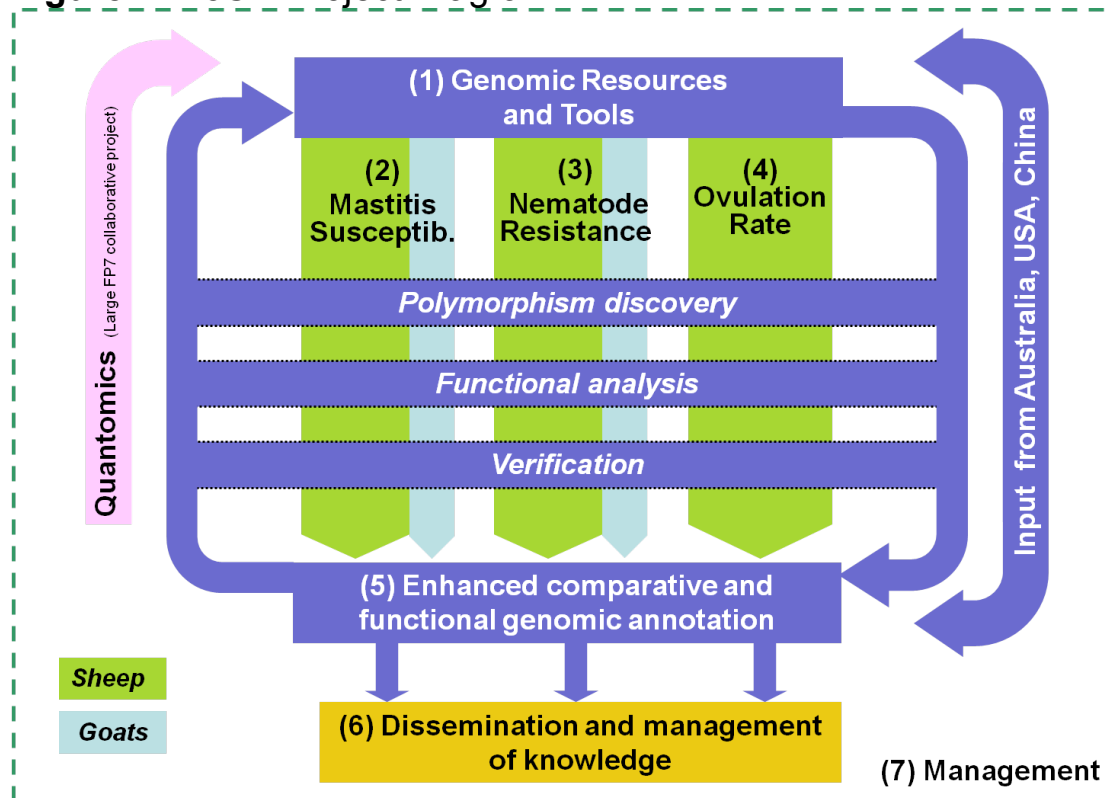


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Figure 1: 3SR Project Diagram



The numbers in brackets indicate the work package numbers

Figure 2: Populations of sheep and goats genotyped in 3SR

Breed	Partner Country	Type	Role in 3SR	Recorded Data	Animals
Sarda-Lacaune	Italy	Dairy	Whole Genome Scanning	Milk yield and composition, milkability, growth, SCC, incidence of mastitis, udder morphology, FEC, ovulation rate, embryo mortality	2,550

Other Sheep Populations used for Mastitis Susceptibility Activity:

Breed	Partner Country	Type	Role in 3SR	Recorded Data	Animals
Lacaune	France	Dairy	Whole Genome Scanning	SCC, milkability, incidence of mastitis, mammary examination, milk bacteriological tests, ovulation rate, litter size	1,770
Churra	Spain	Dairy	Whole Genome Scanning	SCC, Milk yield and composition	1,500
Chios	Greece	Dairy	Validation	SCC, incidence of mastitis, milk bacteriological tests	600

Other Sheep Populations used for Nematode Resistance Activity:

Breed	Partner Country	Type	Role in 3SR	Recorded Data	Animals
Black Belly-Romane cross	France	Meat	Whole Genome Scanning	FEC, plasmatic pepsinogen, hematological parameters, plasmatic IgG, worm burden	800
Scottish Blackface	U.K.	Meat	Whole Genome Scanning	FEC, IgA, monthly liveweights, ultrasound muscle & fat depth, carcass composition data	1,000
Texel	U.K., Ireland	Meat	Validation	FEC, 8 & 20 week weights, ultrasound muscle & fat depths	300
Suffolk	U.K., Ireland	Meat	Validation	FEC, 8 & 20 week weights, ultrasound muscle & fat depths	300
Pampinta	Argentina	Dairy & Meat	Validation	FEC, birth weight and pedigree information	400
Corriedale	Argentina	Meat & Wool	Validation	FEC, pedigree information	80
Manech	France	Dairy	Validation	FEC, milk, fat and protein contents on progeny	300
Blanc du Massif	France	Meat	Validation	FEC	300

Other Sheep Populations used for Ovulation Rate Activity:

Breed	Partner	Type	Role in 3SR	Recorded Data	Animals
Olkuska	Poland	Wool	Whole Genome Scanning	Ovulation rate, litter size, body weight	60
Cambridge	Ireland	Meat		Ovulation rate, litter size, birth and weaning weights, mortality data, ewe weight at joining	60
Davisdale	France	Meat		Ovulation rate, litter size, birth and weaning weights, mortality data, age of puberty	120

Goat Populations:

Breed	Partner Country	Type	Role in 3SR	Recorded Data	Animals
Alpine	France	Dairy	Whole Genome Scanning, Fine Mapping	SCC, production traits, udder type traits, milking speed (subset of population)	3,600
Skopelos	Greece	Dairy	Validation	SCC, milk composition	400
Creole	France	Meat	Whole Genome Scanning, Fine Mapping	FEC, body weight	380

Figure 3: Summary of genotypes available for analysis and proportion of total that were funded through the 3SR project

Trait of interest	Population	Number of genotypes available to the project ⁽¹⁾
Mastitis Susceptibility, Nematode Resistance and Paratuberculosis	Sarda-Lacaune Backcross	2436 (67%)
Mastitis Susceptibility	Sarda-Lacaune Backcross	[2375] ²
	Lacaune grand-daughter design	1013 (0%)
	Lacaune Divergent	334 (56%)
	Churra	1630 (49%)
Nematode Resistance	Sarda-Lacaune Backcross	[2394] ²
	Blackface	752 (100%)
	Blackbelly x Romane	1000 (30%)
Ovulation Rate	Lacaune	78 (100%)
	Grivette	40 (100%)
	Olkuska	64 (100%)
	Davisdale	120 (100%)
	Cambridge	21 (100%)
Paratuberculosis	Sarda-Lacaune Backcross	[2216] ²
TOTAL ANIMALS		7488 (53%)

¹ Proportion of total genotypes available that were funded through the 3SR project

² Number of genotyped Sardinian Back-Cross (BC) animals with relevant phenotypes

Figure 4: Details of animals for which whole genome re-sequencing was performed

Population	Trait of interest	No. animals re-sequenced	Total volume of sequence generated
Lacaune	Mastitis resistance	6 (2 trios)	180GB
Churra	Mastitis resistance	9 (3 trios)	162 GB
Blackface	Nematode resistance	8 (rams)	532.8GB
Sarda-Lacaune Backcross	Nematode resistance	6 (2 trios)	192GB
	Resistance to Para-TB, milk yield and milk contents, udder morphology	15 (5 trios)	514.8 GB
Cambridge	Ovulation rate	2	>60GB
Texel	Animals used in the RNA-Sequencing	3*	>90GB
Total sequence generated			1.73TB

Due to the manner in which the embryo material was collected for the RNAseq analyses it was not possible to sequence the embryo's DNA. However DNA re-sequencing was done for the other three animals.

Figure 5: Number of significant chromosomal regions for LSCS according to the method and the population studied

		Population		
		all	Saanen	Alpine
Method	LD ¹	16	27	17
	LA ²	2	2	2

¹ 1% genome-wide significant QTL

² 5% chromosome-wide significant QTL

Figure 6: Evolution of Faecal Egg Count for resistant (R) and susceptible (S) Creole kids

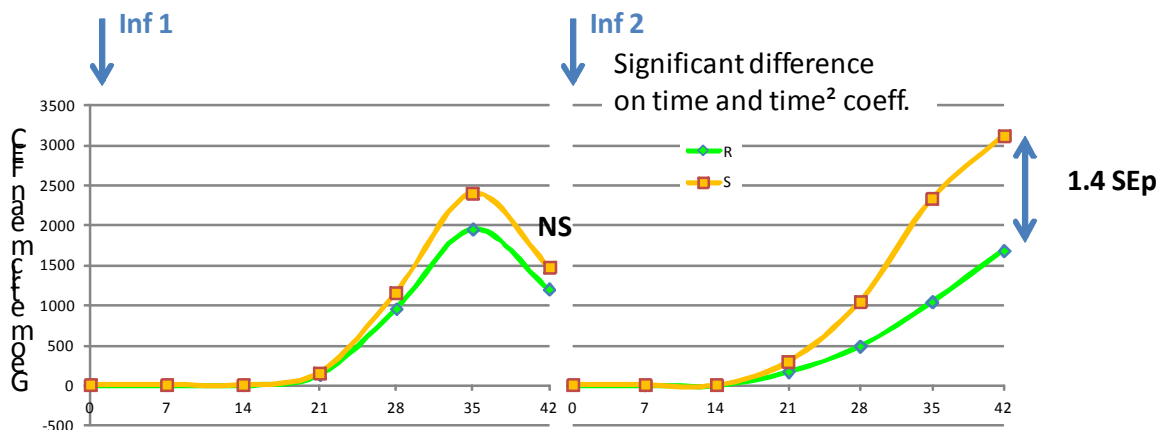


Figure 7: Number of animals genotyped and included in analyses for ovulation rate for each breed

Breed	Number of animals genotyped (and used in the analyses ¹)	Data structure: number of high prolificacy (and controls/carriers)
Lacaune	78 (78)	70 (8)
Davisdale	120 (113)	74 (39) ²
Grivette	40 (40)	29 (11)
Olkuska	64 (64)	29 (35)
Cambridge	21 (16)	7 (9 ³)
Total	323 (311)	209 (102)

¹ remaining samples were not used due to poor quality of genotypes

² includes genotypes for 13 males (some controls, some carriers)

³ includes animals that were sires and dams of homozygous females and therefore known to be heterozygous for the polymorphism of interest

Figure 8: Phenotypes recorded for Map infection

Phenotypic trait	No. animals recorded	Measurement details
Clinical symptoms and death	273	Visual examination confirmed by ELISA test and histo-pathological exam
ELISA in blood serum	2350	Once a year for the first generation; two times per year for further generations
Histo-pathological examination	1738	At the slaughterhouse (at 5 years of age for the first generation and 4 years of age for further generations)
Measurements at the slaughterhouse	650 (all measurements) + 1078 (only carcass weight)	

Appendix 2: Other Supporting Diagrams

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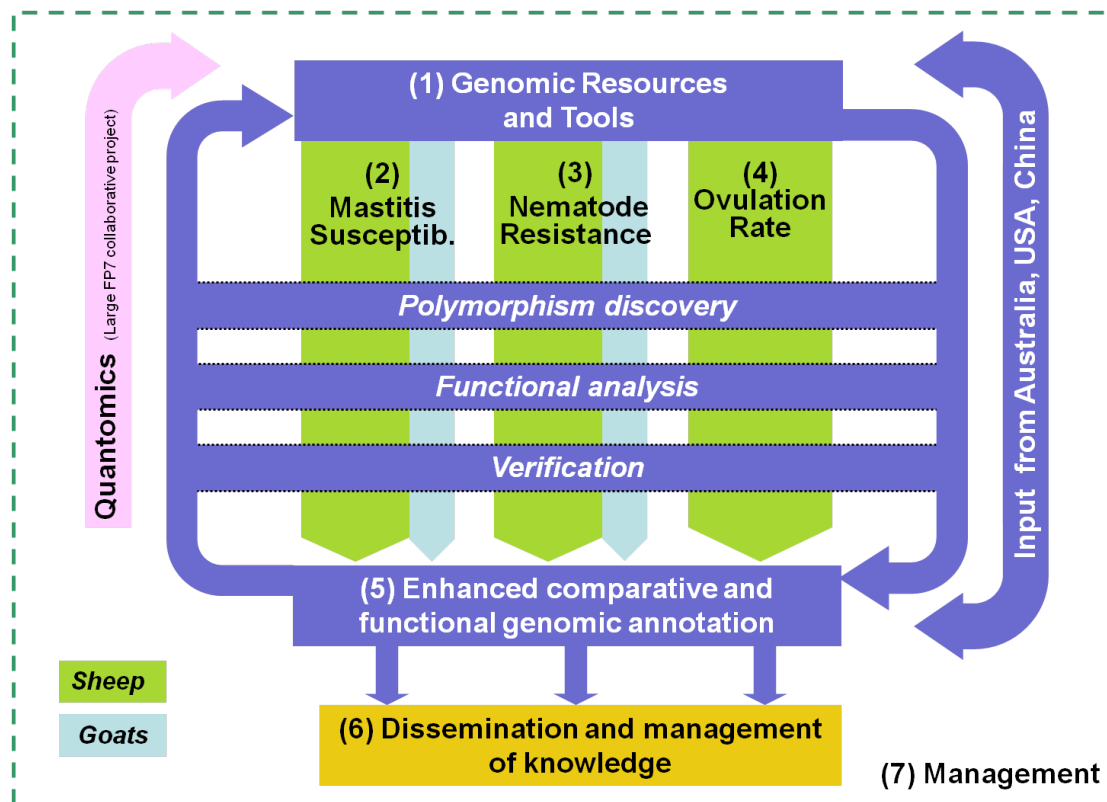
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2. Project Diagram
3. Project Partner Map
4. Project Partner Details
5. 3SR Website Home Page
6. 3SR Outline Poster
7. 3SR Results Poster
8. 3SR Newsletter Front Page (Issue 1)

1. Project Logo



Sustainable Solutions for Small Ruminants

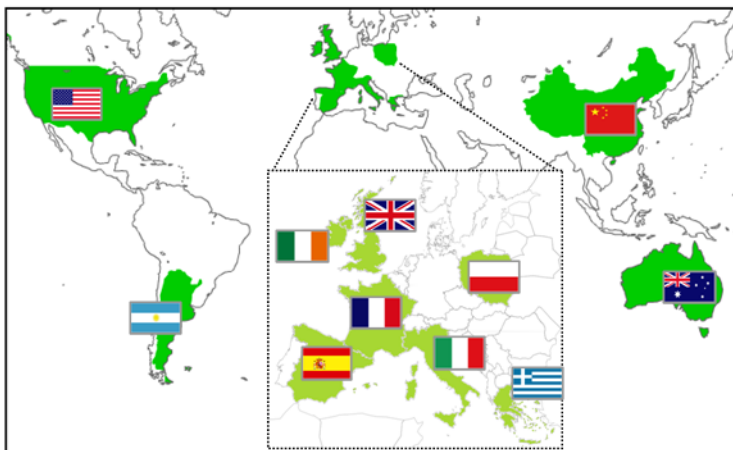
2. Project Diagram



The numbers in brackets indicate the work package numbers

3. Project Partner Map

The 3SR Consortium is comprised of 14 partners from 11 countries around the world:



4. Project Partner Details

Coordinator:

Huw Jones, Biosciences KTN, UK
The Roslin Institute, Easter Bush, Midlothian, EH25 9RG
huw.jones@biosciencektn.com

Partners:

Institut National de la Recherche Agronomique (INRA)

Paris, France
Carole Moreno (Carole.Moreno@toulouse.inra.fr)

University of Edinburgh (UEDIN)

Edinburgh, United Kingdom
Stephen Bishop (Stephen.Bishop@roslin.ed.ac.uk)

Parco Tecnologico Padano (PTP)

Lodi, Italy
Alessandra Stella (Alessandra.Stella@tecnoparco.org)

Aristotelio Panepistimio Thessalonikis (AUTH)

Thessaloniki, Greece
Georgios Banos (Banos@vet.auth.gr)

Utah State University (USU)

Utah, United States
Noelle Cockett (Noelle.Cockett@usu.edu)

Agris Sardegna (AGRIS)

Sassari, Italy
Antonello Carta (ACarta@agrisricerca.it)

Universidad de León (ULE)

Leon, Spain
Juan José Arranz (JJArres@unileon.es)

University of Thessaly (UTH)

Volos, Greece
George Fthenakis (GCF@vet.uth.gr)

Teagasc -The Irish Agriculture and Food Development Authority (TEAG)

Carlow, Ireland
Orla Keane (Orla.Keane@teagasc.ie)

Warsaw University of Life Sciences (WULS)

Warszawa, Poland
Elzbieta Martyniuk (Elzbieta_Martyniuk@sggw.pl)

Commonwealth Scientific and Industrial Research Organisation (CSIRO)

Canberra, Australia

Brian Dalrymple (Brian.Dalrymple@csiro.au)

Huazhong Agricultural University (HZAU)

Wuhan, China (People's Republic of)

Shuhong Zhao (ShZhao@mail.hzau.edu.cn)

Instituto Nacional de Tecnología Agropecuaria (INTA)

Buenos Aires, Argentina

Mario Poli (MPoli@inta.gob.ar)

5. 3SR Website Home Page

Register | Login

3SR Sustainable Solutions for Small Ruminants

Home The Project The Partners News Publications Animal Resource Populations Collaborating Projects

Home

Sustainable Solutions for Small Ruminants

"Delivering long term benefits on animal health, welfare and sustainable agriculture for sheep and goats."

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Click here to access the first 3SR Newsletter (July 2011)

News

The second 3SR Newsletter (April 2013) has been produced: click here to download your copy.

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Contact

Coordinator: Huw Jones
Biosciences KTN
www.innovateuk.org/biosciencesktn

Links

CORDIS FP7 Homepage
International Goat Genome Consortium
International Sheep Genomics Consortium

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6. 3SR Outline Poster

The 3SR Project: Sustainable Solutions for Small Ruminants

Overview

3SR is a 3 year, FP7-funded collaborative project which started on the 1st April 2010 and has a total value of over €5 million.

The main focus of the project is to mine genomic information of sheep and goats to deliver a step-change in the understanding of the genetic basis of three traits that have an important influence on sustainable production, health and welfare (see diagram opposite).

Approaches

As part of the project:

- Over 3200 sheep will be genotyped using a 50K SNP chip
- Sequencing will be carried out to improve the quality of the reference sheep genome in regions of interest
- Any genetic markers that are identified will be verified in commercial populations
- Controlled challenge studies will be carried out for mastitis (in sheep and goats) and for the nematode *H. contortus* (sheep) to help improve the understanding of the mechanisms of resistance
- The project will be conducted in close collaboration with the International Sheep and Goat Genome Consortia

Animal Populations

The project will make use of data from:

- over 10,000 sheep from 15 diverse breeds in 10 countries
- over 4,000 goats from 3 breeds in 3 countries

For example:

What will the project aim to deliver?

Selectable and affordable genetic markers that can be used by sheep and goat breeders

Improved genomics tools and resources for further research on sheep and goats

Dissemination of results to ensure widespread benefits for the EU

14 Partners, 11 countries

- Biosciences KTN, UK
- INRA, France
- University of Edinburgh, UK
- Parco Tecnologico Padano, Italy
- Aristotle University of Thessaloniki, Greece
- Utah State University, USA
- AGRISS Sardegna, Italy
- Universidad de Leon, Spain
- University of Thessaly, Greece
- Teagasc, Ireland
- Warsaw University of Life Sciences, Poland
- CSIRO, Australia
- Huazhong Agricultural University, China
- INTA, Argentina

Visit www.3srbreeding.eu for more

3SR: Sustainable Solutions for Small Ruminants is a Collaborative Project supported by funding from the 7th Framework Programme of the European Union.

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7. 3SR Results Poster

Results from the Sustainable Solutions for Small Ruminants (3SR) Project

Kezia Williamson, Huw Jones, Biosciences KTN; The 3SR Consortium. kezia.williamson@biosciencektn.com

Background

To remain sustainable, sheep and goat producers will need to continue to address the challenges of disease and improved efficiency. Genomic tools and technologies are likely to play a crucial role in helping to address these challenges. In 2009 there was still a need to improve the underpinning genomic tools such as a well annotated and complete reference sequence and effective, affordable selectable genetic markers. The 3SR project was therefore funded to help address this and to develop relevant resources.

Project at a glance

- Total value: >€5m (of which €2.99m EC FP7 grant)
- Consortium: 14 partners in 11 countries
- Duration: 3.5 years from May 2010
- Traits of interest: mastitis, nematode resistance, ovulation rate, paratuberculosis

Key results

Identified causative mutations affecting ovulation rate in Grivette (French) and Olkuszka (Polish) sheep, and 2 candidate genes for sterility were identified in Cambridge sheep and continue to be investigated.

Small regions of the genome were identified that have a significant effect on mastitis susceptibility and nematode resistance. Genetic markers for these regions are being validated in commercial populations.

Helped the ISGC deliver sheep reference genome v3.1.

Produced over a terabyte of RNA-seq data that is being used to annotate the sheep genome.

Confirmed genetic variation to paratuberculosis in sheep (heritability 0.28±0.10)

Open access Genome Browser developed <http://genome.ibt.cnr.it/gb2/gbrowse/ovar3.1/>

A whole-genome radiation hybrid (RH) map was produced for goats, containing more than 30,000 markers ordered across the chromosomes.

Led the establishment of the goat AdaptMap project which aims to coordinate and collate the research data across a number of projects (including 3SR)

Activity highlights

Sequencing of over 50 animals has been carried out to help improve the quality of the reference sheep genome (coordinated by the International Sheep Genomics Consortium – ISGC), while large scale RNA sequencing has been performed to help with the sheep genome annotation.

Helped the International Goat Genome Consortium (IGGC) to develop a high density (50K) SNP chip for goats.

Genotyped over 4000 sheep and 2000 goats using the respective 50K SNP chips.

Over 7000 50K genotypes analysed from 11 sheep populations and over 2000 50K genotypes analysed for goats.

Controlled challenge studies were carried out for mastitis (in sheep and goats) and nematodes (sheep) to explore the mechanisms of resistance.

Functional studies of genes involved in ovulation rate in several sheep breeds were carried out to support the biological understanding of the mutations discovered.

A global consortium

Visit www.3srbreeding.eu for further information

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8. 3SR Newsletter Front Page (Issue 1)

3SR Newsletter

Sustainable Solutions for Small Ruminants Issue 1 - July 2011

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Coordinator's Introduction

Welcome to the first edition of the 3SR newsletter which is aimed at keeping you up to date with project progress and news from the 3SR project, which is focused on developing genomic tools that will help selection to improve the sustainability, health and welfare of small ruminants. In this issue we introduce the project, the website and partners. We also provide information on two key strengths of the project, the wide range of sheep and goat populations that are being used, and the international collaborations that are helping to add value and increase the amount of progress that can be made during its three year duration.

It's now just over a year since the project started and the main focus to date has been on data collection. However, as you will see later, the international collaborations have already played an important role, allowing us to change the project strategy to increase the potential value from the project. You will also see that it has been a busy year for the International Sheep Genome Consortium (ISGC), to whom we have strong links, and we are in the process of reviewing our planned sequencing strategy to take account of the changes that have occurred. All in all it's an exciting time to be working in the area of sheep and goat genetics!

Huw Jones - 3SR Coordinator 

3SR Website and Intranet



The 3SR website (www.3srbreeding.eu) has been developed and launched as a key route for presenting information about the 3SR project to the general public and to those individuals and organisations who are interested in the topics covered by the project. A profile for each project partner including links to their website is also available on the website.

In addition to the publicly available web pages, a password protected area for 3SR consortium members only can be accessed through the 3SR website. The 3SR Intranet includes the Standard Operating Procedures, reports etc as well as a forum for partners to discuss issues relating to the project.

The website will be regularly updated with news and results from the project.

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www.3srbreeding.eu