SAWAGEN: Improving Sorghum Adaptation in West Africa with a Genomics-Enabled Breeding Network

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March 24, 2022
SMIL ANNUAL REVIEW MEETING
An effective and durable R&D network for WA NARS

Researchers
Deliver knowledge that facilitates the breeding programs

Genetic Mapping Research Platform

Physiological Mapping Research Platform

Traits/Lines
Architecture/Markers

Lines
Traits

Local Adaptation Breeding Platform

Broad Adaptation Breeding Platform

Germplasm/Trats
Models/Predictions

Traits
Lines

Traits
Lines

Breeders
Deliver varieties that meet defined product profiles

New local varieties with adaptive traits (5-10 years, to seed system 2023-2028)

New regional varieties with genetic gain (10-25 years, to seed system 2029+)

 Farmers and end-users
SAWAGEN has strong links with the IAVAO crop network

- Common germplasm collectively nominated and evaluated each year in the network
- Traits standardisation across countries and partners (ontology)
- A common database (BMS)
- A common governance (charter)

5 countries: Burkina Faso, Mali, Niger, Sénégal, Togo
Project link with on-going FtF or non FtF initiatives

Sorghum breeding program
Product profiles

End-users
(Farmers, consumers, processors)
Local adaptation breeding platform (LABP)

*Platform lead:* Jacques Faye (ISRA-CERAAS)
Cyril Diatta (ISRA, Senegal)
Nofou Ouedraogo (INERA, Burkina)
Jack Eyanawa Akata (ITRA, Togo)
Ardaly Ousseini, Fanna Maina (INRAN, Niger)
Terry Felderhoff (KSU)
Objective: Deliver improved versions of locally-preferred varieties carrying winning traits (Striga resistance and stay-green) in the 5 to 10 years horizon

- **ARR 1.1, 1.2, 1.4:** Nganda, Sorvato-1, and Mota Maradi carrying \textit{lgs1} Striga resistance allele for Senegal, Togo, and Niger

- **ARR 1.3 and 1.5:** Kapelga and Faourou carrying \textit{Stg1-4} stay-green drought tolerance alleles for Burkina Faso and Senegal
Nganda with \textit{lgsI} striga resistance for Senegal

- Cross between \textbf{Nganda} and \textbf{SRN39} (Striga resistance donor)
- Currently we’re at \textbf{BC2F1} generation
  - Hot off-season (HS) 2022 (\textbf{BC2F2})
  - Rainy season (RS) 2022 (\textbf{BC2F3})
  - \textit{pot evaluation} (cool off-season, CS 2022)
- Striga "hot spot" fields identified; \textit{seed multiplication in HS 2023}
- Rainy season 2023: on \textit{farm evaluation} and participatory variety selection (\textit{PVS})
- Rainy season 2026: \textit{delivered to the seed system}
Sorvato-1 with \textit{lgsI} striga resistance for Togo

- Cross made between Sorvato-1 and SRN39
- Currently at BC2F4 generation
  - → make BC2F5 (Hot off-season 2022)
  - → using \textbf{BC2F5} start field evaluation (Rainy season 2022)
- \textbf{Seed multiplication} in RS 2022 and CS 2022
  - → Provide \textit{seeds to seed producers} for RS 2023

BC2F4 lines at Davié station, Togo

Jack Akata
Mota Maradi with *lgsI* striga resistance for Niger

- Cross between Mota Maradi and SRN39
- Currently at BC4F1/BC4F1 generation
  → BC5F1/BC4F1 (Hot off-season 2022)
  → Field evaluation of BC4F3 in Striga hot spots and PVS (Rainy season 2022)
- **Seed multiplication** in RS 2022
  → to seed system (RS 2023)
Mota Maradi, Sepon82, MR732 with \textit{lgs1} Striga resistance for Niger

<table>
<thead>
<tr>
<th>Country</th>
<th>Variety</th>
<th>Donor</th>
<th>Trait to be added</th>
<th>Generation</th>
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<tbody>
<tr>
<td>KSU/Niger</td>
<td>Mota Maradi</td>
<td>SRN39</td>
<td>Striga resistance</td>
<td>BC3F3/BC1F3</td>
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<tr>
<td>KSU/Niger</td>
<td>MR732</td>
<td>SRN39</td>
<td>Striga resistance</td>
<td>BC5F1/BC3F3</td>
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<tr>
<td>KSU/Niger</td>
<td>Sepon 82</td>
<td>SRN39</td>
<td>Striga resistance</td>
<td>BC2F1</td>
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</tbody>
</table>

- Lines carrying the \textit{lgs1} allele were identified
- Striga germination assay is on-going at Penn-State University
- Field evaluation in hot spot in 5 locations in Niger (rainy season 2022)
Kapelga with stay-green drought tolerance for Burkina Faso

- Cross between Kapelga and B35 (BTx642)
  - Currently at BC2F1/BC1F2 generation → Dry off-season 2022: BC2F2 and BC1F3 lines
  - Rainy season 2022: start field evaluation
- Registration process in 2023
- Registration to National catalog → producers in 2023
- Seed multiplication → to seed system (RS 2024)
Faourou with stay-green drought tolerance for Senegal

- Cross between **Faourou** and B35/BTx642 line
  - Currently at BC3F2 generation → **BC3F3** lines (Hot off-season 2022)
- Rainy season 2022: **field evaluation on station** of the **BC3F3** lines;
- Cool off-season 2022: **Lysimeter experiment** to evaluate effects of stay-green alleles
- Rainy season 2023: on **farm evaluation, PVS** and **field day** on station
- Rainy season 2025: deliver to the **seed system**
Expected progress for the deliverables in 2022

● Effectively establish marker-assisted backcross selection in the 4 breeding programs

● Start field evaluation of lines carrying *lgsI* striga resistance and stay-green alleles and/or pod evaluation for striga resistance

● Verify if the *Stg* alleles predict stay-green phenotype in breeding populations under lysimeter and drought stress experiments

● Challenges:
  ○ Lack of *Striga* infested field in research station: limits field evaluation
  ○ Difficulties to evaluate lines in hot spots (long distance, field variation)
Broad adaptation breeding platform (BABP)

Platform lead: Cyril Diatta (ISRA)
Aissata Mamadou & Ardaly Ousseini (INRAN, Niger)
Nofou Ouedraogo (INERA, Burkina)
Jack Eyanawa Akata (ITRA, Togo)
Objective of BABP

- Develop **broadly-adapted germplasm** as a foundation for long-term varietal delivery

**ARR 4.1**: Development of a West Africa Backcross Nested Association Mapping (BCNAM) resource

**ARR 4.2**: Multi-environmental evaluation and participatory varietal selection of promising Mini-NAM lines in West Africa agro-ecological zones

**ARR 4.3**: Adoption of Breeding Management System (BMS) for data management and sharing in West Africa NARS
Development of Backcross Nested Association Mapping (BCNAM)

**Goal:** Broadly-adapted germplasm (elite and diverse) for long-term genetic gain

- **Four recurrent** parents:
  - **Nganda** (Senegal)
  - **Sepon82** (Niger)
  - **Sorvato1** (Togo)
  - **Sarioso11** (Burkina)

- **Sixteen donor** parents selected based on production constraints and farmer’s preferred traits

<table>
<thead>
<tr>
<th>Recurrent Parent</th>
<th>Donor Parents</th>
<th>Traits</th>
<th>Pays</th>
<th>F1</th>
<th>BC1F1</th>
<th>BC1F2</th>
<th>BC1F3</th>
<th>BC1F4</th>
<th>BC1F5</th>
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<td>Kapelga</td>
<td>Grain quality (Tô)</td>
<td>Burkina</td>
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<td>BC1F1</td>
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<td>B35</td>
<td>Stay green</td>
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<td>BC1F1</td>
<td>BC1F2</td>
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<td></td>
<td>CCAL 1/13-1-1-1</td>
<td>Cecidomyia</td>
<td>Burkina</td>
<td>F1</td>
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<td>Sépon82</td>
<td>CE1516262 (IRAT 204)</td>
<td>Anthracnose</td>
<td>Niger</td>
<td>F1</td>
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<td>Mota Maradi</td>
<td>Long Smut</td>
<td>Niger</td>
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<td>ICSV88032</td>
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<td>Nganda</td>
<td>F2-20</td>
<td>Grain mold and Striga</td>
<td>Senegal</td>
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<td>BC1F1</td>
<td>BC1F2</td>
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<td>Senegal</td>
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<td>Grain mold and foliar diseases</td>
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<td>BC1F2</td>
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<td>BC1F1</td>
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<td>Togo</td>
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<td>BC1F1</td>
<td>BC1F2</td>
<td>BC1F3</td>
<td>BC1F4</td>
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<td>Ni49 (WASAP)</td>
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</table>
Multi-environment & participatory selection of Mini-NAM lines

**On-station Evaluation**

25 promising lines from SMIL Phase-I evaluated at Bambey, Roff, Sinthiou, Sefa (red dots) during the 2019, 2020, 2021 rainy seasons

**On-farm Evaluation**

The 7 lines combining higher yield and resistant to grain mold were evaluated in 13 farmers’ fields (green dots) during the rainy season 2021
Performance and stability

Line **E400** is the best performing followed by **E300-1; E270-1; E269**

Line **E269** is the most stable followed by **E270-2; E400; E300-1**

Average grain yield : 1.5 - 2t/ha
Average grain mold Score : 2
Participatory variety selection of Mini-NAM lines in Senegal

Participatory variety selection (PVS)

PVS at Roff, Séfa, and Sinthiou Maleme in 2021 growing season

Total of 45 farmers
(26 women; 19 men)
Multi-environment & participatory selection of Mini-NAM lines

Best farmers’ preferred lines:

- E319
- E269
- E300-2
- E300-1
- E400

<table>
<thead>
<tr>
<th>LINE</th>
<th>SINTHIOU</th>
<th>SEFA</th>
<th>ROFF</th>
<th>RANK</th>
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<td>1.5</td>
<td>1.2</td>
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<td>E-269</td>
<td>1.4</td>
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<td>1.8</td>
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<td>1.5</td>
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<td>2.7</td>
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<td>2.8</td>
<td>1.7</td>
<td>8</td>
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<tr>
<td>Sureño</td>
<td>1.6</td>
<td>2.2</td>
<td>2.5</td>
<td>9</td>
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</table>
## Participatory selection of Mini-NAM lines

### Farmers' preferred traits

**Men:**
Mostly prioritize agronomic traits

**Women:**
Prioritize both grain quality and agronomic traits

<table>
<thead>
<tr>
<th>FARMERS’ PREFERRED TRAITS</th>
<th>RANKING AT SEFA</th>
<th>RANKING AT ROFF</th>
<th>RANKING AT SINTHIOU</th>
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<td>WOMAN</td>
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<td>Grain yield</td>
<td>1</td>
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<td>1</td>
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<td>Big grain</td>
<td>2</td>
<td>1</td>
<td>5</td>
</tr>
<tr>
<td>Big and open panicle</td>
<td>3</td>
<td>-</td>
<td>7</td>
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<tr>
<td>Short maturity cycle</td>
<td>6</td>
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<td>2</td>
</tr>
<tr>
<td>Medium plant height</td>
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<td>-</td>
<td>4</td>
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<tr>
<td>Biomass yield</td>
<td>-</td>
<td>-</td>
<td>7</td>
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<td>White grain</td>
<td>4</td>
<td>3</td>
<td>6</td>
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<td>Grain quality (suitability for local dishes)</td>
<td>5</td>
<td>2</td>
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<tr>
<td>Grain mold resistance</td>
<td>-</td>
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<td>3</td>
</tr>
<tr>
<td>Plant Vigor</td>
<td>-</td>
<td>6</td>
<td>-</td>
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</tbody>
</table>
Multi-environment & participatory selection of Mini-NAM lines

- Based on agronomic performance and PVS (farmer’s preferences) **05 lines** have been selected

**Next steps:**
- Seed multiplication of the 5 lines
- Tests for suitability for local food
- Start registration for 3 best lines in 2022
- New varieties to **seed system in 2023**

<table>
<thead>
<tr>
<th>LINES</th>
<th>GRAIN YIELD</th>
<th>GRAIN MOLD SCORE</th>
<th>FARMERS’ RANKS</th>
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<td>1917</td>
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<td>E-269</td>
<td>1577</td>
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<td>1683</td>
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<td><em>Nganda</em></td>
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<tr>
<td><em>SURENO</em></td>
<td>1170</td>
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Adoption of BMS for data management and sharing in West Africa NARS

- All NARS Breeders have been trained on BMS
- All 2021 field-books were prepared using BMS
- Historical data are being migrated on the BMS
- Data are being collected with electronic devices
- Barcode reader and field label printers purchased (Senegal)

Next steps

- Implement barcodes field labelling
- Training on seed storage management
Genetic Mapping Research Platform (GMRP)

Platform lead: Fanna Maina (INRAN)
Jacques Faye & Bassirou Sine (ISRA-CERAAS)
Terry Felderhoff (KSU)
Objectives of GMRP

- **Objective:** Deliver genetic knowledge and tools to breeders that solve their roadblocks/gaps
  - Generate genetics knowledge that guides breeding strategy
  - Develop genetic tools to facilitate breeding (trait-predictive and background markers).

- **Anticipated Research Results:**
  - ARR 2.1: KASP markers for *Striga* resistance alleles at the *lgs1* gene
  - ARR 2.2: Genetic maps, KASP markers, and isogenic lines for novel drought resilience traits
Workflow: Genomics discoveries to varietal release

Genomics discoveries → Marker development → Marker testing → Marker-assisted selection → Variety testing & release

Genomics discoveries:
- Quantitative genomics
- Drought
- Striga
- New discoveries
- Existing discoveries

Marker development:
- KASP Marker Design
- Validate markers and develop new markers

Marker testing:
- Diverse sorghum germplasm
- Breeding population

Marker-assisted selection:
- Early generation selection
- Backcrosses
  - NILs
  - RILs

Variety testing & release:
- Testing in farmer's field
  - Drought tolerant varieties
  - Striga resistant varieties
Progress made in 2021

- KASP markers developed and validated *Striga* resistance and drought tolerance → delivered to LABP
- *Striga* resistance evaluation via germination assay to evaluate and validate lines with favorable/unfavorable alleles at *lgs1*
- Quantitative Trait Locus mapping for drought stress in WASAP (Faye et al. 2021, Maina et al., *submitted*)
- Marker development and testing for novel drought tolerance QTLs
**Striga resistance evaluation via germination assay**

- **Hypothesis:** Favorable allele at *lgsl* confers *Striga* resistance by reduced germination stimulant

- *Striga* germination assay in pots for known varieties during rainy season in Niger

- Genotypes tested include SRN39 donor parent variety from breeding programs

- Validation of backcross populations ongoing for *Striga* germination assay at Penn State (Lasky lab)
Evidence of drought adaptation in WASAP

- **Goal:** Discover & deliver drought tolerance markers for West African breeding programs
- Marker traits associations (MTA) with drought response in WASAP
- MTAs colocalized with stay-green genes (Faye et al., 2021, Maina et al., *submitted*)
- Novel loci underlying drought response (Maina et al., submitted)
MTAs for water-use dynamic for drought tolerance

- **Goal**: Discover & deliver predictive markers underlying water use under drought stress
- Water use measured over 12 weekly time points
- Significant genetic variation in water use ($p < 10^{-5}$)
- Several MTAs appear at 2-3 consecutive timepoints
- MTAs could be used as trait-predictive markers used in breeding for climate-resilience

GWAS for water use and its drought response
Testing our novel drought tolerance markers

- Novel markers underlying drought response in WASAP are being tested (11 KASAP markers for validation).
- Evaluation of WASAP drought tolerant varieties under managed environment (Lysimeter at Bambey)
  - Putative drought tolerant accessions
  - Donor accessions of putative MTAs
- Progeny of B35*Nganda (BC3F3) carrying favorable alleles will be evaluated in the lysimeter
Workflow: Genomics discoveries to varietal release

**Genomics discoveries**
- Maina et al.,
- Olatoye et al.,
- Faye et al.,
- GWAS drought
- Lgs1 marker
- Loci associated with traits of interest
- Stg, Lgs1

**Marker development**
- KASP Markers available at Intertek
- Marker-Trait validation Field, Lysimeter, Lab assays

**Marker testing**
- WASAP, global germplasm
- LABP BABP

**Marker-assisted selection**
- Drought
- Striga
- Early generation selection
- Backcrosses NILs RILs

**Variety testing & release**
- Hypothesis testing in farmer's field
- Drought tolerant varieties
- Striga resistant varieties

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An effective and durable R&D network for WA NARS

**Researchers**
*Deliver knowledge that facilitates the breeding programs*

**Breeders**
*Deliver varieties that meet defined product profiles*

**Farmers and end-users**

---

**Local Adaptation Breeding Platform**
- New local varieties with adaptive traits (5-10 years, to seed system 2023-2028)

**Broad Adaptation Breeding Platform**
- New regional varieties with genetic gain (10-25 years, to seed system 2029+)

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**Genetic Mapping Research Platform**
- Traits/Lines
- Architecture/Markers

**Physiological Mapping Research Platform**
- Germlasm/Traits
- Models/Predictions

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**Research Platform**
- Models/Predictions
- Germlasm/Traits
Acknowledgement: This study is made possible through funding by the Feed the Future Innovation Lab for Collaborative Research on Sorghum and Millet through grants from American People provided to the United States Agency for International Development (USAID) under cooperative agreement number AID-OAA-A-13-00047. The contents are the sole responsibility of the authors and do not necessarily reflect the views of USAID or the US Government.
Striga resistance allele for Senegal

- Crosses made between elite and SRN39 line
- Marker-assisted backcross selection at early generations

<table>
<thead>
<tr>
<th>Country</th>
<th>Preferred variety</th>
<th>Donor</th>
<th>Winning trait</th>
<th>Generation 2022</th>
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<tbody>
<tr>
<td>Senegal</td>
<td>Nganda</td>
<td>SRN39</td>
<td>Striga resistance</td>
<td>BC2F3</td>
</tr>
</tbody>
</table>

Genotype | Striga (snpSB00487)
---|----------------
SRN39_1 | A:A
SRN39_1 | A:A
Nganda_1 | G:G
Nganda_1 | G:G
F1(Nganda x SRN39)/1-1 | A:G
F1(Nganda x SRN39)/1-2 | A:G
F1(Nganda x SRN39)/1-3 | G:G
F1(Nganda x SRN39)/1-4 | G:G
Stay-green drought tolerance smallholder farmers

- Cross between elites and B35/BTx642 line
  - Marker-assisted selection at early generations
  - Rainy season 2022: Field evaluation of the BC3F3 lines

MAS has been successfully applied to efficiently select genotypes carrying the Stay-green alleles from B35

<table>
<thead>
<tr>
<th>Country</th>
<th>Preferred variety</th>
<th>Donor</th>
<th>Winning trait</th>
<th>Generation</th>
</tr>
</thead>
<tbody>
<tr>
<td>Senegal</td>
<td>Faourou</td>
<td>B35</td>
<td>Stay-green</td>
<td>BC3F3</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Genotype</th>
<th>Stg3a (snpSB00460)</th>
<th>Stg3b (snpSB00098)</th>
<th>Stg3b (snpSB00468)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Faourou_1</td>
<td>A:A</td>
<td>C:C</td>
<td>G:G</td>
</tr>
<tr>
<td>Faourou_1</td>
<td>A:A</td>
<td>C:C</td>
<td>G:G</td>
</tr>
<tr>
<td>B35_1</td>
<td>C:C</td>
<td>G:G</td>
<td>A:A</td>
</tr>
<tr>
<td>B35_1</td>
<td>C:C</td>
<td>G:G</td>
<td>A:A</td>
</tr>
<tr>
<td>BC2F1(Faourou x B35)/2-1</td>
<td>A:A</td>
<td>C:C</td>
<td>G:G</td>
</tr>
<tr>
<td>BC2F1(Faourou x B35)/2-1</td>
<td>A:A</td>
<td>C:C</td>
<td>G:G</td>
</tr>
<tr>
<td>BC2F1(Faourou x B35)/2-2</td>
<td>C:A</td>
<td>G:C</td>
<td>G:A</td>
</tr>
<tr>
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<td>C:A</td>
<td>G:C</td>
<td>G:A</td>
</tr>
<tr>
<td>BC2F1(Faourou x B35)/2-3</td>
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<td>G:C</td>
<td>G:A</td>
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<td>G:C</td>
<td>G:A</td>
</tr>
<tr>
<td>BC2F1(Faourou x B35)/2-4</td>
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<td>C:C</td>
<td>G:G</td>
</tr>
<tr>
<td>BC2F1(Faourou x B35)/2-4</td>
<td>C:A</td>
<td>C:C</td>
<td>G:G</td>
</tr>
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