

Genetic fingerprints using SSR markers to secure the seed potato production scheme, improvement of the method and database in France

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Why fingerprinting potato varieties using SSR ?

SSR are robust and very informative markers which remain commonly used in cultivar identification and seed testing.

We developed some years ago an efficient kit of markers (Moisan-Thiery et al 2005, Marhadour et al 2014) which is currently used by several labs in France. Around 2700 samples are analyzed each year in the network for different purposes:

- Majority of the samples are processed for the **certification scheme to check initial material and the first generation of the multiplication process**. SOC (the State Service for control and seed certification of France) integrated the method in the seed certification process.
- **Official control of random commercial samples** for fresh consumption (SCL).
- Securing the conservation process of the **Biological Resource Center BrACySol** (Esnault et al 2017)

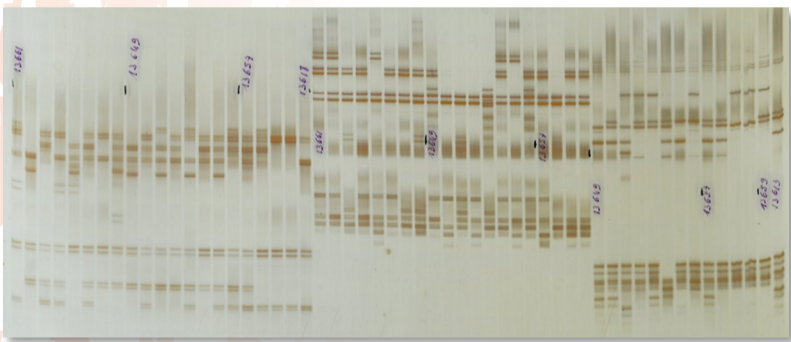
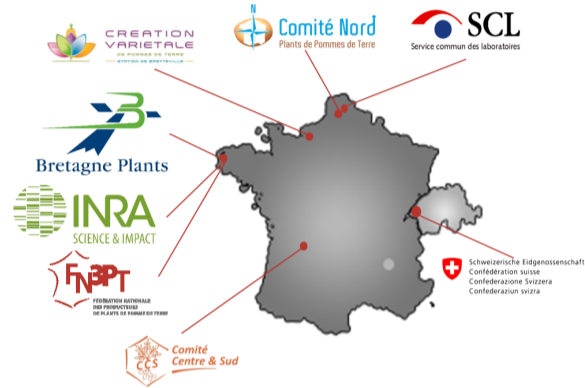


Photo N. Laversin

6 French labs use the same kit; ring tests are regularly organized.

A network of partners is using the same method and a common set of markers (Marhadour, et al. 2014).



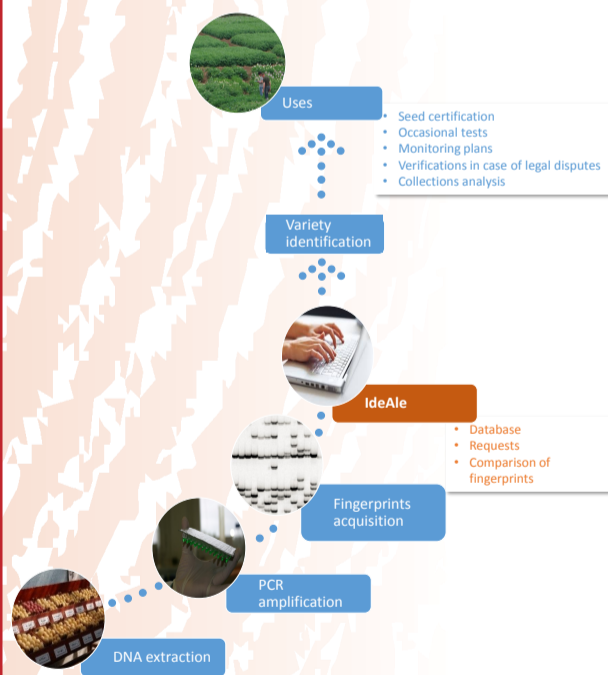
- The seed potato sector in charge of the certification: labs of the professional organisations (Bretagne Plants, Comité Centre & Sud, Comité Nord) and FN3PT (coordinator of the network),
- Inra UMR Igepp, Biological Resource Center BrACySol
- Joint Laboratory Service (SCL).

Agroscope Changins is also involved in our network and participated for the third time to the last ring test jointly organised with the SOC during winter 2016/2017. 6 labs participated. 8 varieties (10 over all labs) were correctly identified in all the labs except one sample which remained anonymous in one lab.

A common database named IdeAle is used by the partners

Number of varieties and then, of fingerprints is continuously increasing. **A common tool allowing real time update and viewing of the data by the users** has become necessary.

An **internet platform** entitled IdeAle was set up by FN3PT in a project supported by the French Ministry of Agriculture between 2008 and 2012 (Marhadour et al 2014).



The access is **secured** by login and password. Consistency of the data is checked by the super administrator. **Data are updated in real time and can be accessed by all the users simultaneously.**

Profiles of more than **1100 varieties and 600 hybrids** are stored in the database. In 2016, the website was visited 635 times and 21 000 pages were downloaded.

The database was recently opened to our Swiss partner.

Characteristics of the kit

Results obtained with the 7 markers of the kit are described in the table.

MARKERS	CHROMOSOME	# ALLELIC PROFILES	#ALLELES	#REGISTERED PROFILES	DISCRIMINATIVE POWER
LEMALX	V	16	5	1550	0.84
SSR1*	VIII	154	17	1692	0.93
STGBSS	VIII	74	13	1489	0.84
STM1097	VII	35	9	1684	0.83
STM2005*	XI	27	8	1692	0.81
STM2020	I	125	12	1655	0.96
STM5136*	I	70	14	1496	0.92
STM5140**	IV	41	8	968	0.90

* markers common to the SASA procedure (Reid et al 2011) ** marker being implemented progressively

Repeatability (3 different PCR obtained by using a single DNA sample) and **reproducibility** (one single PCR obtained from 3 different DNA samples) of the 38 most common alleles revealed by the 7 markers of the current procedure were analysed. For each allele, difference within and between labs were counted.

All markers were highly consistent except one allele of lemalx and stm5136 and 2 alleles of stgbss. Genotyping using stm2020 was less consistent without challenging the identification process thanks to the discriminative power of the kit.

References and acknowledgements



Photo Y. Le Hingrat

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We acknowledge J. Dupeuble (SOC) for the organisation of the ring test.

Prospects

We are now focusing on the improvement of the functionalities associated to the database : sample management, semi automatic consolidation of the data, ... We are also seeking for a new technology able to reveal the profiles and adapted to the medium scale throughput of our analysis.

Addresses

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