

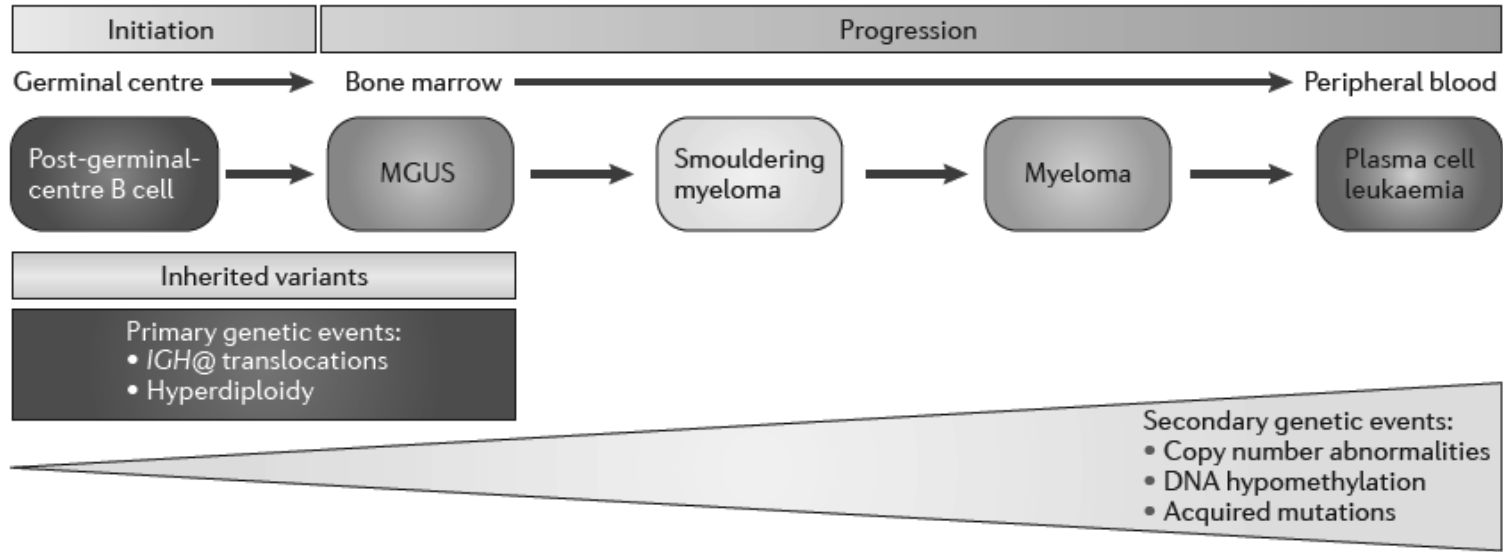


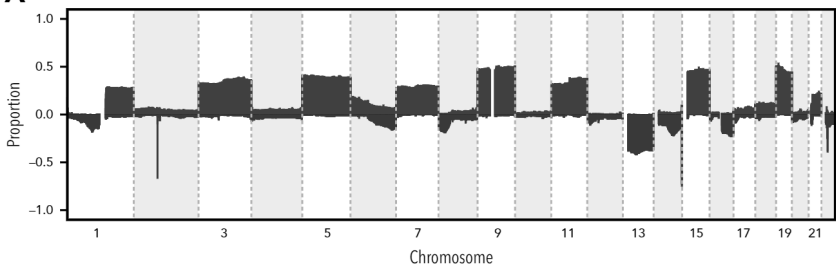
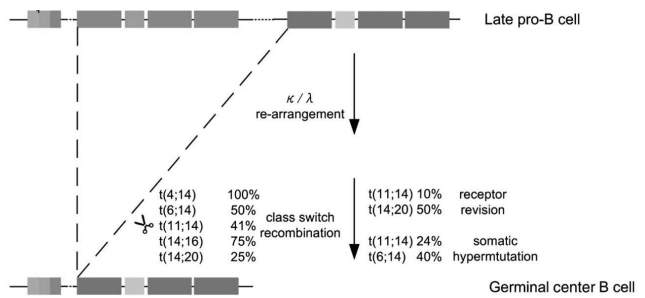
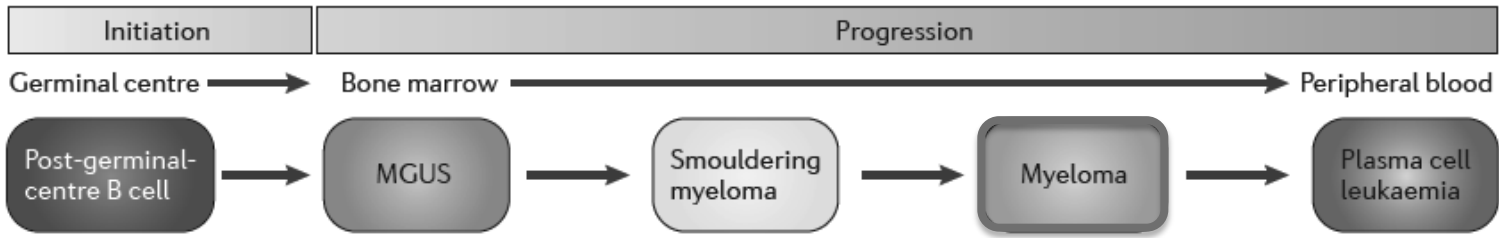
Genomic Evolution – germinal B cell to MGUS/SMM/MM

Dr Brian Walker

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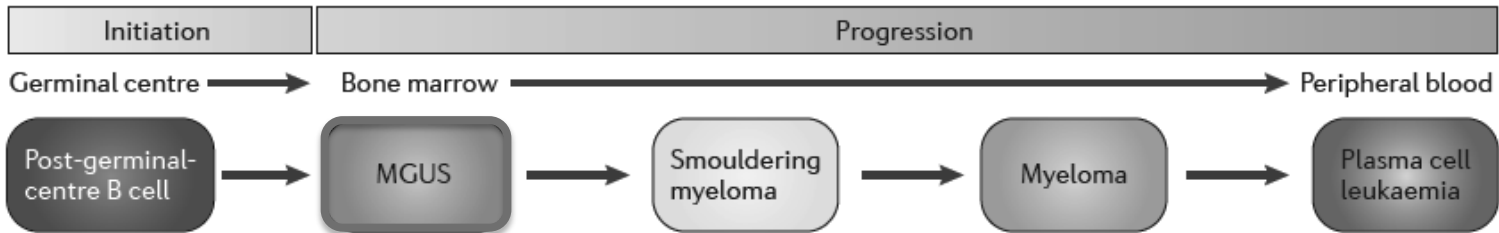
September 8<sup>th</sup> 2021 IMW18





Morgan, Walker & Davies *Nat Rev Cancer* 2012 12:335

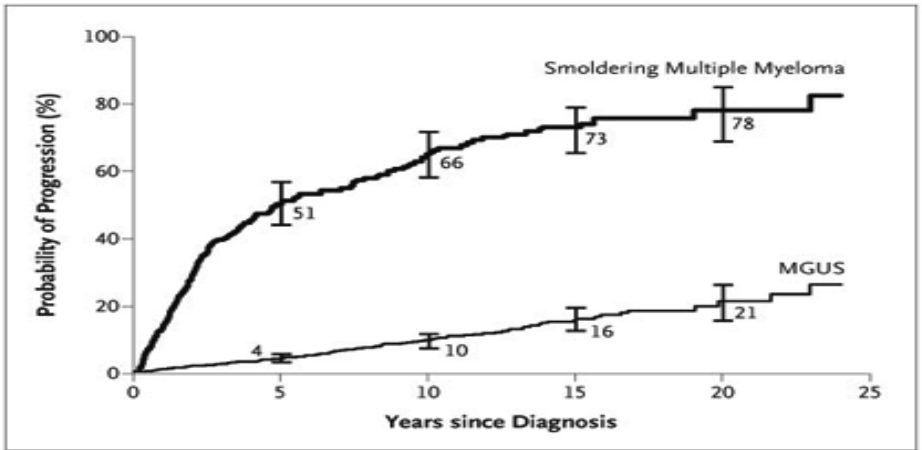




When does MGUS start?

Examine mutation rates

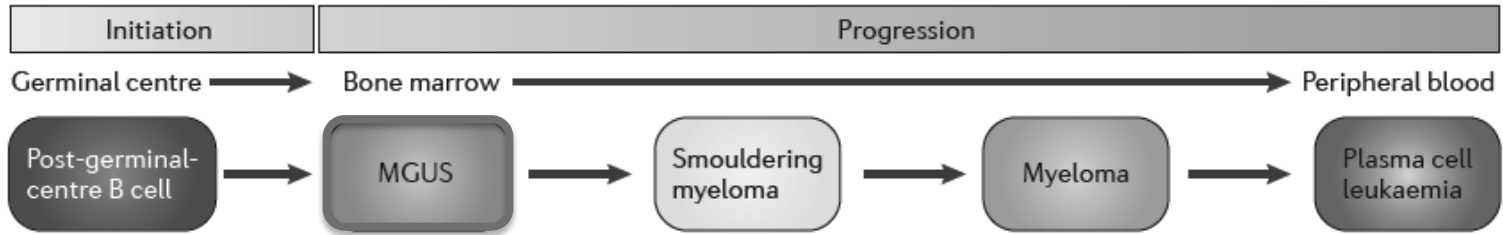
Clock-like mutations correlate with age  
 Myeloma initiation at 20-30 years of age



Rustad et al. *Nat Commun* 2020

Kyle et al. *NEJM* 2007





*IGH* translocations are present

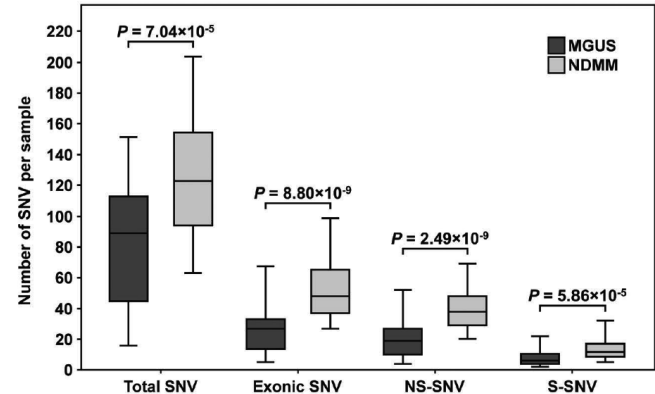
97% of patients have mutations

Mutations happen first, followed by CNAs

Common mutations can be present  
*KRAS*, *NRAS*, *DIS3*, etc.

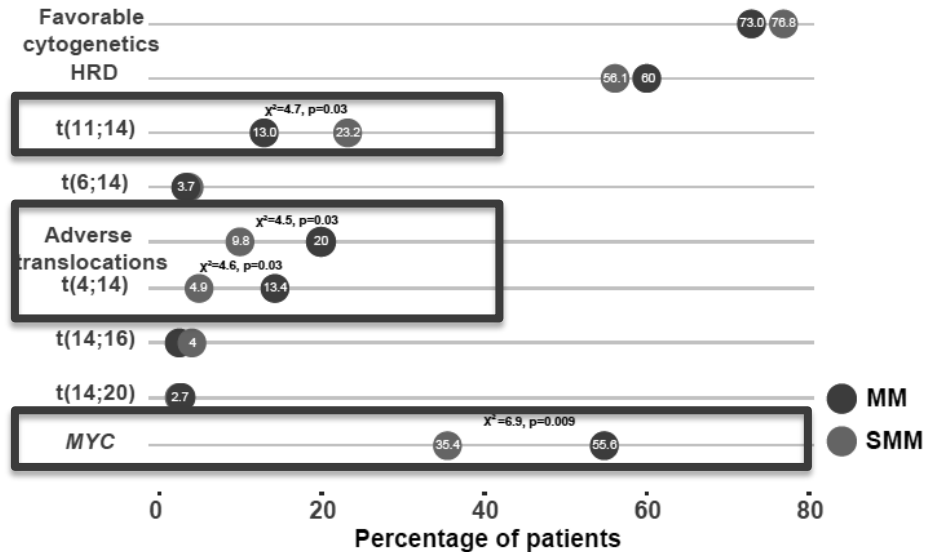
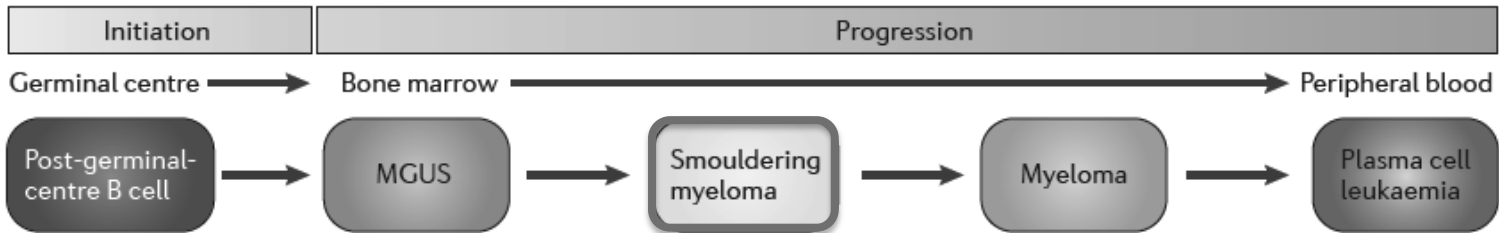
No biallelic deletions in TSGs.  
*CDKN2C*, *TP53*, *CYLD*, *BIRC2/3*

No *TP53* mutations or *MYC* abnormalities



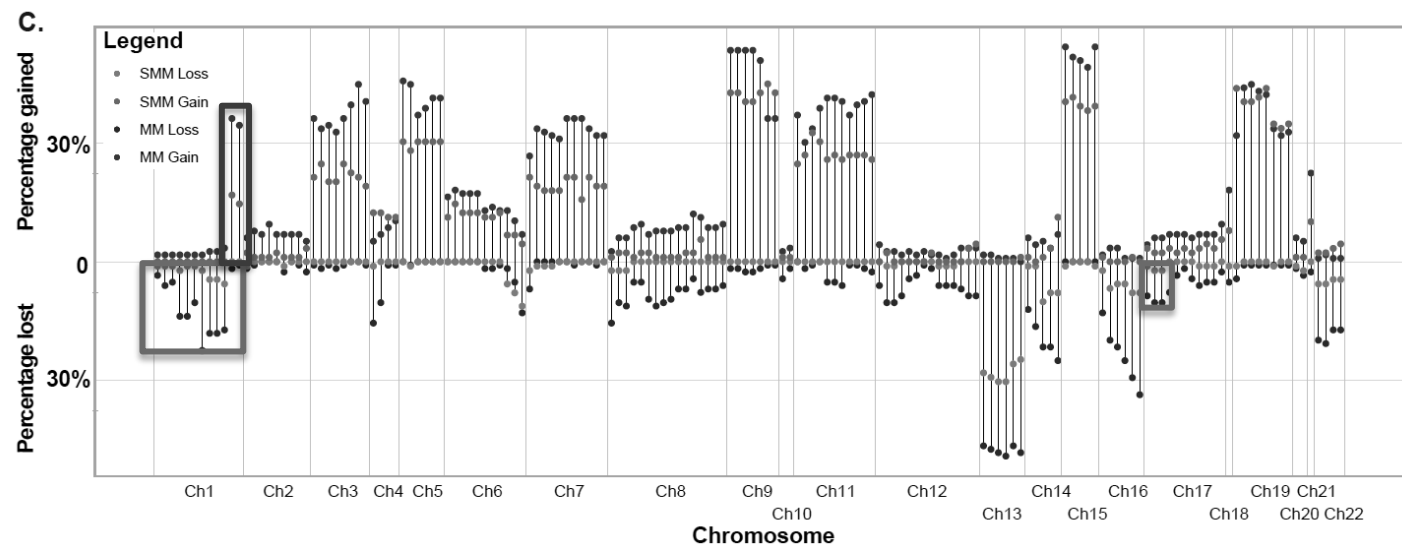
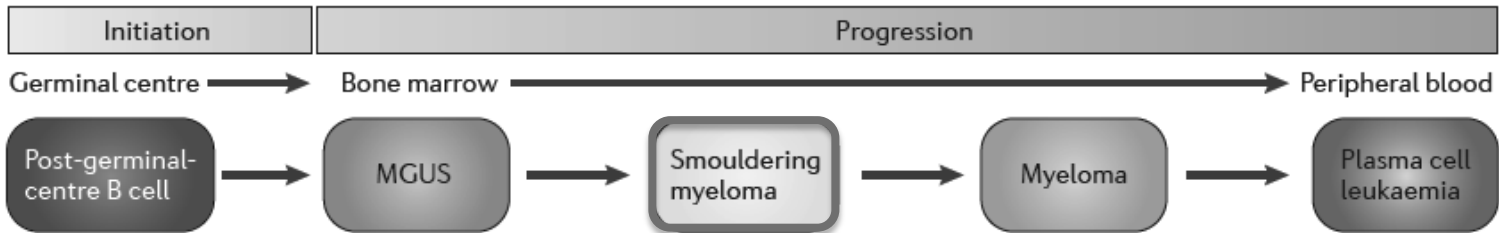
Mikulasova et al. *Haematologica* 2017





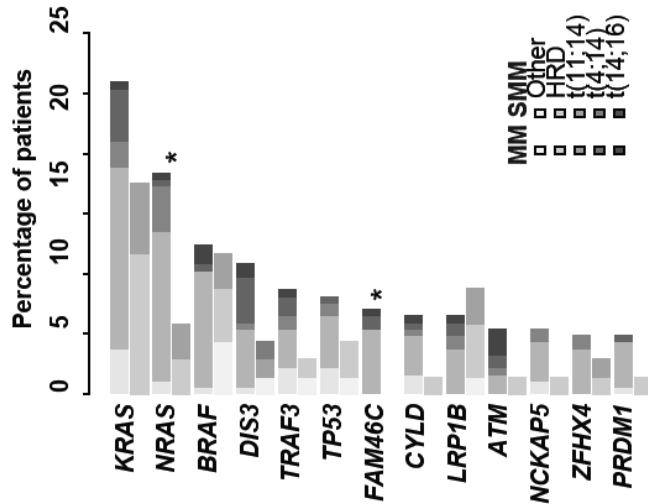
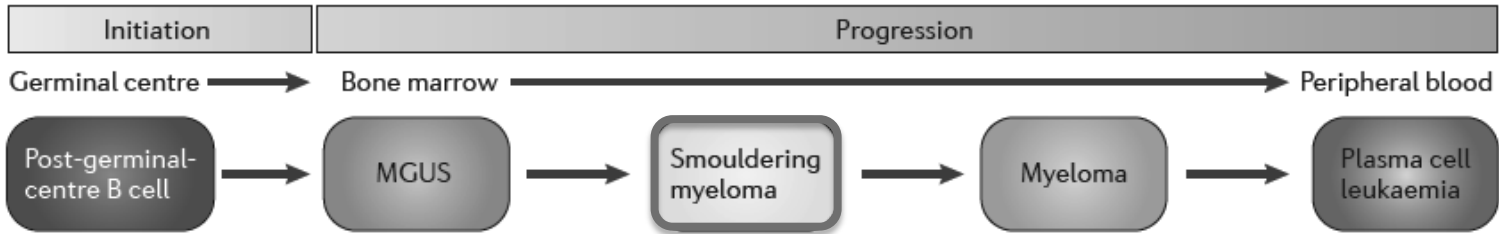
Boyle, Walker et al. Nature Commun. 2021





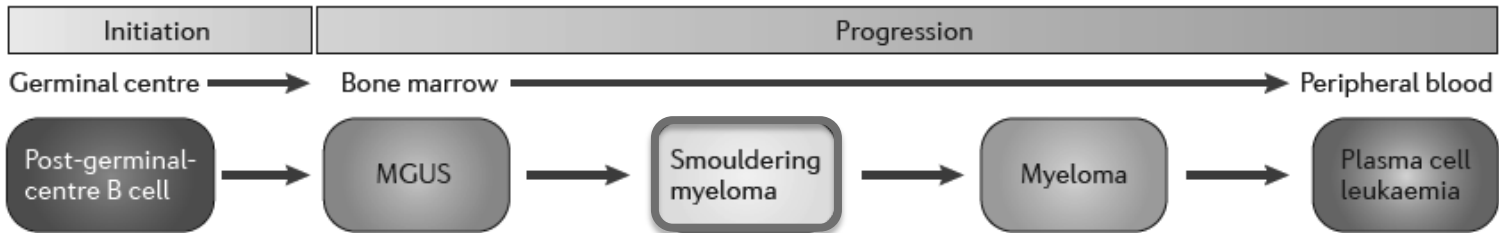
Boyle, Walker et al. Nature Commun. 2021



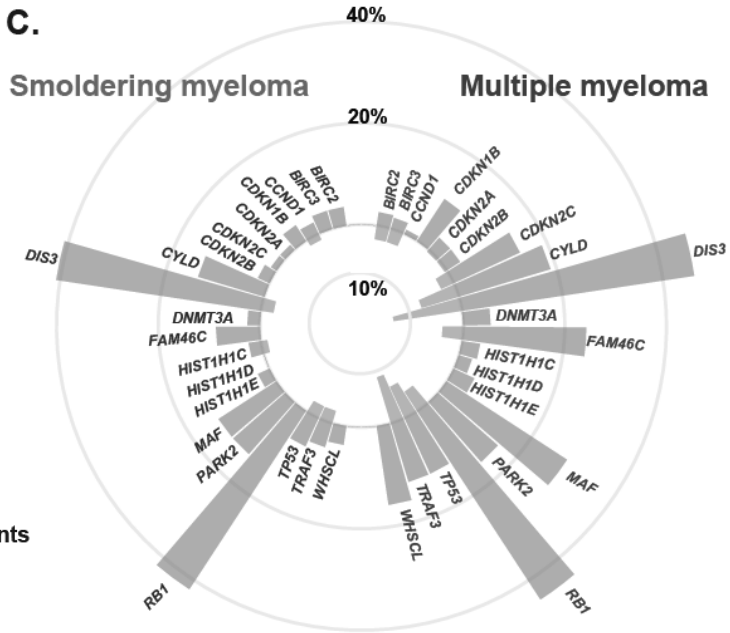


- *NRAS* and *FAM46C* mutations detected at significantly lower frequencies in SMM
- Mutations in *FAM46C* completely absent in SMM





C.

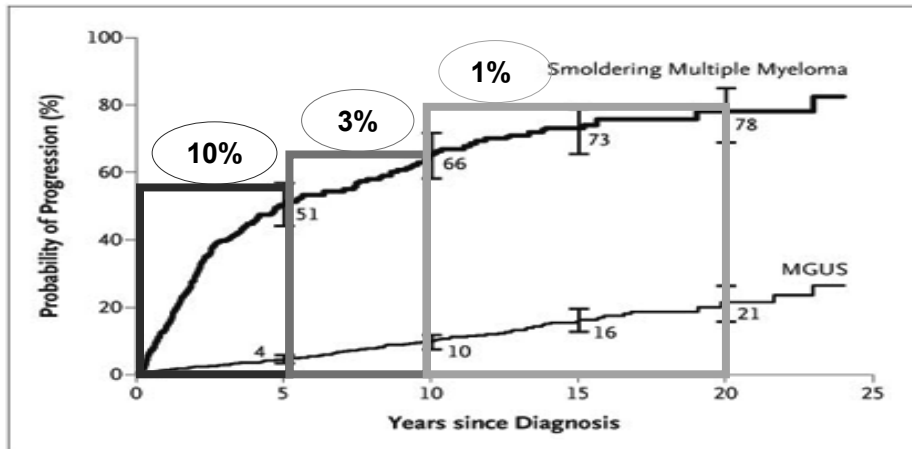
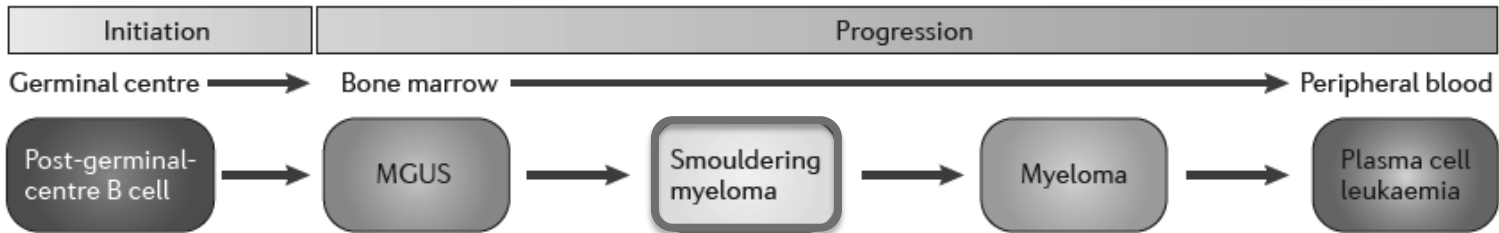


- Total of 103 (64/223 pts) biallelic events identified in MM, compared to 8 (8/82 pts) in SMM,  $\chi^2=10.9$ ,  $p=0.001$
- 1.2% SMM patients with Biallelic *TP53*, compared to 8.1% in MM
- 2% SMM with Biallelic *DIS3*, compared to 5% in MM
- Biallelic inactivation may be a hallmark mechanism in the transition to MM

■ Biallelic events  
■ Monoallelic events

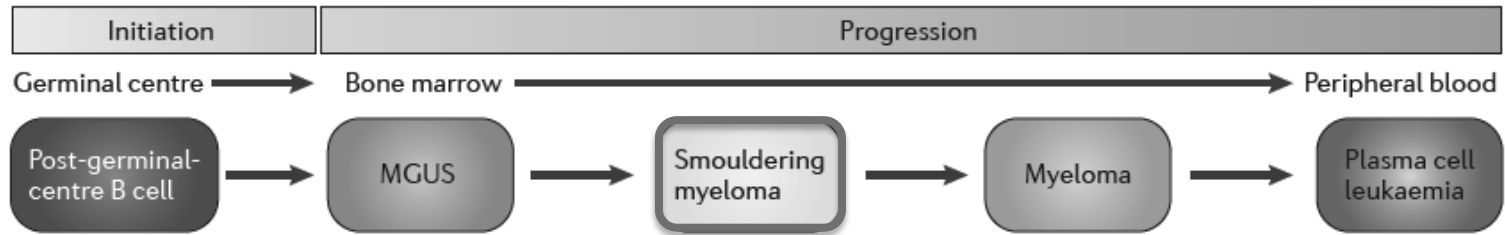
Boyle, Walker et al. Nature Commun. 2021





Are there any genomic risk factors predicting progression to active disease?

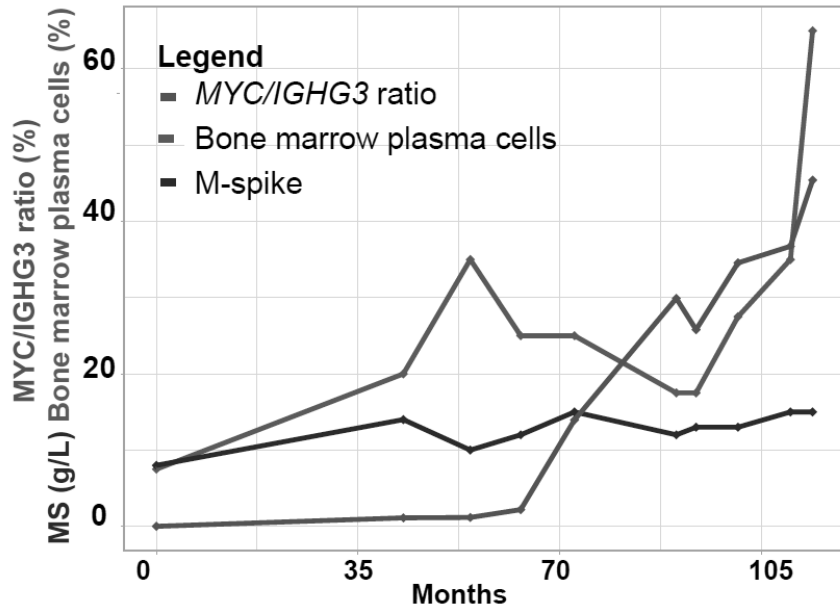
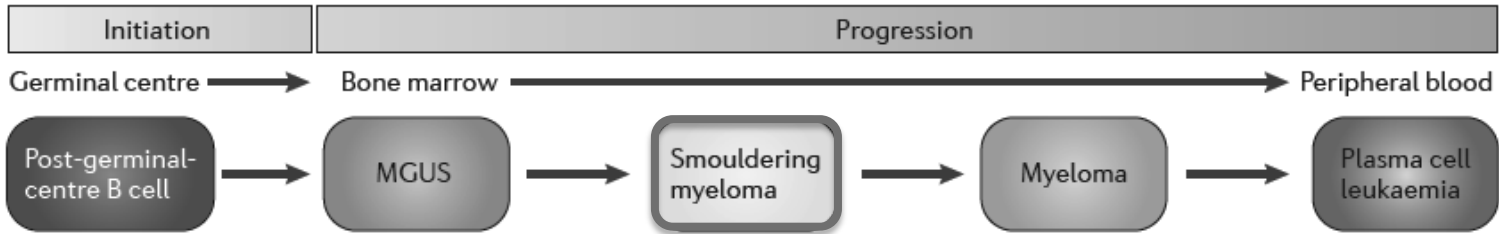




### Markers associated with a short time to progression to MM

	Mutations	CNAs	MYC	IMWG
Boyle et al.	<i>KRAS</i>	del6q		+
Bustoros et al.	<i>KRAS/NRAS</i> <i>TP53/ATM/ATM</i>	Biallelic deletion	+	+
Misund et al	<i>DIS3</i>		+	

N.B. 1q+, del(1p), del(13q), etc. not associated with TTP



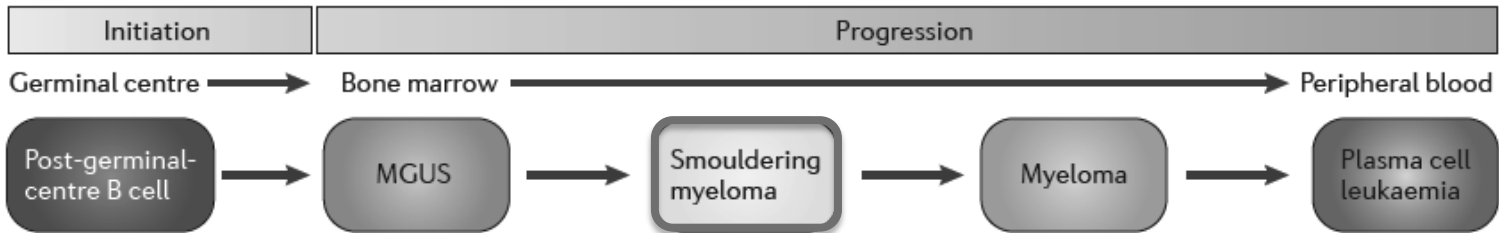
Detected at t(MYC) in one patient, >70 months after SMM diagnosis

Used digital PCR to determine the evolution of the t(MYC), compared to the V(D)J rearrangement

t(MYC) was undetectable at SMM diagnosis and appeared in a subclone (1%) 3 years later, has increased steadily over time and reached 45% of the tumor cells 8.2 years from diagnosis

Increase in t(MYC) clone coincided with an increase in bone marrow plasma cells

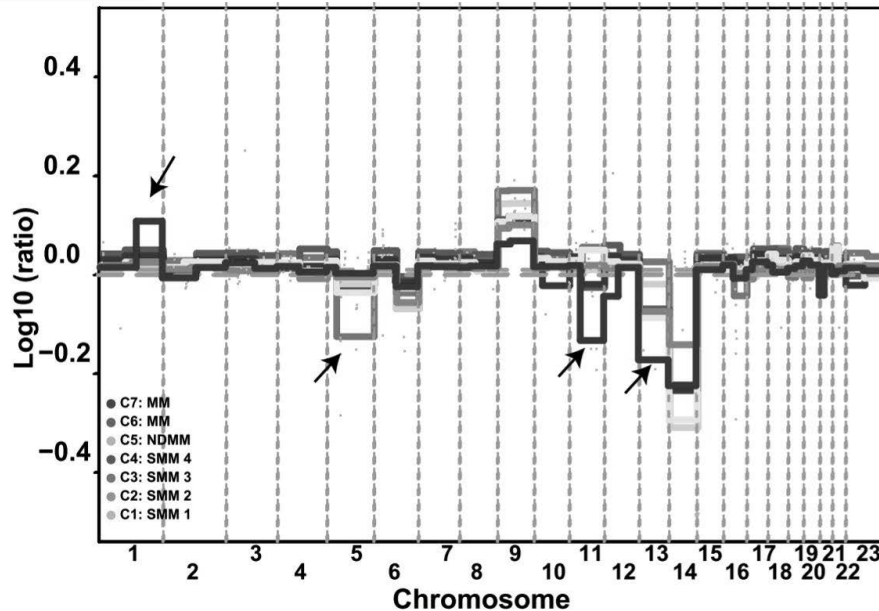




Serial analysis of samples from patients progressing from SMM to MM

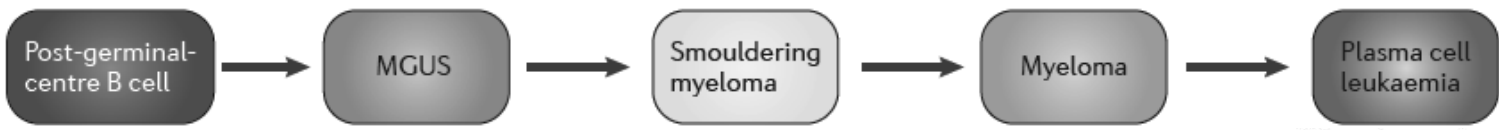
Clonal dominance over time shows changes in copy number

SMM patients are not static and require regular monitoring for high-risk genomic markers.



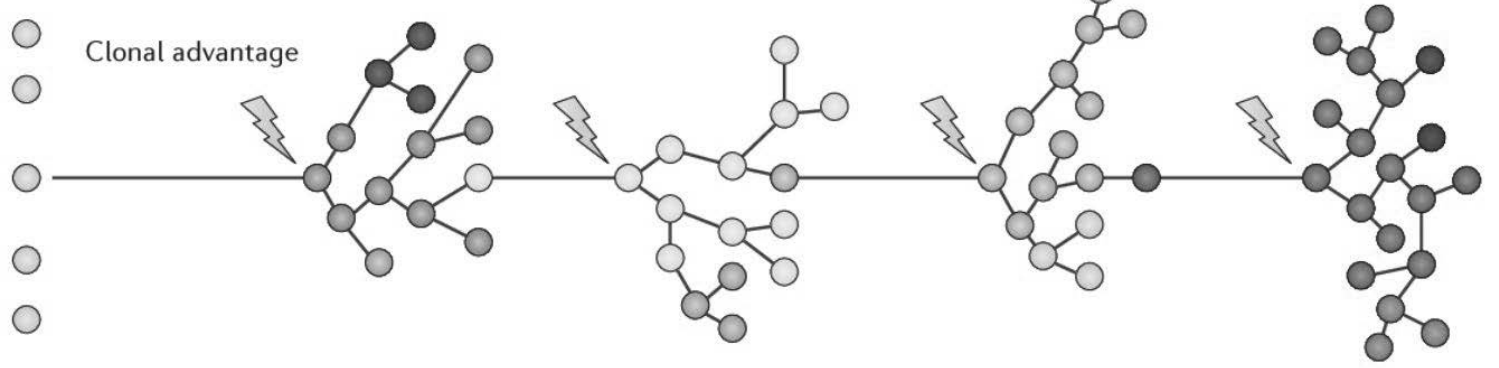
Boyle, Walker et al. Leukemia. 2021





Competition selection for bone marrow niche

Migration and founder effect





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Parvathi Sudha  
Enze Liu  
Nathan Becker

Rafat Abonour  
Mohammad Abu Zaid  
Fabiana Perna  
David Roodman  
Attaya Suvannasankha  
Melissa Stanley



Aneta Mikulasova  
Eileen Boyle

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