulgaria, Spain and Switzerland.

In **2023**, monitoring programs applying bioassays, were carried out in Austria, Croatia, Czech Republic, Switzerland, France, Germany, Hungary, Italy, Portugal and Spain.

Low frequencies of SDHI-adapted strains were detected in Austria, Croatia, Czech Republic, France, Hungary, Italy, Portugal, Spain and Switzerland.

Frequencies in Germany increased to a moderate level.

For the first time, C-A83V was detected in single isolates originating from France and Germany. Mutations B-H242R, B-I244V, C-G169D/S and C-A83V were detected with varying frequencies across different regions. Double mutants were again detected – their impact is under investigation and still unknown. No mutations were detected in Bulgaria, Spain and Switzerland.

1.3 Pomefruit and stonefruit diseases

Apple scab (*Venturia inaequalis*)

(Corteva, Bayer, BASF, Syngenta)

In **2024**, samples were analyzed originating from Croatia, France, Germany, Greece, the Netherlands, Poland, Portugal, Türkiye and Spain. As in previous years, one population with sensitivity slightly above the baseline was detected in France and Greece while all other populations showed high sensitivity.
The following mutation were detected in both samples: B-T253I. Additionally, C-N85S was detected in the sample form Greece.

Historical background:
Extensive monitoring programs were carried out since **2005**.
Data from commercial sites in **2015** show full sensitivity in Bulgaria, Belgium, Switzerland, Germany, Spain, France, Greece, Hungary, Croatia, Ireland, Italy, Latvia, Lithuania, Netherland, Romania, Portugal, Poland, the United Kingdom and Serbia. Single isolates from trial sites with slightly reduced sensitivity were found in Bulgaria, Italy and Spain. Product performance was not affected. For resistant isolates originating from trial sites in Italy, the mutations B-T253I and C-H151R were detected.
In **2016**, analyzed samples showed full sensitivity, coming from the United Kingdom, Germany, Italy, Portugal, Spain, France, Belgium, the Netherlands and Poland.
Samples analyzed in **2017** showed full sensitivity, coming from Germany, Italy, Portugal, Spain, France, Belgium, the Netherlands, Hungary, Ukraine, the United Kingdom, Greece, Austria, Tuerkiye and Poland.
Samples analyzed in **2018** showed full sensitivity, coming from Austria, Belgium, France, Germany, Greece, Hungary, Italy, Poland, Portugal, Romania, Spain, Tuerkiye and the United Kingdom. All samples tested were fully sensitive.
Samples analyzed from **2019** showed full sensitivity, coming from Austria, Belgium, France, Germany, Hungary, Italy, Romania, Spain, Poland, Portugal and the United Kingdom.
Monitoring in **2020** was carried out in Belgium, France, Hungary, Italy, the Netherlands, Poland, Romania, Spain and the United Kingdom and showed full sensitivity.
2021 Monitoring programs are still ongoing. Preliminary data shows overall full sensitivity in the following countries: Austria, Belgium, Denmark, France, Germany, Greece, Hungary, Italy, Ireland, the Netherlands, Poland, Portugal, Romania, Slowenia, Spain, Sweden, Switzerland, Tuerkiye and UK.
In retrospective analyses of samples from 2021, the presence of the mutations C-N85S and C-H151R was found at very low frequencies in one sample originating from Tuerkiye. All other samples were characterized as sdh wild types.
2022 monitoring programs show overall full sensitivity in the following countries: Austria, Croatia, Denmark, France, Italy, Ireland, the Netherlands, Poland, Portugal, Romania, Serbia, Spain, Sweden and the UK.

In spore germination assays, single spores within populations from few locations showed germination outside of the baseline concentrations, originating from the following countries: Belgium, Germany, Greece, Hungary, Switzerland and Tuerkiye. Such samples are under further investigations.
In **2023**, samples were analyzed originating from Austria, Belgium, Germany, Greece, Italy, Poland and Spain. As in previous years, one population with sensitivity slightly above the baseline was detected in Italy while all other populations showed high sensitivity.

Apple powdery mildew (*Podosphaera leucotricha*)
(Bayer, BASF)

Full sensitivity was detected in **2024** samples from Belgium, France, Germany, Italy, Poland, Portugal and Spain.
Single isolates outside the baseline were found in Hungary and Greece. Mutation analysis is ongoing.

Historical background:
All isolates tested in **2014** were sensitive, within the baseline (France, Spain, Austria, Hungary, Germany, Romania, Bulgaria).
All isolates tested in **2015** coming from Belgium, Switzerland, Germany, Spain, France, Italy, Latvia, the Netherlands, Portugal and Poland were sensitive, within the baseline.
In **2016**, all isolates tested showed full sensitivity. Samples originated from Belgium, Bulgaria, Switzerland, Germany, Spain, France, Portugal, Greece, the Netherlands, Czech Republic, Hungary, Italy, Lithuania, Poland and Romania.
In **2017**, all isolates tested showed full sensitivity. Samples originated from Belgium, Germany, Spain, France, Portugal, the Netherlands, Hungary, Italy, Croatia and Poland.
In **2018**, all isolates tested showed full sensitivity. Samples originated from Germany, Spain, France, Portugal, Hungary, Italy, Greece and Poland.
In **2019**, all isolates from France, Italy, Poland and Spain were sensitive. In **2020,** samples originating from Belgium, Germany, France, Greece, Hungary, Italy, Poland, Portugal and Spain showed full sensitivity.
Full sensitivity was detected in **2022** samples from Austria, Belgium, Croatia, France, Germany, the Netherlands, Italy, Poland, Portugal, Spain and Tuerkiye.
One sample from Greece showed a moderate adaptation and carried the mutation C-G149R (homologous to G150R in *S. sclerotiorum* and G151R in *S. fuliginea*).
Full sensitivity was detected in **2023** samples from Belgium, Czech RepublicFrance, Germany, Italy, Poland, Portugal and Spain.

Brown spot on pear (*Stemphylium vesicarium*)
(Syngenta)

No monitoring was carried out in **2024.**

Historic background:

In **2018**, samples were collected in Belgium, Italy, Portugal and Spain. Moderate frequency of resistance was found in Italy. Low frequency was detected in Belgium and Portugal. No resistance was detected in Spain.

2019 samples analyzed from a multi-year trial site in Portugal showed the presence of resistance.
2020 and **2021** samples from Belgium, Italy, Spain, Portugal were analyzed. Single cases with moderate frequencies were found in Italy and Portugal (limited monitoring). Isolated cases of less sensitive strains were reported from Belgium.
2020 and **2021** samples from Belgium, Italy, Spain, Portugal were analyzed. Single cases with moderate frequencies were found in Italy and Portugal (limited monitoring). Isolated cases of less sensitive strains were reported from Belgium.

Brown rot on stonefruit (*Monilinia* spp.)
(BASF, Syngenta)

No monitoring was carried out in **2024.**

Historical background:
Sensitivity of samples from Spain, France, Italy, Germany and Poland was analyzed and showed full sensitivity in **2014**.
In **2015**, samples originating from Belgium, France and Hungary were all sensitive, within the baseline.
In **2015**, samples from Italy, France and Spain were studied (species not confirmed). Single isolates with reduced sensitivity were detected at 3 trial sites in France. Only sensitive phenotypes were reported from Italy and Spain.
In **2016**, samples from Italy, France, Poland, Hungary and Greece were studied (species: *M. laxa*, *M. fructicola*, *M. fructigena*). There is no indication for reduced sensitivity and mutations in the sdh genes.
Samples in **2017** were analyzed originating from Croatia, Czech Republic, France, Germany, Italy, Poland, Romania and Spain, including cherry, nectarines, peach and plum.
Reduced sensitivity was detected in samples coming from Germany, Spain, France, Croatia and Italy. Full sensitivity was observed in the Czech Republic, Poland and Romania.
The analysis of *Monilinia* species present in monitoring samples from **2017** and **2018** highlighted/ showed a higher frequency of *M. fructicola* and *M. laxa* compared to *M. fructigena*.
Samples were analyzed originating from Belgium, Bulgaria, Croatia, Czech Republic, France, Germany, Greece, Hungary, Italy, Poland, Romania and Spain, including cherry, apricots, nectarines, peach and plum.
Reduced sensitivity was detected at low frequency in samples coming mainly from trial sites in the Czech Republic, Germany, Greece, Romania, Spain, France and Italy.
Full sensitivity was observed in Belgium, Bulgaria, Croatia, Hungary and Poland.
The analysis of Monilinia species present in monitoring samples from **2019** showed a higher frequency of *M. fructicola* and *M. laxa* compared to *M. fructigena*.
Samples were analyzed originating from France, Germany, Greece, Hungary, Italy, Poland and Spain including cherry, apricots, nectarines, peach and plum.
Increased EC50 values were detected in single isolates.
2020 samples originating from France, Germany, Greece, Hungary, Italy, Poland, Portugal and Spain showed full sensitivity.
Reduced sensitivity was detected in single *M. fructigena* isolates from one location each in Hungary and Poland.

2021 monitoring included the following countries: Bulgaria, Croatia, Czech Republic, France, Germany, Greece, Hungary, Italy, Poland, Portugal, Romania, Spain and Switzerland.

A broad sensitivity range was again observed, possibly linked with the applied method and *Monilinia* species. The understanding of the results needs further clarification. No impact on field efficacy was reported.

2023 monitoring included the following countries: Belgium, Bulgaria, France, Germany, Greece and Hungary.

The majority of samples was sensitive. Single isolates showed higher EC50 values, possibly linked to the test method or different *Monilinia* species. The understanding of the results needs further clarification. No impact on field efficacy was reported.

1.4. Cucurbit diseases

Cucurbit powdery mildew (*Sphaerotheca fuliginea,* syn. *Podosphaera xanthii, Erysiphe cichoracearum, Golovinomyces cichoracearum)*

(The determination of the species is not part of most monitoring programs)
(BASF, Bayer)

No monitoring was carried out in **2024.**

Historical background:

Extensive monitoring programs were carried out since **2005**.

Monitoring studies in **2014** were carried out in France, Italy, Greece, Germany, Switzerland, China and Spain. Full sensitivity was observed except for Spain, Italy and China, where single resistant isolates were detected.

In **2015**, full sensitivity was observed in Belgium, Bulgaria, Spain and the Netherlands. Resistant isolates were detected in Germany, Czech Republic, Italy, Poland, Greece and France.

P. xanthii samples in **2016** were analyzed originating from zucchini, cucumber, melon and water melon. Single samples showed resistance and were found in Belgium, France and Greece. Decreased sensitivity was reported in a few samples from China. No resistance was detected in Spain, Italy, the Netherlands.

P. xanthii samples in **2017** were analyzed originating from zucchini, cucumber and melon.

Single samples showed resistance and were found in Belgium, Italy, Poland, Germany, France, Spain and Greece. No resistance was detected in Portugal. All samples originating from melon were fully sensitive. Decreased sensitivity was reported in a few samples from China.

P. xanthii samples in **2018** were analyzed originating from zucchini, cucumber and melon.

Single samples showed resistance and were found in Italy, Poland, Germany, Tuerkiye and France. No resistance was detected Spain and Portugal.

In **2018**, samples were collected in 7 provinces in China. Decreased sensitivity was reported from samples at low frequency coming from 2 provinces (Hebei, Liaoning).

P. xanthii samples in **2019** were analyzed originating from zucchini, cucumber and melon.

Samples showing resistance were found in Italy, Tuerkiye and Spain. No resistance was detected in France and Greece.

In **2020**, low frequency of resistance in *S. fuliginea* was observed in samples originated from France, Portugal, Tuerkiye and Spain. Moderate frequencies were observed in Greece and Italy.
In **2021**, moderate to high frequencies of resistance were observed in all countries included in the monitoring program: Greece, Italy, Spain and Tuerkiye.
In **2022**, moderate to high frequencies of resistance were observed in all countries included in the monitoring program: Greece, Italy, Portugal, Spain and Tuerkiye.
In **2023**, moderate to high frequencies of resistance were observed in all countries included in the monitoring program: France, Greece, Italy, the Netherlands and Portugal.

Cucurbits - Target spot (*Corynespora cassiicola*)
(BASF, Syngenta)

No monitoring was carried out in **2024.**
2022 samples, originating from China showed a broad sensitivity with a few resistant isolates. Reported mutations were B-H278Y and C-N75S.
No monitoring data is available for **2021**.
Monitoring of **2020** samples originating from China (province Guangdong) resulted in full sensitivity.

1.5 Other crops

Strawberries and soft fruit – Grey mold (*Botrytis cinerea*)
(Bayer, Corteva, BASF)

Monitoring in **2024** was carried out on samples originating from Germany, Italy, Poland and the United Kingdom.
Overall, there is still a stable sensitivity situation in all monitored countries.
In most countries mentioned, the mutation B-H272R were detected at very low levels. B-P225F was detected at low levels.
The frequencies of B-N230I and C-P80H stayed overall constant at a moderate level with a high variability within and between regional samples.

Historical background:
Extensive monitoring programs were carried out since **2003**.
In **2015**, monitoring was carried out in Germany, Belgium, Hungary, Italy, France, Denmark, Poland, Sweden, the Netherlands (raspberry) and the United Kingdom. Some resistant isolates were detected in Germany, Poland, Belgium and the United Kingdom. When used according to manufacturers' recommendations, field performance of SDHI containing products is good.
In **2016**, the majority of isolates showed full sensitivity, originating from Germany, France and the United Kingdom. In all countries mentioned, the mutations B-H272R and B-H272Y were detected at moderate levels and B-N230I was detected at low levels.
In **2017**, the majority of isolates showed full sensitivity, originating from France.
Low levels found in Germany, United Kingdom, Sweden, Poland and Denmark.
In all countries mentioned, the mutations B-H272R and B-H272Y were detected at moderate levels and B-N230I as well as B-P225F were detected at low levels.
In **2018**, isolates from France showed full sensitivity.
Low levels of mutants were found in Poland and Sweden. Moderate levels were detected in Denmark, Germany, Norway and the United Kingdom.

In **2019**, low levels of mutants were identified in Denmark, France and Germany. Moderate levels were observed in Poland and the United Kingdom.

In all countries mentioned, the mutations B-H272R and B-H272Y were detected at moderate levels and B-P225F was detected at low levels.

The frequencies of B-N230I and C-P80H were observed to increase slightly between **2018** and **2019**.

Monitoring in **2021** and **2022** was carried out on samples originating from France, Germany, Italy, Poland, Spain and Sweden.

Overall, there is a stable sensitivity situation. In bioassays, single adapted isolates were detected in Italy and Spain.

In most countries mentioned, the mutation B-H272R and B-H272Y were detected at low levels. B-P225F was detected at very low levels.

The frequencies of B-N230I and C-P80H stayed overall constant at a moderate level with a high variability within and between regional samples.

Monitoring in **2023** was carried out on samples originating from Belgium, Greece, Italy, the Netherlands, Poland and Spain.

Overall, there is a stable sensitivity situation in all monitored countries. In bioassays, single adapted isolates were detected in Greece and Spain.

In most countries mentioned, the mutation B-H272R and B-H272Y were detected at low levels. B-P225F was detected at very low levels.

The frequencies of B-N230I and C-P80H stayed overall constant at a moderate level with a high variability within and between regional samples.

Grey mold (*Botrytis cinerea*) on other vegetable crops (tomato, lettuce, zucchini, cucumber, beans)

(BASF)

No monitoring data were generated in **2024**.

Historical background:

Monitoring data were reported from **2013** (France, Italy, Portugal, Greece).

Resistant isolates were found in Italy, Greece and Portugal. No cases of reduced field performance were reported.

No monitoring was carried out in **2015, 2016, 2017** and **2018**.

Samples from **2019** and **2020**, originating from China (province Zhejjang) resulted in low frequency of resistant isolates.

No monitoring data are available for **2021**.

Limited monitoring data originating from samples on beans from **2023** in Belgium and France showed a Sensitive situation with few adapted isolates.

Vegetables – *Alternaria* spp. (cabbage, broccoli, carrot)

No monitoring was carried out in since **2019**.

Historical background:

Resistance was detected in **2014** at low frequency in *A. brassicae* and *A. brassicicola* isolated from cabbage in Germany and *A. alternata* sampled from broccoli in Spain.

In **2015**, a single isolate with resistance was detected in *A. alternata* from broccoli in Spain.
No data were reported for **2016**.
In **2017**, samples were analyzed originating from Croatia, France, Lithuania, Denmark, Germany, Italy, Netherlands, Poland, Portugal, Spain, Sweden and Bulgaria, coming from broccoli, cabbage and carrots.
Fully sensitivity was observed in *A. brassica*, *A. brassicicola* and *A. dauci*.
Reduced sensitivity was observed in *A. alternata* samples originating from Croatia, Germany, Netherlands and Poland coming from carrots and cabbage.
No monitoring was carried out in **2018**.

Onion – Stemphylium leaf blight (*Stemphylium vesicarium*)

(Syngenta)

In **2021**, limited monitoring resulted in single cases of decreased sensitivity in Poland, while full sensitivity was reported from Germany.
Single isolates from **2020** originating from Croatia, the Netherlands and Spain were analyzed and showed full sensitivity.

Peas, beans, lettuce – White mold (*Sclerotinia sclerotiorum*)

(BASF, Syngenta)

In **2023**, full sensitivity was reported from Belgium, Germany France and the Netherlands.

Historical background:
In **2015**, samples from the Netherlands and Belgium were all sensitive, within the baseline.
No monitoring was carried out in **2016**.
In **2017**, full sensitivity was observed in samples originating from France, Germany and Poland.
No monitoring was carried out in **2018** and **2019**.
In **2020**, samples from France and Spain showed full sensitivity. One single isolate originating from lettuce on a trial site in Spain showed decreased sensitivity.
In **2021**, full sensitivity was reported from France and the Netherlands.

Oilseed rape – White mold (*Sclerotinia sclerotiorum*)

(BASF, Syngenta)

In **2024**, samples were investigated coming from Germany, France and Lithuania. Full sensitivity was observed in Germany. Biotests confirmed a stable situation in France as in previous seasons with a low number of isolates being outside of the baseline sensitivity. Single isolates with decreased SDHI sensitivity were as well detected in Lithuania. Molecular studies detected low (Lithuania) to moderate (France) frequencies of the mutations B-H273Y, C-H146R, or D-H132R.

Historical background:
Extensive monitoring programs were carried out since **2006**.

In **2014** and **2015**, single resistant isolates were detected in France. No resistant isolates were detected in **2014** in Czech Republic, Germany, the United Kingdom and Poland.
In **2015**, no resistance was detected in the Netherlands, Belgium, France, Poland, Czech Republic, Croatia and Germany.
In the season **2016**, samples were tested from Germany, France, the United Kingdom, Czech Republic, Lithuania, Denmark and Poland. No to low frequency of resistance was detected in France and Germany.
Disease pressure in **2017** was low to moderate. In the season **2017**, samples were tested from Germany, France, the United Kingdom, Czech Republic, Latvia, Sweden, Romania, Denmark and Poland. Full sensitivity was observed in Czech Republic, Romania and Poland. Low frequency of resistance was detected in Germany, France, the United Kingdom, Latvia, Sweden and Denmark.
In the season **2018**, samples were tested from France, Germany, Hungary, Romania, Poland and the United Kingdom.
A low frequency of adapted isolates was detected in France. The following mutations were associated to decreased sensitivity in past monitoring programs: B-H273Y, C-H146R, C-G91R, D-H132R, C-G150R, D-T108K.
In the season **2019**, samples were tested from Czech Republic, Germany, Hungary, Romania, Slovakia, Poland, Ukraine and the United Kingdom. All samples showed full sensitivity. A low frequency of adapted isolates was detected in France.
In **2020**, monitoring was carried out in Bulgaria, Czech Republic, Denmark, France, Germany, Hungary, Latvia, Lithuania, Poland, Romania, Slovakia, Ukraine and the United Kingdom.
Stable and low frequency was observed in France in **2019** and **2020**.
Decreased sensitivity was observed in Germany and Lithuania in single locations at a very low frequency.
In **2021**, results from monitoring programs in Bulgaria, Czech Republic, France, Germany, Hungary, the Netherlands, Poland, Romania and Ukraine show high sensitivity.
Stable and low frequency of sensitivity adaptation was observed in France as in the previous seasons. Decreased sensitivity was observed in Germany in a single location at a very low frequency.
In **2022**, samples were investigated coming from Bulgaria, Czech Republic, Denmark, Estonia, Germany, France, Hungary, Latvia, Lithuania, Poland, Romania and Sweden.
Full sensitivity was observed in Bulgaria, Czech Republic, Denmark, Estonia, Hungary, Latvia, Poland and Romania. A stable situation was observed in France as in the previous seasons with a low frequency of sensitivity adaptation. Decreased sensitivity was observed in samples from Germany, Lithuania Poland and Sweden from single locations at a very low frequency.
In **2023**, samples were investigated coming from Czech Republic, France, Germany, Poland and Romania.
Full sensitivity was observed Czech Republic, Poland and Romania. Single isolates with SDHI-adaptations have been detected in Germany. A stable situation was observed in France as in the previous seasons with a low frequency of sensitivity adaptation.
Samples originating from Canada were collected in **2021** and **2022** and showed full sensitivity.

For information on previously detected mutations please refer to "**link** to mutation table".

Oilseed rape - Blackleg (*Plenodomus lingam* syn. *Leptosphaeria maculans; Plenodomus biglobosus* syn. *Leptosphaeria biglobosa)*

(BASF, Bayer, Syngenta)

Isolates in **2023/24** were analyzed originating from Czech Republic, Denmark, Germany, Latvia, Lithuania, Poland and Romania. All investigated isolates showed full sensitivity.

Historical background:
All isolates tested were sensitive, within the baseline (France, Germany, Poland, United Kingdom and Hungary).
2016 samples coming from France and Germany were all sensitive, within the baseline.
All isolates analyzed from **2017/18** tested were sensitive, within the baseline (France, Germany, Poland and United Kingdom).
Isolates in **2020** were analyzed originating from France, Germany, Poland and the United Kingdom. The majority of isolates was sensitive, within the baseline. Strains from both species showed similar ranges of sensitivity with *P. lingam* showing slightly higher sensitivity values in appropriate testing systems. A few suspicious isolates (both species) with slightly lower sensitivity are currently under investigation.
Isolates in **2021** were analyzed originating from Austria, Bulgaria, Czech Republic, Denmark, France, Germany, Hungary, Latvia, Lithuania, Poland, Romania and the United Kingdom. All investigated isolates were sensitive, within the baseline. Strains from both species showed similar ranges of sensitivity with *P. lingam* showing slightly higher sensitivity values in appropriate testing systems.
Isolates in **2022/23** were analyzed originating from Austria, Czech Republic, France, Germany, Poland, Romania, Sweden and the United Kingdom. All investigated isolates showed full sensitivity with some outliers for *P. biglobosus*. A single SDHI can show different levels of intrinsic activity on the two different species.
Samples from Canada, sampled in **2021** and **2022**, showed full sensitivity.

Oilseed rape – Light leaf spot, *Pyrenopeziza brassicae*

(BASF)

For the first time, a monitoring program was carried out in the UK in **2020**. All tested isolates were fully sensitive. Monitoring data from Denmark, Ireland and the UK are available from **2021, 2022 and 2023** showed full sensitivity. No monitoring was carried out in **2024**.

Potato – Early blight, Alternaria leaf spot (*Alternaria solani, A. alternata*)

(Bayer, BASF, Syngenta)

In **2024**, monitoring was carried out in Belgium, Finland, Germany, the Netherlands, Portugal, Poland, Serbia and Sweden.
A limited monitoring from Portugal and Finland showed a highly sensitive situation.
Low frequency of adapted strains was observed in samples from Serbia.
High frequencies of adapted strains were detected in Germany, Sweden, Belgium, Poland and the Netherlands.
Mutation analysis is ongoing.

No monitoring was carried out on *A. alternata*.

Historical background:
Monitoring studies are carried out since **2009**.
In **2015**, no SDHI resistance was detected in *A. solani* in Austria, France, Greece, Hungary, Italy, Slovakia and Spain. Isolates with reduced sensitivity were detected in Europe in Belgium, Germany, the Netherlands and Denmark. In *A. alternata*, isolates with reduced sensitivity were detected in Austria, Belgium, Germany, Hungary, Italy, Slovakia and the Netherlands. Full sensitivity was found in Finland, France, Greece, Latvia and Spain.
The practical relevance of these mutations and the role of *A. alternata* in the disease complex are still under discussion by the research community.
In *A. alternata*, no resistance was detected in Bulgaria, Romania, Sweden, France, the United Kingdom and Slovakia in **2016**. Low frequency of resistance was detected in Hungary and Poland. Low to moderate frequency of resistance was detected in Switzerland and Germany, and moderate levels in Belgium. In *A. solani*, no resistance was detected in Czech Republic, Spain, Finland, Greece, Hungary and Slovakia. Low frequency of resistant isolates was detected in Poland, Denmark, Italy, Romania and the United Kingdom. Moderate frequency was detected in Belgium, Germany, the Netherlands and Sweden.
In *A. alternata*, no resistance was detected in Hungary in **2017**. Low frequency of resistance was detected in Czech Republic, Germany, Romania and Poland.
In *A. solani*, no resistance was detected in **2017** in Poland, Spain, Hungary and Romania. Low frequency of resistant isolates was detected in Czech Republic and France. Moderate frequency was detected in Denmark, Belgium, Germany, the Netherlands and Sweden.
The following mutations have been detected: B-H278R/Y, C-H134R, D-H133R with B-H278Y and C-H134R being the predominant mutations found.
In **2019**, no resistance in *A. alternata* was detected in Denmark and Latvia. Low frequency of resistance was detected in Germany, Hungary, Italy and Switzerland.
In *A. solani*, no resistance was detected in **2019** in Croatia, Czech Republic, Greece, Ireland, Norway and Poland. Low frequency of resistant isolates was detected in France. Moderate frequency was detected in Austria, Belgium, Germany, Hungary, the Netherlands and the United Kingdom.
Moderate to high frequencies were detected in Denmark and Sweden.
The following mutations have been detected: B-H278R/Y, C-H134R/Q, D-H133R with B-H278Y and C-H134R being the predominant mutations found.
In 2019 monitoring programs, the following new mutation was identified in one single isolate: D-D123E.
In **2020**, *A. solani* samples were analyzed originating from Austria, Belgium, Denmark, Germany, the Netherlands, Norway, Sweden and the United Kingdom.
No resistance was detected in **2020** in Norway and one sample form Germany.
Moderate frequency was detected in Austria, Belgium and the Netherlands.
Moderate to high frequencies were detected in Denmark and Sweden.
The following mutations have been detected: B-H278R/Y, C-H134R/Q, D-H133R, D-D123E with B-H278Y and C-H134R being the predominant mutations found.
In **2021**, *A. solani* samples were analyzed originating from Austria, Bulgaria, Denmark, France, Germany, Hungary, the Netherlands, Norway, Poland, Portugal, Spain and Sweden.
Full sensitivity was observed using bioassays and molecular-biological methods in Bulgaria, Norway, Portugal and Spain.
The following mutations have been detected: B-H278R/Y, C-H134R/Q, D-H133R, D-D123E with B-H278Y and C-H134R being the predominant mutations found.

Target site mutations were found in single samples coming from Hungary and Poland (limited monitoring).
Low frequencies of target site mutations were found in France, Germany and the Netherlands.
Moderate frequencies were found in Austria.
Moderate to high frequencies were detected in Denmark and Sweden.
In **2022**, *A. solani* samples were analyzed originating from Austria, Denmark, and Norway.
The following mutations have been detected: B-H278R/Y, C-H134R, D-D123E with B-H278Y and C-H134R being the predominant mutations found.
Low frequencies of target site mutations were found in Norway.
Moderate frequencies were found in Austria.
High frequencies were detected in Denmark.
In **2023**, monitoring was carried out in Austria, Belgium, Denmark, Germany, the Netherlands and Sweden. Based on in vitro assays, no sensitivity changes were observed. Mutation analysis resulted in comparable results as in **2022**. The following mutations were detected for the first time: B-H278V/L. Double mutations C-H134R+D-D123E were detected as well.
High frequencies were detected in Denmark.

No monitoring was carried out on *A. alternata*.

For information on previously detected mutations please refer to "**link** to mutation table".

Potato – Silver scurf (*Helminthosporium solani*)
(Syngenta)

No monitoring was carried out in **2023** and **2024**.

Historical background:
In **2014**, single resistant isolates were detected in Belgium and the Netherlands. No resistant isolates were detected in the United Kingdom, France and Germany.
Monitoring data from **2016** from Germany, France and the USA showed a low frequency of resistance. Full sensitivity was reported from the United Kingdom.
Samples in **2019** were analyzed coming from mainly commercial fields in Bulgaria, France, Germany, Hungary, Italy, the Netherlands and the United Kingdom.
Single resistant isolates were detected in France, Germany and the Netherlands. Considering long-term monitoring, the frequency of resistance is stable in the mentioned countries.
Samples in **2020** were analyzed coming from mainly commercial fields in Germany, Hungary, Italy, Latvia, Lithuania, the Netherlands, Spain and the United Kingdom.
All strains collected in **2020** from Spain, Hungary, Italy, Latvia and Netherlands were sensitive. Single resistant strains were observed in Germany, Latvia and United Kingdom in **2020**.
Samples in **2021** were analyzed coming from mainly commercial fields in Denmark, France, Germany, Hungary, Italy, Latvia, the Netherlands, Poland, Romania, Spain, Sweden and the United Kingdom.
All strains collected in **2021** from Denmark, Germany, Italy, Latvia, Romania and Sweden were sensitive. Single resistant strains were observed in Italy, the Netherlands, Poland, Spain and United Kingdom.
Low frequency of mutations was detected in France.

Monitoring from **2022** showed full sensitivity in Italy and some resistant strains in Belgium, Germany, Spain, France, Hungary, the Netherlands and the United Kingdom.

Potato – Stem canker/ Black scurf *(Rhizoctonia solani*)
(Syngenta, Sumitomo)

In **2020, 2021, 2023 and 2024**, full sensitivity was observed in France, Germany, the Netherlands, Spain and the United Kingdom.

Historical background:
All samples analyzed from the United Kingdom, the Netherlands, France and Germany in **2014** showed full sensitivity.
In **2016**, samples from Germany, France, The United Kingdom and Netherlands showed full sensitivity.
Samples were analyzed in **2018** originating from Germany, the Netherlands, Spain and the United Kingdom. Full sensitivity was observed.
In **2019**, full sensitivity was observed in Germany, Spain, the United Kingdom, Hungary, Italy, the Netherlands, Romania and Sweden.
In **2020, 2021 and 2023**, full sensitivity was observed in France, Germany, the Netherlands, Spain and the United Kingdom.

Sunflower – Blight of sunflower (*Alternaria helianthi*)
(BASF)

2022 samples originating from Romania showed full sensitivity.

Isolates originating from **2019** and **2020** from Czech Republic, Slovakia and Romania showed full sensitivity.
2021 samples originating from France, Hungary and Romania showed full sensitivity.

***Sclerotinia sclerotiorum*, sunflower**
(BASF)

Full sensitivity was reported from Poland, Hungary and Romania in **2021, 2022** and **2023**.

Black stem of sunflower, *Plenodomus lindquisti*
(BASF)

2022 samples from Romania showed full sensitivity.

Tomato – Early blight, Alternaria leaf spot (*Alternaria solani, A.alternata*)
(Syngenta)

Data were presented from *A. solani* strains from the USA, collected in **2021**, showed a low frequency of less sensitive strains.

No monitoring data are available for **2020** for *A. alternata* and *A. solani*.

Historical background:
In **2015**, no SDHI resistance was detected in *A. solani* in Poland, Bulgaria and Spain. In *A. alternata*, a single isolate from Italy showed reduced sensitivity. No SDHI resistance was reported from Spain and Bulgaria.
In *A. solani*, no resistance was detected in Poland and Italy in **2016**. In *A. alternata*, few isolates showing reduced sensitivity were detected in Poland, Italy and Greece.
In **2017**, full sensitivity was found for *A. alternata* in Spain, Hungary and Romania. Low frequency of resistance was observed in Italy.
No monitoring data are available for **2018**.
In **2019**, single *A. alternata* resistant strains were detected in Italy, Poland and Portugal. Full sensitivity was found in Spain. For *A. solani*, full sensitivity was found in Croatia, Italy and Spain.
Data were presented from *A. solani* strains from the USA, collected in **2021**, showed a low frequency of less sensitive strains
No monitoring data are available for **2020** for *A. alternata* and *A. solani*.

For information on previously detected mutations please refer to "**link** to mutation table".

Tomato – Powdery mildew (*Oidium neolycopersici*)
(Syngenta)

All **2016** samples originating from Belgium, Spain, France and the Netherlands showed full sensitivity.

Almonds – Leaf spot (*Alternaria alternata*)

In samples originating from **2015** and **2016**, resistance was confirmed in California/ USA.

Rice – Sheath blight (*Rhizoctonia solani*)
(Syngenta)

Full sensitivity was observed in **2020, 2023** and **2024** samples in a monitoring program conducted on samples originating from Vietnam. No known target site mutations were detected.

False smut on rice (*Ustilago virens*)
(Syngenta)

Samples from a first monitoring program in **2023** in China showed high sensitivity.

Cercospora leaf spot on sugarbeet (*Cercospora beticola*)
(BASF)

First sensitivity data from samples taken in **2017, 2018, 2023** and **2024** were reported for European countries, including Austria, Belgium, Czech Republic, France, Germany, Lithuania, the Netherlands, Poland, Romania, Russia, Slovakia, Spain, Sweden, Switzerland, Ukraine and the United Kingdom and showed a homogenous distribution.

Soybean – Asian soybean rust (*Phakopsora pachyrhizi*)

(Syngenta, Bayer, BASF, FMC, Corteva, Sumitomo)

Soybean rust samples have been tested for sensitivity to SDHI fungicides since 2007 in Brasil and adjacent countries.
Disease pressure in **2023/24** was high in the Southern states and low in the Cerrado region.

The evaluation of soybean rust field control showed that even under high I86F-mutation frequencies, SDHIs continue to contribute to disease control and are valuable partners for resistance management.
Substantial SDHI-sensitivity monitoring programs were running with samples from the season **2023/24**. These were based on detached leaf tests and the detection of mutations in the SDH genes. In most cases there was a good correlation between detached leaf assays and genetic evaluations. Genetic studies based on pyrosequencing, illumina sequencing, qPCR and whole SDH gene sequencing showed that the C-I86F mutation is the prevalent resistance mechanism and the main driver for observed sensitivity changes in the field. However, also other mutations (C-N88S/D, C-H154R, C-G92R) have been identified at very low frequency from beginning of SDHI-adaptation in soybean rust. These mutations do not increase in frequency over the last years. Their implication on SDHI sensitivity is therefore believed to be limited. Since such homologous mutations can be found and are relevant in other plant pathogens (e.g. *Zymoseptoria tritici* C-N86S, C-H152R; *Corynespora cassiicola* C-N75S ; *Pyrenophora teres* C-G79R), they will be further monitored.

Results from Brazil : Analyzed samples originated from both, commercial and trial sites (both treated and untreated plots) from the following states: Bahia, Mato Grosso do Sul, Mato Grosso, Parana, Sao Paulo, Minas Gerais, Goias, Rio Grande do Sul, Santa Catarina, Maranhao and Tocantins.
Over the last years, the frequency of C-I86F increased slightly each year until season 2022/23, reaching moderate to high frequency levels in most monitored regions. Frequencies in 2023/24 showed a stable, unchanged level compared to last season.Results from Paraguay : Monitoring studies including samples from 2021/22 and 2022/23 (sensitivity tests and mutation analysis) showed that the frequency of SDHI adaptation was moderate.

Species can carry different mutations which affect SDHIs. A few mutations can lead to different sensitivities depending on the chemical structure of the active ingredient.
As all SDHIs are cross-resistant, resistance management must be the same for all SDHIs. All monitoring and guideline related statements refer to the entire group of SDHIs.
Historical background:
The initial characterization of populations collected in **2015/16** indicated a mutation in the C-subunit at position I86F. The relevance and distribution of this mutation for the reduced SDHI sensitivity partly observed as well in **2016/17** samples is still under investigation.
Intensive monitoring programs are running to investigate the magnitude and relevance of the findings.
In **2016/17**, in many hundreds of trials as well as in commercial fields analyzed throughout Brazil the performance of SDHI-containing fungicides was as expected based on experience from previous years.
For the first time in the season **2015/16** and more frequently in **2016/17** at sites with a history of intensive SDHI-use and very high disease pressure, cases of reduced performance have been detected. Further analyses of populations from **2016/17** have shown reduced sensitivity to varying degrees. No to high frequencies of less sensitive populations were observed in the South of Brazil (Rio Grande do Sul, Parana, Mato Grosso do Sul). A low proportion of less sensitive

populations was found in Goias, Minas Gerais, Sao Paulo and Mato Grosso. No to very low frequency of less sensitive populations was found in Bahia, Maranhao and Tocantins.

Samples from the season **2016/17** from Bolivia were sensitive, whereas the target site mutation was detected in samples from Paraguay. Analysis on volunteer soybeans also showed the presence of the target mutation in Paraguay and Brasil, but not in Bolivia.

SDHI-sensitivity in monitoring programs from the season **2017/18** was comparable to the previous season and no further spread of the resistant mutation I86F was observed.

In some areas, even a reduction in the frequency of less sensitive populations was observed. If these findings are related to improved resistance management practices needs to be further clarified. Samples originating from volunteer plants collected in Brasil during the soybean-free period in **2018** showed the presence of the mutation I86F at a comparable level to the previous monitoring programmes.

Disease pressure in **2018/19** was (compared to the last season) lower in the beginning and disease development was delayed. Disease pressure at the end of the growing season was high. Field efficacy of SDHI-containing fungicides remains generally good. Substantial monitoring programs have been carried out and are still ongoing.

SDHI-sensitivity in monitoring programs from the season **2018/19** was heterogeneous compared to the previous season depending on sample timing, sampling location and seasonal factors.

The majority of samples contained the I86F mutation. However, the frequency of the mutation within the analyzed samples was highly heterogeneous, ranging between 0 and very high as in the past.

First evidence for fitness penalties in the I86F mutants were observed in monitoring studies by FRAC member companies and are further investigated. The relevance of these findings for SDHI field performance will be further investigated.

Soybean rust samples have been tested for sensitivity to SDHI fungicides since 2007 in Brasil and adjacent countries.

Disease onset was late and disease pressure in **2019/20** compared to last season was low to moderate.

Field efficacy of SDHI-containing fungicides remains generally good.

Substantial SDHI-sensitivity monitoring programs were running with samples from the season **2019/20**. These were based on detached leaf tests and the detection of mutations in the SDH genes. In most cases there was a good correlation between detached leaf assays and genetic evaluations. Genetic stuidies based on pyrosequencing, illumina sequencing, qPCR and whole SDH gene sequencing showed that the C-I86F mutation is currently the prevalent resistance meachnism and the main driver for observed sensitivity changes in the field. However also other mutations (C-N88S/D, C-H154R, C-G92R) have been identified at very low frequency from beginning of SDHI-adaptation in soybean rust. Their implication on SDHI sensitivity is currently not understood. Since such homologous mutations can be found and are relevant in other plant pathogens (e.g. *Zymoseptoria tritici* C-N86S, C-H152R; *Corynespora cassiicola* C-N75S ; *Pyrenophora teres* C-G79R), they will be further observed.

Disease onset was late and disease pressure in **2020/21** compared to last season was moderate.

Field efficacy of SDHI-containing fungicides remains generally good.

Substantial SDHI-sensitivity monitoring programs were running with samples from the season **2020/21**. These were based on detached leaf tests and the detection of mutations in the SDH genes. In most cases there was a good correlation between detached leaf assays and genetic evaluations. Genetic studies based on pyrosequencing, illumina sequencing, qPCR and whole SDH gene sequencing showed that the C-I86F mutation is still the prevalent resistance mechanism and the main driver for observed sensitivity changes in the field. However also other mutations (C-N88S/D, C-H154R, C-G92R) have been identified at very low frequency from beginning of SDHI-adaptation in soybean rust. Their implication on SDHI sensitivity is currently not understood. Since such homologous mutations can be found and are relevant in other plant pathogens (e.g. *Zymoseptoria tritici* C-N86S, C-H152R; *Corynespora cassiicola* C-N75S ; *Pyrenophora teres* C-G79R), they will be further monitored.

Results from Brazil : Analyzed samples originated from both, commercial and trial sites (both treated and untreated plots) from the following states : Bahia, Mato Grosso do Sul, Mato Grosso, Parana, Sao Paulo, Minas Gerais, Goias, Rio Grande do Sul, Santa Catarina and Tocantins.
In general, the sensitivity range was observed to be similar to the previous year but the frequency of the C-I86F mutation increased slightly .Results from Paraguay : Limited monitoring studies (sensitivity tests and mutation analysis) showed that the frequency of SDHI adaptation was low to moderate.Results from Bolivia : Limited monitoring studies were performed and all samples analyzed did not indicate any SDHI-adaptation. The results were based on sensitivity analysis by detached leaf assays.
Disease onset was late and disease pressure in **2021/22** compared to last season was comparable, i.e. moderate.
Field efficacy of SDHI-containing fungicides remains generally good.
Substantial SDHI-sensitivity monitoring programs were running with samples from the season **2021/22**.
Results from Brazil: Analyzed samples originated from both, commercial and trial sites (both treated and untreated plots) from the following states: Bahia, Mato Grosso do Sul, Mato Grosso, Parana, Sao Paulo, Minas Gerais, Goias, Rio Grande do Sul, Santa Catarina and Tocantins.
Over the last years, the frequency of C-I86F was observed to increase slightly each year, reaching moderate to high frequency levels in most monitored regions.
SDHIs still contribute to disease control and antiresistance strategies.
Results from Paraguay: Monitoring studies including samples from **2021/22** (sensitivity tests and mutation analysis) showed that the frequency of SDHI adaptation was moderate.
Results from Bolivia: Limited monitoring studies from the last 2 seasons (**2020/21** and **2021/22**) were performed and all samples analyzed did not indicate any SDHI-adaptation. The results were based on sensitivity analysis by detached leaf assays.

Substantial SDHI-sensitivity monitoring programs were running with samples from the season **2022/23**. These were based on detached leaf tests and the detection of mutations in the SDH genes. In most cases there was a good correlation between detached leaf assays and genetic evaluations. Genetic studies based on pyrosequencing, illumina sequencing, qPCR and whole SDH gene sequencing showed that the C-I86F mutation continues to be the prevalent resistance mechanism and the main driver for observed sensitivity changes in the field. However, also other mutations (C-N88S/D, C-H154R, C-G92R) have been identified at very low frequency from beginning of SDHI-adaptation in soybean rust. These mutations do not increase in frequency over the last years. Their implication on SDHI sensitivity is therefore believed to be limited. Since such homologous mutations can be found and are relevant in other plant pathogens (e.g. *Zymoseptoria tritici* C-N86S, C-H152R; *Corynespora cassiicola* C-N75S ; *Pyrenophora teres* C-G79R), they will be further monitored.
Results from Brazil : Analyzed samples originated from both, commercial and trial sites (both treated and untreated plots) from the following states: Bahia, Mato Grosso do Sul, Mato Grosso, Parana, Sao Paulo, Minas Gerais, Goias, Rio Grande do Sul, Santa Catarina and Tocantins.
Over the last years, the frequency of C-I86F continues to increase slightly each year, reaching moderate to high frequency levels in most monitored regions.
Results from Paraguay : Monitoring studies including samples from 2021/22 (sensitivity tests and mutation analysis) showed that the frequency of SDHI adaptation was moderate.
Results from Bolivia : Limited monitoring studies from the last 2 seasons (2020/21 and 2021/22) were performed and all samples analyzed did not indicate any SDHI-adaptation. The results were based on sensitivity analysis by detached leaf assays.

Soybean – Target spot (*Corynespora cassiicola*)

(BASF, Syngenta, Bayer, Corteva, FMC)

Monitoring programs have been carried out since **2018**.
The following states were included in monitoring programs: Bahia, Tocantins, Parana, Sao Paulo, Minas Gerais, Goias, Rio Grande do Sul, Rodonia, Santa Catarina, Mato Grosso, Mato Grosso do Sul and Maranhao.
The evaluation of target spot control in the field showed that even under high C-N75S-mutation frequencies, SDHIs continue to contribute to disease control and are valuable partners for resistance management.
The majority of analyzed populations in Brasil in **2023/24** carry the C-N75S mutation at high frequency and the mutation B-H278Y was observed at low frequencies as in the previous season. Other mutations have been detected in the past in single isolates, including sdh B-H278R, B-I280V and the newly detected mutation D-V152I.
Historical background:
All samples analyzed from Brazil in **2014/15** showed full sensitivity.
Monitoring programs have been carried out for the season **2016/17** and **2017/18**. Preliminary results showed the presence of single isolates with reduced sensitivity. Further molecular analysis is needed to confirm the sensitivity phenotypes.
Status update, December **2018**:
Molecular analysis confirmed the presence of target site mutations B-H278Y and C-N75S in isolates with reduced sensitivity. These isolates were detected in Mato Grosso and at single sites in Rio Grande do Sul and Bolivia. All sites analyzed from Goias, Minas Gerais and Parana were sensitive.
Monitoring programs have been carried out for the seasons **2018/19** and **2019/20**. The studies for season **2019/20** are not fully completed, but the present data indicate an increase in the frequency of isolates with reduced sensitivity in the last two seasons compared to the past.
Molecular analysis confirmed the presence of target site mutations B-H278Y and C-N75S in isolates with reduced sensitivity. These isolates were detected in Mato Grosso and Mato Grosso do Sul at moderate frequencies and at lower frequencies in other states (Parana, Sao Paulo, Tocantins, Goias, Minas Gerais, Rio Grande do Sul, Rodonia).
Compared to **2019/20**, monitoring data from **2020/21** indicate a slight increase in mutation frequency.
Isolates with sdh mutations were observed in Mato Grosso and Mato Grosso do Sul at moderate to high frequencies and at lower frequencies at other states (Bahia, Tocantins, Parana, Goias, Minas Gerais, Rio Grande do Sul, Rodonia). Full sensitivity was observed in Sao Paulo and Santa Catarina (based on limited number of locations).
The same states as in previous years were included in monitoring programs in **2022/23** (Bahia, Tocantins, Parana, Sao Paulo, Minas Gerais, Goias, Rio Grande do Sul, Rodonia, Santa Catarina, Mato Grosso, Mato Grosso do Sul, Maranhao).
The evaluation of target spot control in the field showed that even under high C-N75S-mutation frequencies, SDHIs continue to contribute to disease control and are valuable partners for resistance management.
The majority of analyzed populations in Brasil in **2022/23** carry the C-N75S mutation at high frequency and the mutation B-H278Y was observed at low frequencies. Other mutations have been detected in single isolates, including sdh B-H278R, B-I280V and the newly detected mutation D-V152I.

Anthracnose - *Colletotrichum* spp, involved in stem and pod rot anomalies
(Syngenta)

First monitoring data are available for *Colletotrichum* spp. strains collected during **2021/22** and **2022/23** from Maranhao, Minas Gerais, Mato Grosso, Mato Grosso de Sul, Parana, San Paolo and Tocantins showing full sensitivity. Comparable sensitivity range was observed for both *C. gloeosporioides* and *C. siamense*.

The following states were included in monitoring programs in **2022/23**: Bahia, Tocantins, Parana, Sao Paulo, Minas Gerais, Goias, Rio Grande do Sul, Rodonia, Santa Catarina, Mato Grosso, Mato Grosso do Sul, Maranhao.
The majority of analyzed populations in Brasil carry the C-N75S mutation at high frequency. In comparison to last year, the frequency of the mutation B-H278Y was observed to decrease reaching low frequencies, while the mutation C-N75S shows increasing frequencies. Other mutations have been detected in single isolates, including sdh B-H278R, B-I280V and the newly detected mutation D-V152I.
SDHI's do still contribute to disease control and resistance management.

Soybean – *Diaporthe* spp. (Phomopsis), involved in stem and pod rot anomalies

(Syngenta)

Monitoring data from single *Diaporthe* spp. strains collected during **2021/22** and **2022/23** showed full sensitivity.

Cotton – Ramularia leaf spot (*Ramularia areola*)

(BASF, FMC)

Monitoring programs since the season **2019/20** showed an overall stable situation with the detection of single outliers. Outliers have been found in Bahia and Mato Grosso. Investigations on the genetic background of the outliers are still ongoing.

Historical background:
Monitoring programs were carried out with samples originating from **2017/18** and **2018/19** coming from Mato Grosso, Goias, Bahia, Mato Grosso do Sul. All samples were fully sensitive.
Monitoring studies from **2019/20** showed full sensitivity in Mato Grosso, Mato Grosso do Sul, Goias and single outliers were observed in Bahia which are under further investigation.
Monitoring studies from **2019/20** showed full sensitivity in Mato Grosso, Mato Grosso do Sul, Goias and single outliers were observed in Bahia.
Monitoring programs from **2020/21** showed most isolates being fully sensitive. Single outliers were found again.
Monitoring studies from **2019/20** showed full sensitivity in Mato Grosso, Mato Grosso do Sul, Goias and single outliers were observed in Bahia.

Monitoring programs from **2020/21** showed most isolates being fully sensitive. Single outliers were found again.

Cotton – Target spot (*Corynespora cassiicola*)
(Syngenta, Bayer, BASF, FMC)

High frequency of strains carrying the mutations C-N75S were observed in **2023/24** from Mato Grosso, Mato Grosso do Sul, Goias, Maranhao and Bahia. The mutation B-H278Y was detected at low frequencies. These findings are similar to the results reported in soybean.
This shows the importance of crop-specific recommendations linking these two important crops.

Historic background:
Sensitivity tests and molecular analysis on Brasilian populations confirmed the presence of isolates with reduced sensitivity and these carried the target site mutation B-H278Y and C-N75S, as it has been found for *C. cassiicola* from soybeans. Such isolates were detected in Mato Grosso and Mato Grosso do Sul at moderate frequencies. In general, the frequency of SDHI adaptation in populations from cotton was lower than in populations from soybeans.
High frequency of strains carrying the mutations B-H278Y and C-N75S were observed in **2019/20** from Mato Grosso, Mato Grosso do Sul, Goias and Bahia.
Meanwhile, the frequency of sdh mutations is higher in cotton compared to soybean populations. This shows the importance of crop-specific recommendations linking these two important crops. These are under preparation.
High frequency of strains carrying the mutations B-H278Y and C-N75S were observed in **2021/22** from Mato Grosso, Mato Grosso do Sul, Goias, Maranhao and Bahia (comment: check states!). The last season showed an frequency increase of the mutation C-N75S and a decrease of the mutation B-H278Y as reported for target spot in soybean.
This shows the importance of crop-specific recommendations linking these two important crops.
High frequency of strains carrying the mutations C-N75S were observed in **2022/23** from Mato Grosso, Mato Grosso do Sul, Goias, Maranhao and Bahia. The mutation B-H278Y was detected at low frequencies. These findings are similar to the results reported in soybean.
This shows the importance of crop-specific recommendations linking these two important crops.

Banana – Black sigatoka (*Mycosphaerella fijijensis*)
(Syngenta, Bayer, BASF)

In vitro monitoring studies have revealed first isolates with reduced sensitivity in Ecuador and Costa Rica. No information on target site mutations is available at this point in time. Field performance was not affected.
More details are published by the Banana FRAC working group (Link).

2. Detection of Resistance (other monitoring data sources, non-FRAC)

A complete overview on resistant plant pathogenic organisms, including published cases of SDHI resistance, can be viewed in the publications area of the FRAC website. See the List of Resistant Plant Pathogens.

See following table for detected mutations: (link).

3. SDHI – Use Recommendations

3.1 SDHI – General SDHI Guidelines (all crops)

Strategies and General Guidelines for the 2021/22 season:

- Strategies for the management of SDHI fungicide resistance, in all crops, are based on the statements listed below. These statements serve as a fundamental guide for the development of local resistance management programs.
- Resistance management strategies have been designed in order to be proactive and to prevent or delay the development of resistance to SDHI fungicides.
- A fundamental principle that must be adhered to when applying resistance management strategies for SDHI fungicides is that:

  The SDHI fungicides (benodanil, benzovindiflupyr, bixafen, boscalid, carboxin, cyclobutrifluram, fenfuram, fluindapyr, fluopyram, flutolanil, fluxapyroxad, furametpyr, inpyrfluxam, isofetamid, isoflucypram, isopyrazam, mepronil, oxycarboxin, penflufen, penthiopyrad, pydiflumetofen, sedaxane, thifluzamide) are in the same cross-resistance group.
- Fungicide programs must deliver effective disease management. Apply SDHI fungicide based products at effective rates and intervals according to manufacturers' recommendations.
- Effective disease management is a critical component to delay the build-up of resistant pathogen populations.
- The number of applications of SDHI fungicide based products within a total disease management program must be limited.
- When mixtures are used for SDHI fungicide resistance management, applied as tank mix or as a co-formulated mixture, the mixture partner:
    - should provide satisfactory disease control when used alone on the target disease
    - must have a different mode of action

- Mixtures of two or more SDHI fungicides can be applied to provide good biological efficacy; however, they do not provide an anti-resistance strategy and must be treated as a solo SDHI for resistance management. Each application of such a mixture when used in a spray program counts as one SDHI application.
- SDHI fungicides should be used preventively or at the early stages of disease development.
- Please refer to the “mixture document” (link) for more information on fungicide mixtures for resistance management.
- Species can carry different mutations which affect SDHIs. A few mutations can lead to different sensitivities depending on the chemical structure of the active ingredient.
- As SDHIs are cross-resistant, resistance management must be the same for all SDHIs.
- All monitoring and guideline related statements refer to the entire group of SDHIs.

3.2 SDHI-Guidelines – Grapes

- Apply SDHI fungicides according to manufacturers’ recommendations.
- When mixtures are used for SDHI fungicide resistance management, applied as tank mix or as a co-formulated mixture, the mixture partner:
    - should provide satisfactory disease control when used alone on the target disease
    - must have a different mode of action
- Apply a max. of 3 SDHI-containing fungicides per year over all diseases, solo or in mixture with effective mixture partners from different cross-resistance groups but not more than 50% of the total number of applications.
- A maximum of 4 SDHI fungicide applications may be used where 12 or more fungicide applications are made per crop.
- If used solo, apply SDHI fungicides in strict alternation with fungicides from a different cross-resistance group.
- If used in mixture, apply SDHI fungicides in a maximum of 2 consecutive applications.
- Apply SDHI fungicides preventively.
- For SDHI fungicide applications specifically targeted against grey mold, Botrytis cinerea, refer to the table below.

SDHI – Grey mold (*Botrytis cinerea*) spray table:

Total number of *Botrytis cinerea* spray applications per crop	1	2	3	4	5	6	>6

Maximum recommended Solo SDHI fungicide sprays **(apply in strict alternation)**	1	1	1	2	2	2	3
Max. recommended SDHI fungicide sprays in mixture **(apply a max. of 2 consecutive applications)**	1	1	2	2	2	3	3

3.3 SDHI-Guidelines – Pomefruit

- Apply SDHI fungicides according to manufacturers' recommendations.
- When mixtures are used for SDHI fungicide resistance management, applied as tank mix or as a co-formulated mixture, the mixture partner:
    - should provide satisfactory disease control when used alone on the target disease
    - must have a different mode of action
- Apply SDHI fungicides using not more than 2 consecutive applications.
- Apply SDHI fungicides preventively.

The following spray table shall be used as a guideline irrespective of the targeted disease in pomefruits.

Total number of spray applications per crop	1	2	3	4	5	6	7	8	9	10	11	12	>12
Maximum recommended Solo SDHI fungicide sprays	1	1	1	1	2	2	2	2	2	3	3	3	3
Max. recommended SDHI fungicide sprays in mixture	1	1	2	2	2	3	3	3	3	3	3	4	4

3.4 SDHI-Guidelines – Stone fruits

- Apply SDHI fungicides according to manufacturers' recommendations.
- When mixtures are used for SDHI fungicide resistance management, applied as tank mix or as a co-formulated mixture, the mixture partner:
    - should provide satisfactory disease control when used alone on the target disease
    - must have a different mode of action

- Apply a max. of 3 SDHI-containing fungicides per year over all diseases, solo or in mixture with effective mixture partners.
- If used solo, apply SDHI fungicides in strict alternation with fungicides from a different cross-resistance group.
- If used in mixture, apply SDHI fungicides in a maximum of 2 consecutive applications.
- Apply SDHI fungicides preventively.

3.5 SDHI-Guidelines – Other multi-spray crops (e.g. vegetables, including small berries and strawberries)

- When mixtures are used for SDHI fungicide resistance management, applied as tank mix or as a co-formulated mixture, the mixture partner:
  - should provide satisfactory disease control when used alone on the target disease
  - must have a different mode of action

The following spray table shall be used as a guideline irrespective of the targeted disease in the crops specified above.

Total number of spray applications per crop	1	2	3	4	5	6	7	8	9	10	11	12	>12
Maximum recommended Solo SDHI fungicide sprays **(apply in strict alternation)**	1	1	1	1	2	2	2	3	3	3	3	4	*
Max. recommended SDHI fungicide sprays in mixture **(apply a max. of 2 consecutive applications)**	1	1	1	2	2	3	3	3	3	3	4	4	*

* When more than 12 fungicide applications are made, observe the following guidelines:

- When using a SDHI fungicide as a solo product, the number of applications should be no more than 1/3 (33%) of the total number of fungicide applications per season.

- For programs in which tank mixes or pre-mixes of SDHI are utilized, the number of SDHI containing applications should be no more than 1/2 (50%) of the total number of fungicide application per season.
- In programs where SDHIs are made with both solo products and mixtures, the number of SDHI containing applications should be no more than 1/2 (50%) of the total no. of fungicide applied per season.
- If used solo, apply SDHI fungicides in strict alternation with fungicides from a different cross-resistance group.
- If used in mixture, apply SDHI fungicides in a maximum of 2 consecutive applications.

3.6 SDHI-Guidelines - Banana

Guidelines for the use of SDHI fungicides in banana are published by the Banana FRAC working group (link) (next meeting scheduled for 2022).

3.7 SDHI-Guidelines – Cereals

3.7.1. Foliar applications

- Apply SDHI fungicides always in mixtures
- The mixture partner:
  - should provide satisfactory disease control when used alone on the target disease
  - must have a different mode of action
- Apply a maximum of 2 SDHI fungicide containing sprays per cereal crop (see below for specifics on seed treatments).

Apply the SDHI fungicide preventively or as early as possible in the disease cycle. Do not rely only on the curative potential of SDHI fungicides. Strongly reduced rate programs including multiple applications must not be used. Refer to manufacturers' recommendations for rates.

3.7.2. Seed treatment applications

SDHIs are and will be used as seed treatment products.
It is FRAC's objective to protect this fungicide group and integrate all uses into technical recommendations. These minutes contain a recommendation on seed treatments, including those which have efficacy on foliar pathogens.
These recommendations will be reviewed regularly and supported by monitoring. When an SDHI fungicide is used as a seed treatment on cereals, there should be no implications regarding SDHI FRAC guidelines on the use of foliar SDHI fungicides on the same crop as long as the SDHI seed treatment is directed by rate and efficacy against

seed and soil borne diseases or ‘low risk’ foliar pathogens (Link to FRAC pathogen risk list).

SDHIs used as a seed treatment in cereals providing foliar efficacy against pathogens with moderate/ high resistance risk count against the total number of foliar SDHI sprays.

3.8 SDHI-Guidelines – Soybeans

Species can carry different mutations which affect SDHIs. A few mutations can lead to different sensitivities depending on the chemical structure of the active ingredient. As all SDHIs are cross-resistant, resistance management must be the same for all SDHIs. All monitoring and guideline related statements refer to the entire group of SDHIs.

- Apply SDHI fungicides always in mixtures
- The mixture partner:
    - should provide satisfactory disease control when used alone on the target disease
    - must have a different mode of action
    - The use of additional, non-cross-resistant modes of action should also be considered (ready-mixtures and tank-mixtures where legally possible)
- Apply a maximum of 2 SDHI fungicide containing sprays per soybean crop (no soy after soy/ double cropping)
- Apply the SDHI fungicide preventively or as early as possible in the disease cycle. Do not rely only on the curative properties of SDHIs, or SDHI-containing mixtures
- Strongly reduced rate programs including multiple applications must not be used. Refer to manufacturers’ recommendations for rates
- Respect the spray intervals according to the manufacturers’ recommendations.

Good agricultural practices must be considered to reduce the source of inoculum, disease pressure and resistance risk, e.g. no multiple cropping, implement and respect soybean-free periods, consider partially resistant soybean varieties, reduce the planting window, give preference to early-cycle varieties and endorse the destruction of volunteers and harvest residues from previous crops such as cotton.

3.9 Cotton SDHI recommendation

Adhere to the general use guidelines for SDHI-fungicides.

- Apply SDHI always with a mixing-partner
    - The mixture partner:
    - Should provide satisfactory disease control when used alone on the target disease
    - Must have a different mode of action (including multisites)

    - ready-mixtures and tank-mixtures can be considered as “mixtures” (where legally possible)
- Apply a maximum of 3 SDHI containing sprays per cotton crop, according to the table below.
- Apply SDHI fungicides in a maximum of 2 consecutive applications.
- Apply the SDHI fungicide preventively or as early as possible in the disease cycle.

Total number of spray application per crop	1	2	3	4	5	6	7	8	9	≥10
Max. recommended SDHI spray in mixture **(apply a max. of 2 consecutive applications)**	1	1	1	2	2	3	3	3	3	3

Good agricultural practices must be considered to reduce source of inoculum, disease pressure and resistance risk, e.g. no multiple cropping, give preference to disease-tolerant varieties and endorse the destruction of harvest residues from previous crops such as soybean.

3.10 SDHI-Guidelines – All other crops

- Refer to the general guideline for the use of SDHI fungicides.

SDHI – Oilseed rape

Extensive monitoring programs have been carried out. Reduced sensitivity has been detected in *S.sclerotiorum*.

Further monitoring programs will continue and clarify the necessity for a specific crop guideline.
The general guidelines for the use of SDHIs are currently considered to be sufficient because current data shows sporadic detection, no consistent increase and spread of resistant mutations. In addition, the life cycle of the pathogen, its distribution and rotation with non-host crops confirm that *Sclerotinia* in OSR justify the classification as a low risk pathogen (Link to FRAC pathogen risk list).

3.10 SDHI-Guidelines – Seed treatment for other crops

There are no guidelines for additional crops because currently the relevant pathogens are not considered as high-risk pathogens. Monitoring programs will continue to be carried out and serve as basis for regular reviews of the need for specific guidelines.