



Comité de pilotage GRIPAVI

Bilan année 1, perspective année 2

Virology Section, UMR-15 CIRAD/INRA



- Virologie : Détection, isolement et caractérisation moléculaire des souches du virus de la grippe aviaire et de la maladie de Newcastle à partir de prélèvements faits sur terrain.

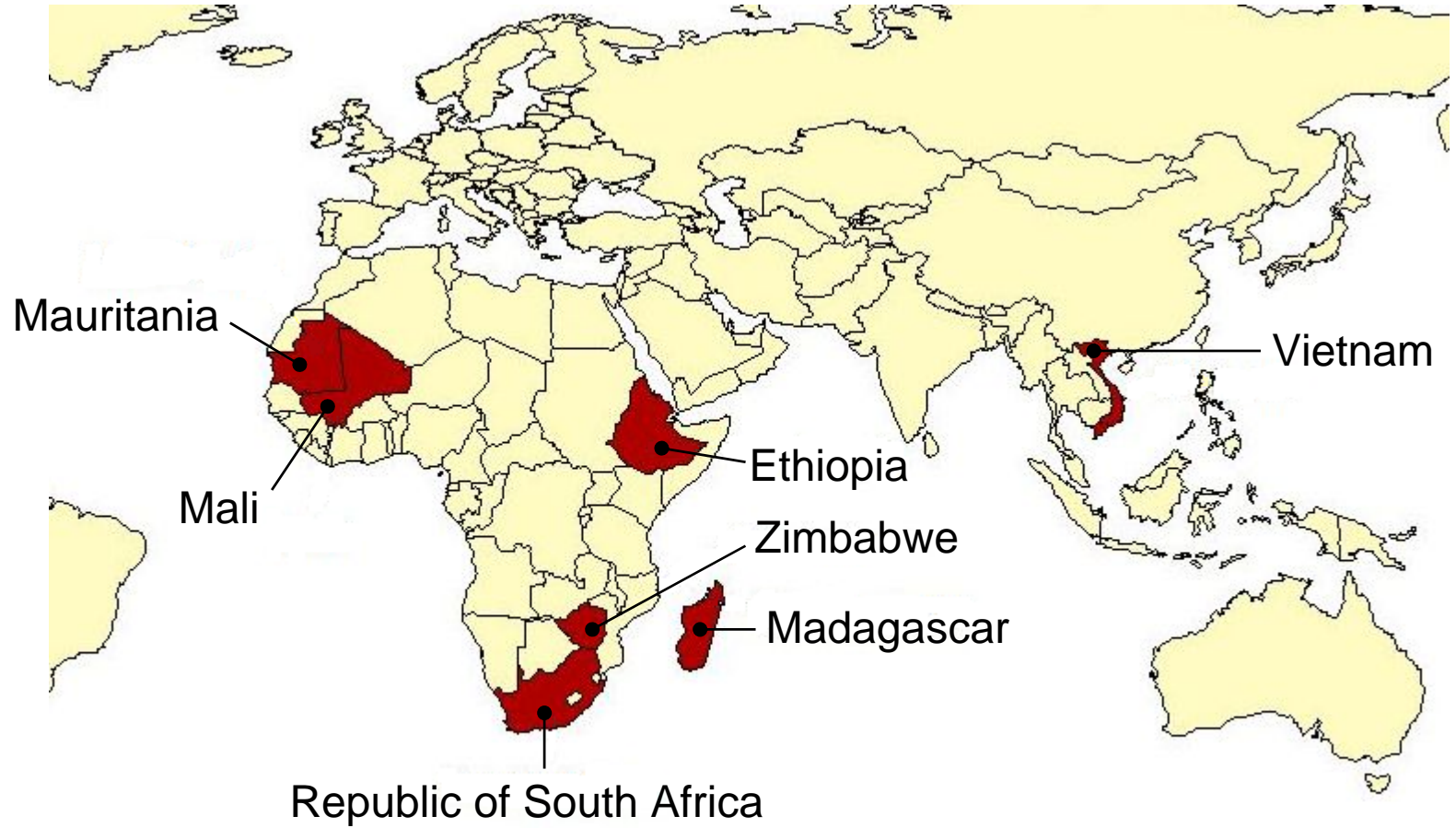
- → 2880 prélèvements testés
- → 4 isolats NDV

Retards prélèvements dans certains pays/ retard analyses dans certains pays/ état des capacités d'analyses RT-PCR par pays effectué sur « Mesures d'urgence »



FSP GRIPAVI

- 7 countries included



- UMR-15: virological testing for 4 partners

High throughput detection and characterization of ortho and paramyxoviruses



Swab in liquid nitrogen

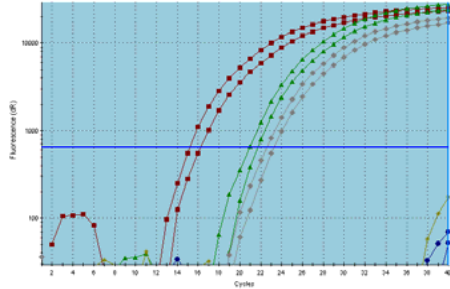
-80°C

96-wells microplate



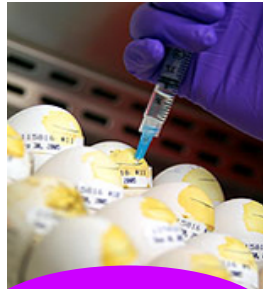
Extraction
150 µl RNA, 88 samples in 50 min

Real-time RT-PCR:
AIV M gene
NDV: F gene
~4h

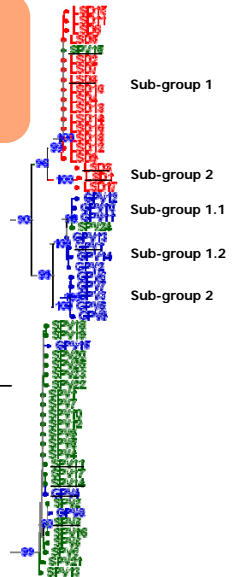


AIV/NDV⊕

Isolation
7-25 days



Sequencing & Phylogeny
~5d



Real-time RT-PCR:
AIV H5, H7, N1
~2h

Pathotyping:
sequencing of cleavage site
~5d



Overall results

	Mali 2007	Mali 2008	Mauritania 2008	Madagascar 2008	Total
Domestic birds tested	223	315	28	547	Birds 223 in 2007 1622 in 2008
Wild birds tested	0	362	370	0	
% of birds AIV+ (% H5 & H7 positive)	3.13% (0)	0% domestic 0.28% wild	0% domestic 0.27% (0) wild	0.55%	0 – 3.13% 0.27%
Number of AIV isolates	0	0	0	0	0
% of wild birds NDV + (pathotype)	1.3% (all velogenic)	0.95% domestic (all velogenic) 3.31% wild	0% domestic 6.8% wild (9 velogenic, 4 lentogenic)	5.3% (7 velogenic, 5 lentogenic)	0 – 5.3% 3 – 7%
Number of NDV isolates	3	3	0	1	7



MALI

Sequencing of Malian isolates:

- 2007: fragment of 670 nt (end of M, beginning of F)
 - ML029 & ML031 are 100% identical
 - ML038 has 87.5% homology with the two others
- 2008: fragment of 670 pb
 - ML225 & 230 are 100% identical
 - ML007 has 91.7% homology with the two others

Isolate	Cleavage site motif	Pathotype
ML029	G/RRRKR/FV	V
ML031	G/RRRKR/FV	V
ML038	G/RRQKR/FI	V
ML1/1/225	G/RRQKR/FI	V
ML/1/230	G/RRQKR/FI	V
ML/2/007	G/RRQKR/FI	V



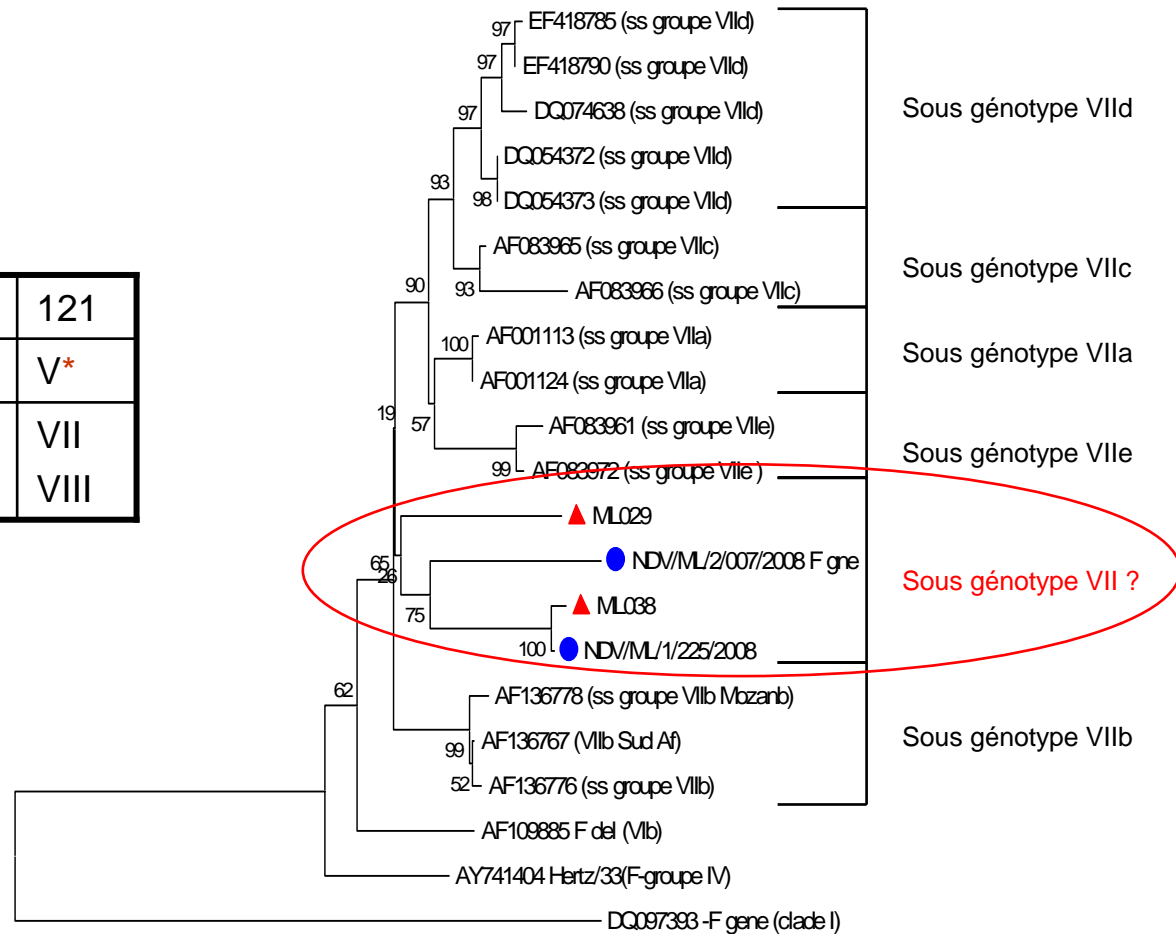
Phylogenetic analysis within sub-genotype VII

MALI

Seq ML029

10	16	23	101	114	118	121
L	V	S	K	R	V	V*
VIII	VIII	VIIa	VII a-e	VIIe VIII	V VI f	VII VIII

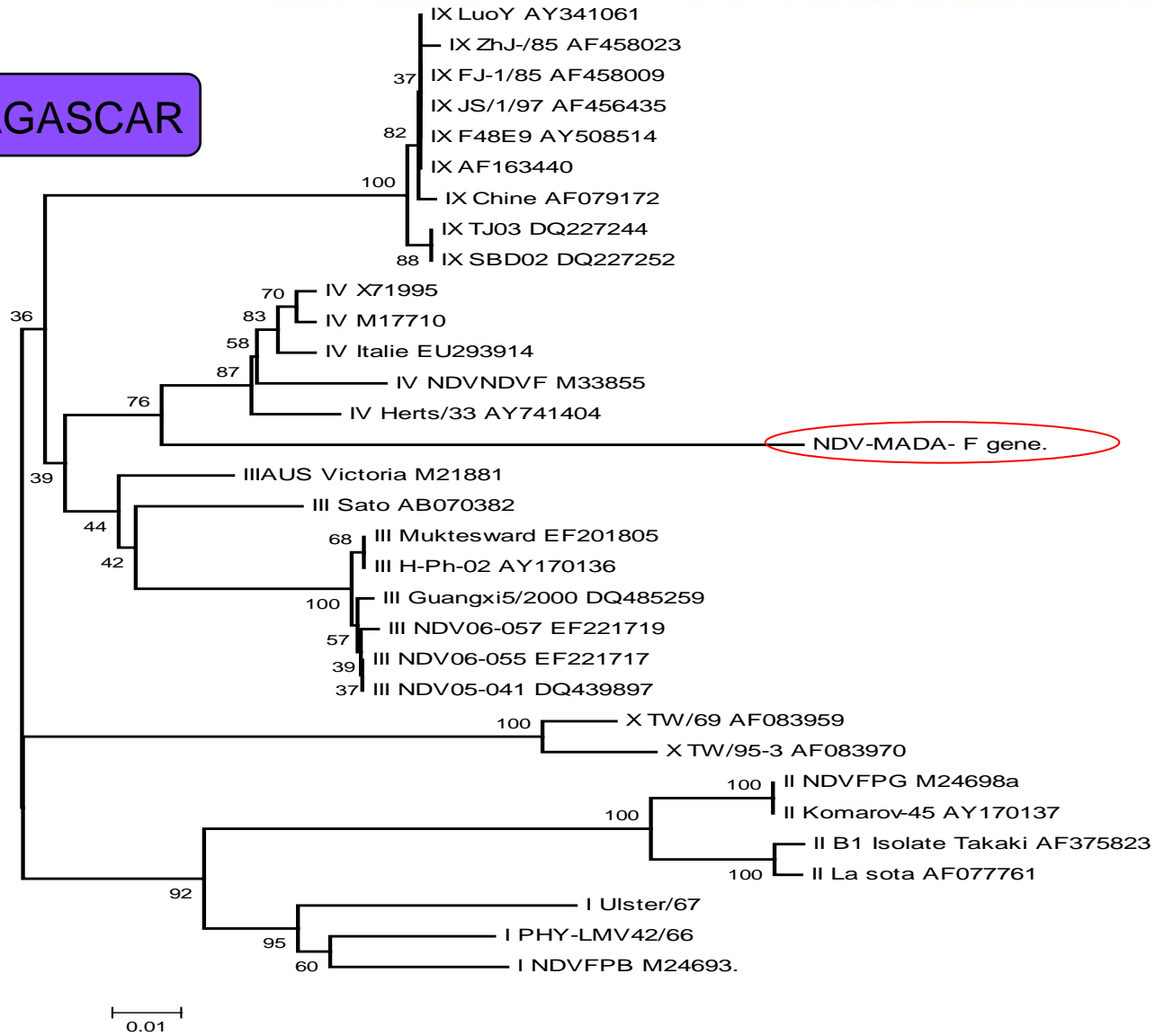
* V121 = feature of genotypes VII and VIII



0.05



MADAGASCAR



Phylogenetic tree based on nt sequence of F gene (partial = 374 nt)



Conclusions

- Low level of AIV detection, higher level for NDV
- Almost similar detection in tracheal and cloacal swabs, no bird with both swabs positive
- **Mali:**
 - Isolates close to genotype VII and sub-genotype b
 - New sub-genotype?
- **Madagascar:**
 - Original motif of cleavage site RRRRR*FVG
 - Isolates close to the old genotypes III and IV appeared more than 50 years ago during first panzootics
 - New genotype or sub-genotype?



Autre activités

- Recrutement allocataire en virologie: non fait
- Essai interlaboratoire PCR: participants NIVR, LCV, NAHDIC
- Inventaire capacités diagnostiques NIVR (juillet 2008)
- Sessions de formation sur sites (Mesures d'urgence) : LCV et NAHDIC (juin 2008)



- **Perspectives year 2:**

- More sequencing for better genetic characterization of NDV isolates
- Assessment of in vivo pathogenicity for some NDV isolates
- Acquisition of more isolates from the African:
 - 3700 PCR AI et NDV
 - 30 isolements et séquençage
 - PCR Inventaire Lac Alaotra (Madagascar)
- PhD or post doc in Virology