



Development of Photo-Switching Ocean-Degradable Plastics with Edibility

⑤ Development of Sorghum Varieties Optimized as Feedstock for Photo-Switching Ocean-Degradable Plastics

(5)-1

Development of varieties optimized root systems for high biomass yield

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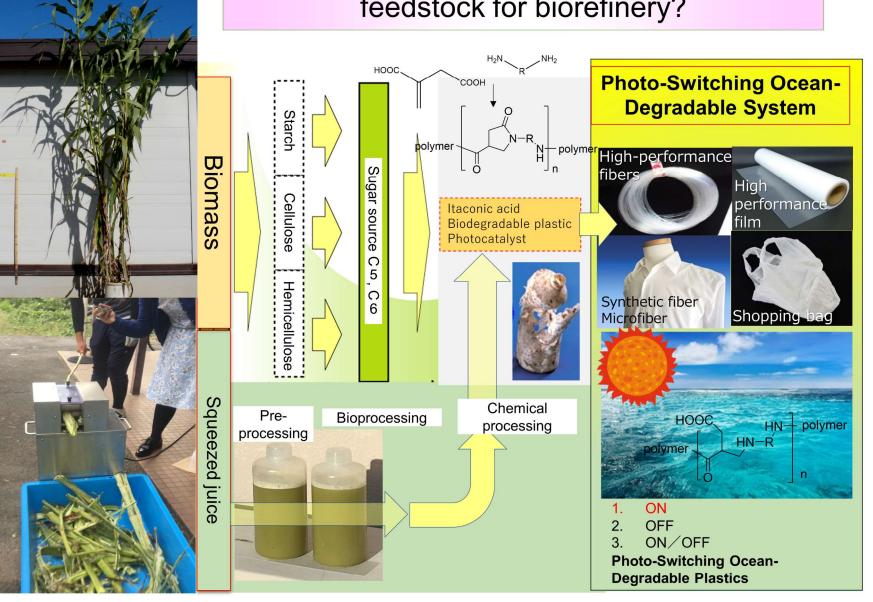
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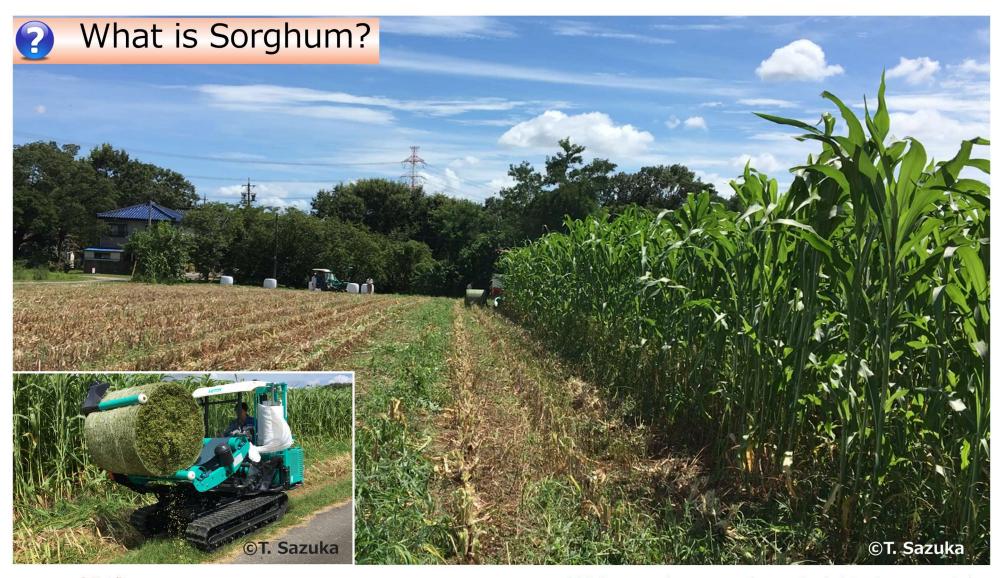
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How to produre the "carbon source" as the feedstock for biorefinery?





- ~85 t/ha
- Diploid (ideal for genomic breeding)
- C4 Plant
- Stem and leaf are used for Livestock feed
- Sweet sorghum accumulates sugar in stems

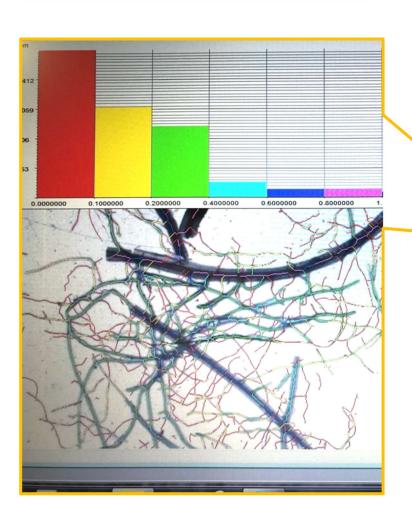
- Wide growing area (equatorial to temperate)
- Drought and salt tolerances
- · Use of abandoned cultivated zone

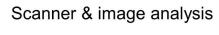
Schedule: Development of varieties with an optimized root system for high biomass yield

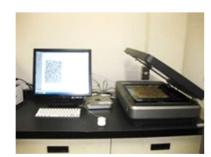
	FY2020	FY2021	FY2022	FY2023	FY2024	FY2025-2029	
(Yamauchi, Inukai)				0 _ 0			-
	Analysis	of root systems incre biomass	asing culm				
	Preliminary study of root system using model varieties	Evaluation of root systems of 20-30 varieties					
Set up infrastructure of genome information (Nishiuchi)		astructure of nformation					
	Genome sequencing of the sorghum collection	Additional sequencing					

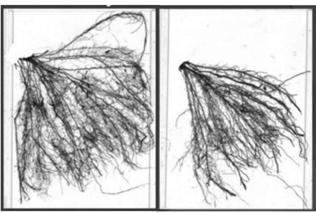
Analysis of root morphology with WinRHIZO

Establishment of a root system evaluation system using 10 varieties

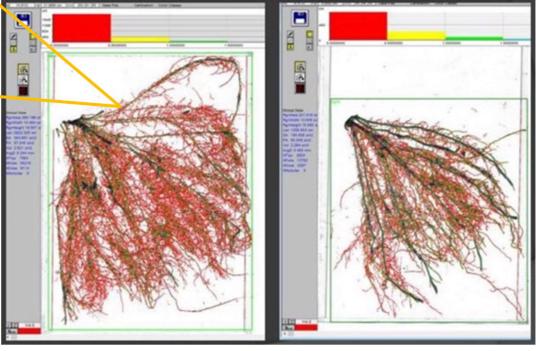








Length measurements each root types



Results: Root system are highly diversed On going: 50 varieties **Crown root:** Variety J Variety H Mainly provides physical support to the underground and helps to increase the absorption of nutrients Lateral roots: Increases the surface area of roots, contributing to increased efficiency of nutrient water absorption 250 (%) 200 150 100 50 Average diameter S-type lateral root lengthL-type lateral root length Crown Root Length Root surface area Root volume Root ratio ■A アメリカ ■B メキシコ ■C スーダン ■D 南アフリカ ■E オーストラリア ■F ハンガリー ■G 日本 ■H 中国 ■I インド ■J アフガニスタン USA Sudan South America Australia Mexico Hungary Japan China India Afghanistan

Development of genome database

World-wide collection (255 strains)



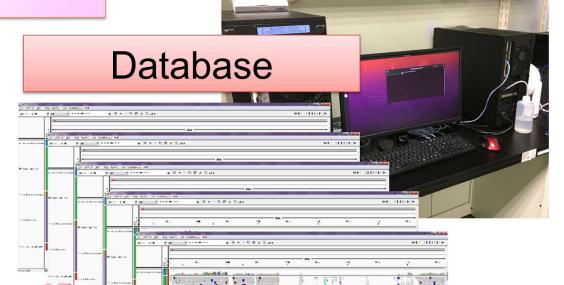
Extraction of genomic DNA of 255 varieties





Whole genome sequencing (247 strains)

(Genome size ~732Mb)



BAM

SAM

Assemble of the sequence fragments of the 247 strains (bwa-0.7.17)

New varieties with high biomass by "optimized roots"



Maximizing biomass for biorefinery

